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S67307 Ca(2+)-sens
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175054 Human man
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Norway rat.
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
1 (bases 1 to 2520)
                                                                             Rattus norvegicus putative taste receptor TR1 mRNA, partial cds. AF127389 GI:4337085
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AR012623 Sequence
AR028466 Sequence
175052 Sequence 2
U20760 Human extra
G28586 human STS
AF110178 Mus muscu
AR012625 Sequence
175054 Sequence
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175058 Partus norv
AF110179 Mus muscu
A73577 Sequence
1 S81755 Calcium rec
18810876 Fugu rubr
AB008857 Fugu rubr
AB008857 Fugu rubr
AB008859 Fugu rubr
AB008859 Fugu rubr
AF083084 Carassius
AF158763 Carassius
AF15877 Fugu rubr
AF0008857 Fugu rubr

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Mammalia; Rattus.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (10-FEB-1999) Taste and Smell Unit, Drive MSC 1188, Bethesda, MD 20892-1188, USA
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Hoon, M.A., Adler, E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Putative mammalian taste receptors: a with distinct topographic selectivity cell 96 (4), 541-551 (1999) 99159821

2 (bases 1 to 2520)
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                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MLFWAAHLLISLQLVYCWAFSCQRTESSPGFSLPGDFLLAGLFS
LHGDCLQVRHRPLVTSCDRPDSFNGHGYHLFQAMRTTVEEINNSSALLPNITLGYELY
DVCSESANVYATLRVLALGGPRHIEIQKDLRNHSSKVVAFIGPENNSSALLPNITLGYELY
DVCSESANVYATLRVLALGGPRHIEIQKDLRNHSSKVVAFIGPDNTDHAVTTAALLGP
FLMPLYSYEASSVVLSAKRKPPSFLRTVPSDRHGVEVMVQLLQSFGWWATSLIGSYGD
YGQLGVQALEELAVPRGICVAFKDIVFFSARVGDPRMQSMMQHLAQARTTVVVVFSNR
HLARVFFRSVVLANLTGKVWASEDAATSTY ITSVTGIGGIGTVLGVRVQQCQVFGCK
EFESSYVRANTAAPSACPEGSRGSTNQLCRECHTFTRRNMFTLGAFSMSAAYRTVEAV
YAVAHGLHQLLGCTSEICSRGPVYPWQLLQQIVKVNFLLHENTVAFDDNGDTLGYYDI
IAWDWNGPEWTFEIIGSASLSPVHLDINKTKIQMHGKNNQVPVSVCTTDCLAGHHRVV
VGSHHCCFECVPCEAGTFLNMSELHICDPCGTEEMAPKESTTCFPRTVEFLAWHEPIS
LVLIAANTLLLLLLVGTNGLFAMHFHTPVVRSAGGRLCFUMLGSLYAGSCSFYSFGE
PTVPACLLRQPLFSIGFAIFLSCLTIRSFQLVIIFKFSTKVPTFYRTWAQNHGAGLFV
IVSSTVHLLICLTWLVMWTPRFTREYQREPLLVIIEKTENNSVGFLLAFTHNILLSIS
TFVCSYLKELPENXNBAKCVTFSLLNHEVSWTLAFTTMASIYGGSYLPAVNVLAGLTT
LSGGFSGYFLPKCYVILCRPELNNTEHFQASIQDYTRRCGTT"

1 SGGFSGYFLPKCYVILCRPELNNTEHFQASIQDYTRRCGTT"

1 SGGFSGYFLPKCYVILCRPELNNTEHFQASIQDYTRRCGTT"
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/protein_id="AAD18069.1"
/db_xref="GI:4337086"
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Rattus norvegicus |
AF127390 AF127390.1 GI:433
    Putative
                          Hoon,M.A., Adler,E., Lindemeier,J.,
Zuker,C.S.
                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
1 (bases 1 to 2529)
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LSVLGFSFAYMGKELPTNYNAEAFFITSMTFSFTSSISICTFMSVHDGVLVTIMDLL
LSVLGFSFAYMGKELPTNYNAEAFFITSAYFNSMIQGYTMRKS"
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VERSION KEYWORDS ACCESSION

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AUTHORS

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DEFINITION ACCESSION VERSION KEYWORDS RESULT G09859/c SOURCE ORGANISM

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REFERENCE AUTHORS TITLE Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Cl Tetrapoda; Amniotae; Mammalia; Theria; Eutheria; Archonta; Catarrhini; Hominidae; Homo.

1 (bases 1 to 270)

Murray,J., Sheffield,V, Weber,J.L., Duyk,G. and Buetow,K.l Cooperative Human Linkage Center Unpublished (1995) G09859 270 bp DNA
human STS CHLC.GCT15G02.P16729 clone GCT15G02.
G09859
G09859.1 GI:941708
STS sequence; primer; sequence tagged site.
human vector-pJCP1 host-E.coli dut+ung+ (DH10B)
genomic DNA prepared from XY individual of Frence Homo sapiens Marker Selected ch nationality. 15-AUG-1995 Choanata;

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Primer B: TGGTGTTTTTGGCTTTGC
STS size: 124
PCR Profile:
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                                   Human Kruppel-related 3
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               cctaagtgctacgtgatcctctgccgcccagacctcaacagcacagagcacttccaggcc
                                                   CCTAAGTGCTACGTGATCCTCTGCCGCCCAGACCTCAACAGCACAGAGCACTTCCAGGCC
TCCATTCAGGACTACACGAGGCGCTGCGGCTCCACCTGA 218
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Maris,J.M., Jensen,S.J.,
Allen,C., Biegel,J.A., Br
Direct Submission
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1 (bases 1 to 3106)

Maris, J.M., Jensen, S.J., Sulman, E.P., Beltinger, C.P., Allen, C., Biegel, J.A., Brodeur, G.M. and White, P.S. Cloning, chromosomal localization, physical mapping, Characterization of HXR3 Genomics 35 (2), 289-298 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (09-JAN-1996) John M. Maris, Children's Hospital of Philadelphia, Al Street, Philadelphia, PA 19104-4318, U Location/Qualifiers
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/gene="HKR3"
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/clone="P1-4184,
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/db_xref="taxon:9606"
/chromosome="1"
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Bos taurus
Eukaryota; Metazoa;
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Location/Qualifiers
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Ca(2+)-sensing receptor
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/db_xref="taxon:9913"
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Sequence
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Nemeth, E.F., Brown, E.M., Hebert, S.C., Garret
Wagenen, B.C., Balandrin, M.F. and Del Mar, E.G
Method of screening calcium receptor active
Patent: US 5858684-A 1 12-JAN-1999;
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Pred. No. 1.5e-21;
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                              AACTGCAGTCGAGACTGCCTGGCAGGGACCAGGAAAGGAATCATTGAGGGGGGAGCCCACC
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Unclassified.
1 (bases 1 to 5275)
Brown, E.M., Fuller, F.H., Hebert, S.C.
Calcium receptor-active molecules
Patent: US 5688938-A 118-NOV-1997;
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Sequence 1 from patent
175051
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Pred. No. 1.5e-21;
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AR012624 Sequence AR012624 AR012624.

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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

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ATCCTCTTCAAGCCTTCCCGGAACACCATCGAGGAGGTGC
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                            ACCTGCCTGCTGCCATCTGCTTCTTTGCCTTCAAGTCCCGGAAGCTGCCGGAG
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1 (bases 1 to 3809)
Brown,E.M., Hebert,S.C. and Garrett Calcium receptor active molecules
Patent: US 5763569-A 3 09-JUN-1998;
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Pred. No. 1.7e-20;
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                cotgtggtgaggtcagcaggggccgcctgtgctttcttatgctgggctccctggcagca
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Sequence
AR028467
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Nemeth, E.F., Brown, E.M., Hebert, S.C., Garrett, J.E.
Wagenen, B.C., Balandrin, M.F. and Del Mar, E.G.
Method of screening calcium receptor-active molecul
Patent: US 5858684-A 3 12-JAN-1999;
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Pred. No. 1.7e-20;
0; Mismatches 556;
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Brown, E.M., Fuller, F.H., Hebert, S.C.
Calcium receptor-active molecules
Patent: US 5688938-A 3 18-NOV-1997;
Location/Qualifiers
                                                                                                                                                                                                    Unclassified
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H. sapiens | X81086 X81086.1 G:

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ECPDGEYSDETDASACNKCPDDDWSNENHTSCIAKEIEFLSWTEPGIALTLFAVLGI
FLIAFVLGVFIKFRNIP IVKATNRELSYLLLFSLLCCESSSLFIGEPDDWTCRLRQP
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GLQGPVGDQQPRAVEDPELSPALVVSSSQSFVISGGGSTVTENVVNS"
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YIPQVSYASSSRLLSNKNQFKSFLRTIPNDEHQATAMADIIEYFRWNWVGTIAADDDY
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

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Molecular cloning of a
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KKVHPRKSVHNGFAKEFWEETFKOLLOGGAKGPLPVDTFLGGIEEGGDRESNSSTAFR
PLCTGJENISSVETPYLDYTHLRISTNYLAVFSIAHALODIYTCLGGRELFINGSCA
DIKKVEAMQVLKHLRHLNFTNNNGEQVTFDECGDLVGNYSIINMHLSPEDGSIVFKEV
GYYNVYAKKGERLFINEEKILMSGFSREVPFSNCSRDCLAGTEKGI LEGEPTCGFECV
ECPDGEYSDETDASACNKCPDDFWSNENHTSGLIAKEIFFLSWTEPFGIATLFAVLGF
FLTAFVLGVFIKRRNTPIYKATNRELSYLLLFSLLCCFSSSLFFIGEDDWTCRLRQF
AFGISFYLCISGLIVKUNRVLLVFEAKIFSTHKKWMGLNLOFLVFLCTFANGIVICV
IMLYTAPPSSYRNQELEDEIIFITCHEGSLAGFFIKSTTCLLAAIGFFFAKSTLLF
ENFNEAKFITESMLIFTIVMISFIPAYASTYGKEVSAVEVIAILAASGFCLLACIFFIK
TYILLFKPSRNYTEEVRCSTAHAFKYAARAILRRSNYSRKRSSSLGGSTGSTPSSSI
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VTFSLSFDEPQKNAMAHRNSTHQNSLEAQKSSDTLTRHQPLLPLQCGETDLDLTVQET
GLQGPVGGDQRPEVEDPEELSPALVVSSSQSFVISGGGSTVTENVVNS"
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/protein_id="BAA09453.1"
/db_xref="GI:904210"
/translation="MARYSCCWVLLALTWHTSAYGPDQRAQKKGDIILGGLFPIHFGV
AAKDQDLKSRPESVECIRYNFRGFRWLQAMIFAIEEINSSPALLPNLTLGYRIFDTCN
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YIPQVSYASSSRLLSNKNQFKSFLRTIPNDEHQATAMADIIEYFRWNWVGTIAADDDY
GRPGIEKFREEAEERDICIDFSELISQYSDEEEIQHVVEVIQNSTAKVIVVFSSGPDL
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                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 3783)
Garrett, J.E., Capuano, I.V., Hammerland, L.G., Hung, B. Hebert, S.C., Nemeth, E.F. and Fuller, F. Molecular cloning and functional expression of human molecular cloning and functional expression of human
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Submitted (07-FEB-1995) James E. Garrett, Molecular Biology, NPS
Pharmaceuticals, Inc., 420 Chipeta Way, Salt Lake City, UT 84108
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YIPOVSYASSSRLISNKNOFKSEIRTIPUDEHQATAMADIIEYERMINWOTIAADDDY
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KKVHRRKSVHNGFAKEEWEEFINCHLQBEAKGPLPVDDTFLIGHEESGDRESNSSTAF
PLCTGDENISSVETPYIDYTHLRISYNVYLAVYSIAHALQDIYTCLPGREIFTNGSCA
DIKKVEAWQVLKHLRHLINFTNNMGEQVTFDEGGDLVGRYSIINMHLSPEDGSIVFKEV
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FLTAFYLGVFIKFNNFDIVKAINRELSYLLLFSLLCGFSSSLFFIGEPDDWTCKLRQP
AFGISFVLCISGILVKTNRVLLVFEAKIFTSFHKWMGLNLQFLLVFLCTFTMQIVICV
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ENFNEAKFITFSMLIFFIVMISFIPAKAASTSCKEVSAKENSESGGGTGSTESSSI
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VTSLLSFDEPOKNAMAGNSTHONSLEAQKSSDTLTRHOPGLPPLOCGETDLDLTVQET
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/protein_id="AAA6503.1"
/db_xref="G1:683745"
/translation="MAFYSCCWVLLALTWHTSAYGPDQRAQKKGDIILGGLFPIHFGV
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/db_xref="taxon:9506"
/clone="phPCaR-4.0"
/clone="ib="lambdaZ-hPG2ss"
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                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 3234) Freichel, M., Zink-Lorenz, A., Holloschi, A., Hafner, M
Endocrinology
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                                                   Expression of a calcium-sensing thyroid carcinoma cell line and
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                                                                  agatgccagccttgtggaacagaagagtgggcacctgagggaagccagacctgcttcccg
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VTFSLSFDEPOKKAMAHRNSTHONSLEAOKSSDTLTRHOPLLPLOCGETDLDLTVOET
GLOGPVGGDQREPEEDBFPLVSSSQSFVISGGGSTVTENVVNS"
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FLTAFYLGVFIKFRNTPIVKANNRELSYLLLFSLLCGESSLFFIGEPODWTCRLROP
AFGISFVLCISCILVKTNRVLLVFEAKIPTSFHKWWGLNGLLOFLLVFLCTFMQIVICV
IWLYTAPPSSYRNQELEDEIIFITCHERGSLMALGFLIGYTCLLAAICFFAFKSRKLP
ENFNEAKFITFSMLIFFIVWISFIPAYASTYGKFVSAVEVIAILAASFGLLACIFFNK
IYIILFKPSRNTIEEVRCSTAAHAFKVAARATLRRSNVSRKRSSSLGGSTGSTPSSSI
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DIKKVEAWQVLKHLRHLNFTNNMGEQVTFDECGDLVGNYSIINWHLSPEDGSIVFKEV
GYYNYYAKKGERLFINEEKILMSGFSREVPFSNCSRDCLAGTRKGIIEGEPTCCFECV
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GRPGIEKFREEAERDICIDFSELISQYSDEEEIQHYVFWYIQNGTAKVIYVFSSGPDL
EPLIKEIVRRNITGKIWLASEAWASSSLIAMPQYFHVVGGTIGFALKAGQIPGFREFL
EKKNHPRKSYHNGFAKEFWEETFNCHLQEGAKGPLPVDTFLRGHEESGDRFSNSSTAFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="mafysccwvllaltwhtsaygpdqraqkkgdiilgglfpihfgv
aakdqdlksrpesvecirvnfrgfrwlqamifaieeinsspallpnltlgyrifdtcn
tvskaleatlsfvaqnkidslnldefcncsehipstiavvgatgsgvstavanllglf
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/translation="MARYSCGWVLLALTWHTSAYGPDQRAQKKGDIILGGLFFIHFGV
/translation="MARYSCGWVLLALTWHTSAYGPDQRAQKKGDIILGGLFFIHFGV
AAKIQDLKSREESVECIRSYWFPFADSSATRINSSLSSEPSPMKSTRPLPWQTSSSIS
AGTGWAQLQLMTTMGGRGLRNSERKLRKGISASTSVNSSPSTLMRKRSSMW"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="calcium-sensing
/protein_id="AAB46873.1"
/db_xref="GI:1836094"
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/gene="CaSR"
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/protein_id="AAB46874.1"
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Search completed: March 19, 2000, 01:24:13 Job time: 3887 sec

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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108	131.6	178.2	195.8	210.4	279	380	Score
4.6	5.6	7.6	8.4	9.0	12.0	16.3	Query Match
514	247	298	421	525	496	562	Length
105	26	48	40	45	39	51	BU
AQ615201	W18663	AI562167	AI415100	AI390993	AA853967	AI742401	DB ID
AQ615201 HS_5138_B	W18663 mb98d01.rl	AI562167 vw73di0.x	AI415100 mb98d01.x	AI390993 mb98d01.y	AA853967 aj51e10.s	AI742401 Wg40e02.x	Description

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RESULT 1
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Unpublished (1997)
On Dec 20, 1995 this sequence version replaced gi:1130951.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
                                                                                                                                                                               Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 562)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGA
                                                                                                                                                                                                                                                                                        AI742401 562 bp mRNA EST 21-JUN-1999 wg40e02.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2367578 3' similar to TR:093557 093557 PUTATIVE ODORANT RECEPTOR; mRNA sequence.
AI742401 GI:5110689
                                                             Email: Robert_Strausberg@nih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Seq.primer: -40UP from Gibco
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                                    quality sequence stop: 468.
Location/Qualifiers
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/db_xref="taxon:9606"
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 496)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Pro-
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AJ51e10.s1 Soares_testis_NET Homo aj51e10.s1 Soares_testis_NET Homo 3' similar to SW:CASR_RAT P48442 E RECEPTOR PRECURSOR; mRNA sequenc AA853967

AA853967.1 GI:2941505
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Similarity 99.7%;
80; Conservative (
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/clone_lib="Soares_NSF_F8_9W_OT_PA_P_S1"
/lab_bost="bH108"
/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from five normalized libraries were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 5 libraries. The pools consisted of the following libraries and cloneIDs: Soares NbHSF pool 1: 309384-310919, 332208-325895 Soares NbHFP pool 1: 45032-147355, 147720-148103, 148872-149255, 15002 - 150407, 151176-152327 Soares NbHFP apool 1: 758280-760583, 772104-774407 Soares NbHPA pool 1: 725880-760583, 772104-774407 Soares NbHPA pool 1: 72580-760583, 772104-774079 Soares NbHPA pool 1: 72580-760583, 772104-774079 Soares NbHPA pool 1: 72580-760583, 772104-7740999 Subtraction by Bento Soares and M. Fatima Bonaldo."
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No. 4.8e-83;
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EXTRACELLULAR
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clone IMAGE:1393866
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                                                                                        GGCGCTGCGGCTCCACCTGA 178
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AI390993 525 mb98d01.yl Soares
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Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 223.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA Sequencing by: Washington University Genome Clone distribution: NCI-CGAP clone distribution found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: Robert_Strausberg@nih.gov
cDNA Library Preparation: M. Ben
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1997)
On Jan 14, 1998 th
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA Library Arrayed by: Greg Lennon,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             an 14, 1998 this sequence version act: Robert Strausberg, Ph.D. (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note-"Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand was prepared from mRNA obtained from Clontech
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="Taxon:9606"
/clone="IMAGE:1393866"
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95.9%;
mouse
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Pred. No. 2.8e-58;
0; Mismatches 11;
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Local Similarity
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CALCIUM-SENSING F
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on Jan 17, 1998 this sequence version replaced gi:2044280
contact: Maarra M/WashU-NCI Mouse EST Project 1999
washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 525)

Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y.,
Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R.,
Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
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This clone is available royalty free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
This read is a RESEQUENCE of a previously sequenced mouse clone
This read has been verified (found to hit its original self in t
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Fax: 314 286 1810
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Location/Qualifiers
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//Clone_lib="Soares mouse p3NMF19.5"
//clone_lib="Soares mouse p3NMF19.5"
//dev_stage="19.5 dpc total fetus"
//dev_stage="19.5 dpc total fetus"
//lab_host="DH10B (ampicillin resistant)"
//lab_host="DH10B (ampicillin resistant)"
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AI415100.1
EST.
                                                                                                                                                                                                                                                 Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
This clone was previously sequenced on the 5' end only, this new
data is from the 3' end
                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1999)
On Apr 21, 1998 this sequence version replaced g1:3073000.
Contact: Marra M/Mashu-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla; Eutherla; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 421)

Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.

Waterston,R. and Wilson,R.

The WashU-NCI Mouse EST Project 1999
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                                                                                                                                                                              Possible reversed clone: similarity on High quality sequence stop: 373.
Location/Qualifiers
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Mus musculus
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314 286 1810
/clone_lib="Soares mouse p3NMF19.5"
/dev_stage="19.5 dpc total fetus"
/lab_host="DH10B (ampicillin resistant)"
/note="Vector: pT7T3D (Pharmacia) with a modified
                                                                                          /organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:337441"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1999)
On Mar 10, 1998 this sequence version replaced Contact: Marra M/WashU-NCI Mouse EST Project 19 Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis,
                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 298)

Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                     A1562167 298 bp mRNA EST vw73d10.x1 Stratagene mouse heart (#937316) Mus muscullus cDNA of IMAGE:1260595 3' similar to SW:CASR HUMAN P41180 EXTRACELLULAR CALCIUM-SENSING RECEPTOR PRECURSOR; mRNA sequence.
                                             Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further:
This clone was previously sequenced data is from the 3' end
                               IMAGE Consortium MGI:663147
                                                                                               Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                       house mouse.
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Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
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                         on May 9, 1995 this sequence version repla
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
                                                                                                                                     The WashU-HHMI Mouse EST Project Unpublished (1996)
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/dev_stage="13 day embryos"
/lab_host="SOLR (kanamycin resistant)"
/lab_host="SOLR (kanamycin resistant)"
/note="Organ: heart; Vector: pBluescript SK-; Site_1:
/note="Organ: heart; Vector: pBluescript SK-; Site_1:
/note="Organ: heart; Vector: pBluescript SK-; Site_1:
/note="Organ: heart; Vector: pBluescript Site_2: XhoI; Cloned unidirectionally. Primer:
/note="Driver Site_1" Cloned unidirectionally. Primer:
/note="Driver Site_
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/strain="NIH/Swiss"
/db_xref="ftaxon:10090"
/clone="MAGE:1260595"
/clone_lib="Stratagene mouse heart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /sex="pooled"
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                                            Sequence-tagged connectors: scanning the human genome Proc. Natl. Acad. Sci. U. S.
                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutherla; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 514)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S.,
                              99380589
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314 286 1810
Mahairas GG,
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Pred. No. 3.1e-22;
0; Mismatches 64;
  Wallace JC,
                                                  U. S. A. 96 (17),
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Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact
IMAGE Consortium (info@image.llnl.gov) for further informati
double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. RNA was kindly provided by Dr. Minoru Ko (Wayne State University)."
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1661 cototatgcottotttggggaacccacaaggcotgcgtgcttgctacgccaggccctctt 1720 Length 247; 0, Gaps 0

TTCTCTCGGGTTTGCCATTTTCCTCTCTCTGTCTGACAATCCGCTCCTTCCAACTGGTCAT 128 tgcccttggttttcaccatcttcctgtcctgcctgacagttcgctcattccaacctaatcat 1780 CCACCAGGGAGTACCAGCGCTTCCCCCCATCTGGTGATTCTTGCTGCGTCACGCCCTCTT 1840 83

CATCTTCAAGTTTTCTACCAAGGTACCCACATTCTACCACACTTGGGCCCAAAACCATGG

tgctggcctgtttgtgatgatcagctcagcggcccagctgcttatctgtctaac 1894 242

189 TGCCGGAATATTCGTCATTGTCAGCTCCACGGTCCATTTGTTCCTCTGTCTCAC AQ615201 514 bp DNA GSS 15-JUN-1999 HS_5138_B2_C04_SP6E RPCI-11 Human Male BAC Library Homo sapie genomic clone Plate=714 Col=8 Row=F, genomic survey sequence.

sapiens

Mammalia;

A sequence approach Swartzell,S., g,J., Zhao,S., 9739-9744 (1999) mapping Adams, M.D. Holzman, T., and

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BASE COUNT
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Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pleter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
http://www.htsc.washington.edu
Plate: 714 row: F column: 8
Seg primer: SP6
                                                                                                                                                                                                                                                                                             AA937218 464 bp mRNA EST 09-JUN-1998 okl3f08.sl Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:1507719 3' similar to SW:CASR_HUMAN P41180 EXTRACELLULAR CALCIUM-SENSING RECEPTOR PRECURSOR ;, mRNA sequence.

AA937218
AA937218.1 GI:3095329
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index Unpublished (1997) On Jan 19, 1998 this sequence version replaced gi:2150441. Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550 Email: Robert_Strausberg@nih.gov This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                               NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap
                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 464)
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                                                                                                                                                                                                                                           Homo sapiens
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(206) 616-3887
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/db_xref="taxon:9606"
/clone="Plate=714 Col=8 Row=F"
/clone_lib="RPCI-11 Human Male
/sex="male"
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77.38;
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Pred. No. 2.8e-16;
0; Mismatches 41;
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                                                                                                                                                                                                                            AW051287 498 bp mrnA EST 20-SEP-1999 wy83912 x1 Soares_NSF_F8_9W_OT_PA_P_S1 Home cDNA clone IMAGE:255206 3' Similar to SW:CASR_HUMAN P41180 EXTRACELLULAR CALCIUM-SENSING RECEPTOR PRECURSOR ;, mrnA sequence.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 498)
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High quality sequence stop: 398.
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/clone_lib="Soares_NSF_F8_9W_OT_PA_P_S1"
/clone_lib="Soares_NSF_F8_9W_OT_PA_P_S1"
/lab_MSGt="DH108"
/note="Organ: pooled; Vector: pT773D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Ecc RI; Equal amounts of plasmid DNA from five normalized libraries were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was pcR-amplified cDNAs from pools of 5,000 clones made from the same 5 libraries. The pools consisted of the following libraries and cloneIDs: Soares NbHFP pool 1:
1050407, 153176-15237 Soares NbHPP pool 1:
1150407, 153176-15237 Soares NbHPP pool 1:
150407, 153176-15237 Soares NbHPP pool 1:
1758280-760583, 772104-774407 Soares NbHPA pool 1:
30476-305311, 320136-322823, 326280-326663 Soares NbHOT pool 1:
73720-72407, 739180-740999 Subtraction by Bento Soares and M. Fatima Bonaldo."
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53.5%;
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0; Mismatches
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                                                                                                                                                                              GATATCTGCATCGACTTCAGTGAACTCATCTCC
                                                                                                                                                                                                        ggcatctgcattgctttcaaggacatcatgccc
                                                                                                                                                                                                                                                                         GCTGATGACGACTATGGGCGGGCCGGGGATTGAGAAATTCCGAGAGGAAGCTGAGGAAAGG
                                                                                                                                                                                                                                                                                                          agcagtgacgactatgggcagctagggggtgcaggcactggagaaccaggccctggtcagg
                                                                                                                                                                                                                                                                                                                                                                           CTCAGCAACAAGAATCAATTCAAGTCTTTCCTCCGAACCATCCCCAATGATGAGCACCAG
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AL040113 732 bp
DKFZp434C2213_r1 434 (;
DKFZp434C2213 5', mRNA
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On Dec 20, 1995 this sequence version replaced Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This clone is available royalty-free through LLNL; IMAGE Consortium (info@image.llnl.gov) for further: Seg primer: -40UP from Gibco High quality sequence stop: 440.
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105032-147335, 147720-148103, 148872-149255, 15002 -
150407, 151176-152327 Soares NDHRF pool 1:
758280-760583, 772104-774407 Soares NDHPA pool 1:
304776-305311, 320136-322823, 326280-326663 Soares NDHOT |
304776-305311, 320136-3228023, 326280-326663 Soares NDHOT |
304776-305311, 320136-3228023, 326280-326663 Soares NDHOT |
304776-305311, 320136-3228023, 326280-326663 Soares NDHOT |
304776-305311, 320136-322823, 326280-32663 Soares NDHOT |
304776-305311, 320136-328011, 320136-32
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Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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/clone_lib="Soares_NSF_F8_9W_OT_PA_P_S1"
/lab_host="DH10B"
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/db_xref="taxon:9606"
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Pred. No. 1.2e-10;
0; Mismatches 155;
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Matches 285;
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1563 ggcctgtttgcctggcacctagacacccctgtggtgaggtcagcaggggggccgcctgttgc 1622
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                                                ctgggcttcatactggccttcctctacaatggcctcctctccatcagtgcctttgcctgc
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GCAAGTATGTTGGGCCTCGCCTGCCCTACAATGTGCTCCTCATCGCGCCTCTGCACGCTTTAT
                                                                                                                                                                                                                                                                                                                                                                               gtacctacattctaccacgcctgggtccaaaaccacggtgctggcctgtttgtgatgatc 1862
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cccacaaggcctgcgtgcttgctacgccaggccctctttgcccttggtttcaccatcttc 1742
                                                                                                          GGCAAGGAGACAGCCCCCGAACGGCGGGGGGGTGGTGACACTGCGCTGCAACCACCGCGAT
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                                                                                                                                                                                                                                                                                                                               GGTGCCCAGCGGCCACGCTTCATCAGTCCTGCCTCACAGGTGGCCATCTGCCTGGCACTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clone from S. Wiemann, Molecular Genome Analysis, German Can
Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de;
sequenced by BMFZ within the cDNA sequencing consortium of t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EST (Koehrer, et al.)
Unpublished (1999)
On Jul 7, 1999 this sequence
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Similarity 45.5%;
85; Conservative
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This is the 5' sequence of the clone insert
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 732)
Koehrer,K., Beyer,A., Mewes,H.W., Gassenhuber,J. and Wiemann,
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/clone="DKF2p434C2213"
/clone="lb="434" (synonym: h
/tissue_type="testis"
/dev_stage="adult"
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/db_xref="taxon:9606"
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Pred. No. 1.6e-06;
0; Mismatches 339;
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Conservative

0;

Pred. No. 9.5e
); Mismatches Score 61;

201;

0

Gaps

0

61; DB 70; No. 9.5e-05

Length 497; Indels

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ACCESSION
VERSION
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AW157397/c
BASE COUNT
ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisei, G., Jost Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AW157397 497 bp mRNA EST 04-NOV-1999 au95a09.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783992 3' similar to gb:J02984 408 RIBOSOMAL PROTEIN S15
                                                                                                                                                                                                                                                                                                                                                                                                           IMAGE Consortium (info@image.llnl.gov)
Seq primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                      Email: est@watson.wustl.edu
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL;
This clone is available royalty-free through LLNL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished
On Dec 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WashU-NČI human EST Project
Unpublished (1997)
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AW157397
AW157397.1 GI:6228798
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                                                                                                                                                                                                                                                                                                                                                                              quality sequence stop: 467
Location/Qualifiers
              74
                                       /note="Organ: brain; Vector: pBluescript SK (Stratagene);
Site_1: SstI; Site_2: XhoI; Double-stranded cDNA was
prepared from human fetal brain tissue. 5' and 3'
adaptors were used in cloning as follows: 5' adaptor
            Science Park, Tr
                                                                                                                                                                    sequence:
                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                           /dev_stage="5 months post-conception"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                       /clone_lib="Schneider fetal brain 00004"
                                                                                                                                                                                                                                                                                                                  /clone="IMAGE: 2783992"
                                                                                                                                                                                                                                                                       tissue_type="frontal lobe"
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L50 g 121 t
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AW157806/c
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Best Local S
Matches 181
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Similarity 47.4%;
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366 gcgcaccatccccaatgacaagtaccaggtggagaccatggtgctgctgctgcagaagtt 425
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                                                                                                                                                                                                                                                                                                 Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

This clone is available royalty-free through LLNL; contact the

This clone is available royalty-free through further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WashU-NCI human EST Project
Unpublished (1997)
On May 18, 1998 this sequence version
Other_ESTs: au80f01.y1
Contact: Wilson RK
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au80f01.x1 Schneider fetal
IMAGE:2782585 3' similar t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jos. Krizman, D., Kucaba, T., Lacy, M., Le, N., Lenon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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AW157806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis,
                                                                                                                                                                                                                                                                              IMAGE Consortium (info@image.linl.
Seq primer: -40UP from Gibco
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                                                                                                                                                                                                                                                    quality sequence stop: 343
/tissue_type="frontal lobe'
                                /sex="male"
                                                                /clone_lib="Schneider fetal brain
                                                                                             /db_xref="taxon:9606"
/clone="IMAGE:2782585"
                                                                                                                                                          /organism="Homo sapiens"
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brain 00004 Homo sapiens cDNA clone
o gb:J02984 40S RIBOSOMAL PROTEIN S15
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RESULT 13
AI090099/c
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AUTHORS
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DEFINITION
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Tumor Gene Index
Unpublished (1997)
On Jan 14, 1998 this sequence version replaced
Contact: Robert Strausberg, Ph.D.
                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 476)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Pro
                                                                                                                                                                                                                                                                                                            gb28a01.x1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone
IMAGE:1697544 3' similar to gb:J02984 40S RIBOSOMAL PROTEIN S15
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5'-GAGAGAGAGACICGAGTITTTITTTTTTTTTTTTT-3'. The library was size-selected for >0.5 kb inserts and has an average insert size estimated at 1.2 kb. This library was constructed using the CAP-trapper method for full-length enrichment and has not undergone amplification. Librar was constructed by Dr. Claudio Schneider (LNCIB-Area Trieste. Italy). "
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/lab_host="DH10B"
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Pred. No. 9.5e-05;
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Best Local Similarity 47.4%;
Matches 181; Conservative
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                                                         qf98a02.x1 Soares_placenta_8to9weeks_2NbHP8to9w
clone IMAGE:1758026 3' similar to qb:J02984 40S
S15 (HUMAN);, mRNA sequence.
a1200353
                                            AI200353.1
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                                                                                                                        AI200353
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Email: Robert_Straus
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/clone_lib="Soares_pregnant_uterus_NbHPU"
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/lab_host="DH10B"
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/db_xref="taxon:9606"
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Pred. No. 0.00013;
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   AI283030
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 544 Std Error: 0.00
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[ [ bases 1 to 438]
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National Cancer Institute, Cancer Genome Anatomy
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                                                                GGTGGGCAGCATGGTGGGCGTCTACAACGGCAAGACCTTCAACCAGGTGGAGATCAAGCC
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Score 60.4; DB 44 Pred. No. 0.00013; 0; Mismatches 201

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DB 44;

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gm56h04.x1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA
clone IMAGE:1892791 3' similar to gb:J02984 40S RIBOSOMAL PROTEIN
S15 (HUMAN);, mRNA sequence.
a1283030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1997)
On Jan 17, 1998 this sequence version replaced Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 592 Std Error: 0.00
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National Cancer Institute, Cancer Genome Anatomy
                                                                                                                                                                                                                                                                                                                                                                                                High quality sequence stop: 452
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                               Seq primer: -40UP from Gibco
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                         Gene Index
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(Pharmacia). Library constructed by Bento Soares and M.Fatima Bonaldo."
145 c 148 g 125 t 1 others
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query Match Length DB	Query Match Length DB ID	80	ID	Description
O	_	333.6	12.0	421	46	AI415100	AI415100 mb98d01.x
	N	301.4	10.9	525	₽	AI390993	AI390993 mb98d01.y
ი	ω	294.8	10.6	562	51	AI742401	AI742401 wg40e02.x
Ω	4	229.2	8. 3	298	84	AI552167	AI562167 vw73d10.x
O	S	212.8	7.7	496	39	AA853967	AA853967 aj51e10.s
	σ	175.6	6.3	247	25	W18663	W18663 mb98d01.rl
	7	140.6	5.1	260	71	AV278654	AV278654 AV278654

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TITLE
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                                                                     Unpublished (1999)
on Apr 21, 1998 this sequence version replaced gi:3073000 Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108,
                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 421)

Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,
   Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                  AI415100
AI415100.1
                                                                                                                                                            Waterston, R. and Wilson, R.
The WashU-NCI Mouse EST Project 1999
                                                                                                                                                                                                                                                                                                                                                                     AI415100 421 bp mRNA EST 09-FEB-1999 mb98d01.x1 Soares mouse p3NMF19.5 Mus musculus cDNA clone IMAGE:337441 3' similar to SW:CASR_RAT P48442 EXTRACELLULAR CALCIUM-SENSING RECEPTOR PRECURSOR; mRNA sequence.
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AL131864 Fugu rubr
AL004753 F.rubrige
AL131871 Fugu rubr
AL131873 Fugu rubr
AL131876 Fugu rubr
AL131880 Fugu rubr
AL108298 Drosophil
AL131884 Fugu rubr
AL108616 Drosophil
AL398650 tx15all.x
AL108616 Drosophil
AA252399 zs12h01.s
AL108616 Drosophil
AA252399 zs12h01.x
AL169085 tm06c01.x
AL1060029 UI-R-C1-k
AA170693 ms85h09.x
AN087570 xb31h05.x
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AL060767 Drosophil
AL099741 Drosophil
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AL1659872 tc77605.x
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/organism="Mus musculus"
/organism="Mus musculus"
/olone="IMAGE:337441"
/clone="IMAGE:337441"
/clone=lib="Soares mouse p3NMF19.5"
/clone="IMAGE:337441"
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/clone=lib="Soares mouse p3NMF19.5"
/clone=lib=lib="Soares mouse 
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Pred. No. 4e-69;
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Best Local
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                                                                                                                                     ttgctcatctgtctcacatggcttgtaatgtggaccccacgacccaccagggaataccag 2183
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                                                                                                                                                                                                       CACACTTGGGCCCAAAACCATGGTGCCGGAATATTCGTCATTGTCAGCTCCACGGTCCAT
                                                 cgcttcccccatctggtgattctcgagtgcacagaggtcaactctgtaggcttcctgttg 2243
                                                                                                                                                                                                                                                                                                                                                                                                            ATCCGCTCCTTCCAACTGGTCATCATCTTCAAGTTTTCTACCAAGGTACCCACATTCTAC 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               443;
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This clone is available royally-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
This read is a RESEQUENCE of a previously sequenced mouse clone
This read has been verified (found to hit its original self in t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
Waterston,R. and Wilson,R.
The WashU-NCI Mouse EST Project 1999
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Fax: 314 286 1810
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/dev_stage="19.5 dpc total fetus"
/lab_host="DBIOB (ampicillin resistant)"
/note="Vector: pT7T3D (Pharmacia) with a modified
/note="Vector: pT7T3D (Pharmacia) with a modified
polylinker; Site=1: Not I: Site=2: Eco RI: 1st strand cDNA
/ras primed with a Not I - oligo(dT) primer [5'
/ras primed with a Not I - oligo(dT) primer [5'
/ras primed with a Not I - oligo(dT) primer [5'
/ras primed cDNA
/ras size selected, ligated to Eco RI
/ras adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT7T3 vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. RNA was kindly provided by Dr. Minoru Ko (Wayne State University)."

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/clone="IMAGE:337441"
/clone_lib="Soares mouse p3NMF19.5"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1997)
On Dec 20, 1995 this sequence version
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota: Metazoa;
Eutheria; Primates;
1 (bases 1 to 562)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IMAGE Consortium (info@image.llnl.gov) for further is Seg primer: -400P from Gibco
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         High quality sequence stop: 468 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: Robert_Strausberg@nih.gov
This clone is available royalty-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
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                                                            /note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Ecc RI; Equal amounts of plasmid DNA from five normalized libraries were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 5 libraries. The pools consisted of the following libraries and clonelDs: Scares NDSHP pool 1: 309384-310919, 332088-325895 Soares NDSHP pool 1: 145032-147335, 147720-148103, 148872-149255, 15002 - 158280-760583, 772104-774407 Soares NDSHP pool 1: 758280-760583, 772104-774407 Soares NDSHP pool 1: 758280-760583, 772104-774407 Soares NDSHP pool 1: 732720-726407, 739080-740999 Subtraction by Bento Scares and M Father a Romaldo "740999 Subtraction by Bento
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gene Index
                       Soares and M. Fatima Bonaldo." 161 \text{ c} 167 \text{ g} 117 \text{ t}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:9606"
/clone="IMAGE:2367578"
/clone=lib="Soares_NSF_F8_9W_OT_PA_P_S1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                        /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
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Catarrhini; Hominidae;
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                       1 others
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RESULT 4
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         Unpublished (1999)
On Mar 10, 1998 this sequence version replaced gi:2948814.
Contact: Marra M/MashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, UTel: 314 286 1810
Fax: 314 286 1810
                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodenita; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 298)

Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R., and Wilson, R.
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AI562167.1
                                                                                                          Waterston, R. and Wilson, R. The WashU-NCI Mouse EST Project 1999
                                                                                                                                                                                                                                                                                                               AI562167 298 bp mRNA EST 25-MAR-1999 vw73d10.xl Stratagene mouse heart (#937316) Mus musculus cDNA (IMAGE:1260595 3' similar to SW:CASR_HUMAN P41180 EXTRACELLULAR CALCIUM-SENSING RECEPTOR PRECURSOR ; mRNA sequence.
                                                                                                                                                                                                                                                               EST.
house mouse
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Pred. No. 7.8e-60;
0; Mismatches 153
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hes 255;
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             Tumor Gene Index
                                                                                                     Homo sapiens
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                                    Eukaryota; Metazoa; Chordata; Craniata; Ve
Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 496)
                                                                                                                                                                              AA853967 496 bp mRNA aj51e10.s1 Soarse_testis_NHT Homo sapiens 3' similar to SW:CASR_RAT P48442 EXTRACELL RECEPTOR PRECURSOR; mRNA sequence.
AA853967
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Possible reversed clone: similarity Possible reversed clone: spolyT not f High quality sequence stop: 286.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:663147
MGI:663147 was previously sequenced on the 5' end only, this new
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus"
/strain="NIH/Swiss"
/db_xref="raxon:10090"
/clone="IMAGE:1260595"
/clone_lib="Stratagene mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /sex="pooled"
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Pred. No. 2.3e-44;
0; Mismatches 43
                                                                                                                                                                                                                 o sapiens cDNA clone IMAGE:139:
EXTRACELLULAR CALCIUM-SENSING
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2682 cagcttacgatgtataagcacgcggaagaatccagtgca 2720
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2262 ctcctctccatcagtaccttcgtctgcagctacctgggtaaggaactgccagagaactat 2321
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      493 CTCCTTCCCATCAGTGCCTTTCCCTGCAGCTACCTGGGTAAGGACTTGCCAGAGAACTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 72.1 nes 331; Conservative
                                                                                                                                                 | CgCtgCggcaCtacCtgatCcaCtggaaaggtgcagacgggaaggaaggctCtCtttttt
                                                                                                                                                                                                                                                                                                                                                                                                                   AACGAGGCCAAATGTGTCACCTTCAGCCTGCTCTTCAAATTCGTGTGCTGGATCGCCTTC
                                                                                                                                                                                                TGCCGCCCAGACCTCAACAGCACAGAGCACTTCCAGGCCTCCATTCAGGACTACACGAGG
                                                                                                                                                                                                                  CTGAGCAGCCTGAGCAGCGGCTTCGGTGGGTATTTTCTGCCTAAGTGCTACGTGATCCTC
                                                                                                                                                                                                                                                                                                                                            TTCACCACGGCCAGGTCCTACGACGGCAAGTA-ANCCTTGCGGCCAACATGATGGC-TGG
                                                      TGAGGGTCGAAGGTCGAGCAGGCCGGGGGGGTGTCCGGGAGGTCTTTGGG-CATCGCGGTCT
                                                                                     tgctgaaggtggcgggtccagtggggccgagagcttgaggtgtctgggagagctccggca 2681
                                                                                                                         CGCTGCGGCTCCACCTGACCAGTGGGTCAGCAGGCAAC--GCTGGCAGCCTTCTCTGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Possible reversed clone: similarity on wrong strand Insert Length: 878 Std Error: 0.00 Seq primer: -40ml3 fwd. Er from Amersham High quality sequence stop: 223.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bonaldo, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: Robert_Strausberg@nih.gov cDNA Library Preparation: M. Bento Soares,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     On Jan 14, 1998 this sequence version replaced Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        www-bio.llnl.gov/bbrp/image/image.html
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DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL at:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not and Eco RI sites of the modified pT773 vector. Library went through one round of normalization to Cot5, and was constructed by Bento Soares and M. Fatima Bonaldo. " 145 c 148 g 100 t 1 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1393866"
/clone_lib="Soares_testis_NHT"
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Pred. No. 2.3e-40;
0; Mismatches 123;
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 247)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubu
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.
The WashU-HMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     W18663 247 bp mann mb98d01.rl Soares mouse p3NMF19 IMAGE: 337441 5', mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1996)
On May 9, 1995 this sequence version replaced contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     High quality sequence stop:
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This clone is available royalty-free through LLNL; IMAGE Consortium (info@image.llnl.gov) for further
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus
                                                                                                                                                                                                                       Similarity 92.9
84; Conservative
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Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                             Dr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:337441"
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/dev_stage="19.5 dpc total fetus"
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89 c 42 g 72 t
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mouse p3NMF19.5
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Unpublished (1999)
On Mar 10, 1988 this sequence version replaced gi:2948605.
Genome Exploration Research Group, Life Science Tsukuba Center,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hayashizaki,Y.

Transcriptional sequencing: A method for DNA sequencing using RNA polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998) Itoh,M., Kitsunai,T., Aklyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.

Okazaki,Y. and Hayashizaki,Y.

Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)

System. Genome Res. 9 (5), 463-470 (1999)
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AV278654 RIKEN full-length enriched, adult male testis (DH10B)
musculus cDNA clone 4933403B08 3', mRNA sequence.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fax: +81-298-36-9098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3-1-1 Koyadai,
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The Institute of Physical and Chemical Research (RIKEN), Genomic
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1 (bases 1 to 260)
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+81-298-36-9013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  visit our web site (http://genome.rtc.riken.go.jp) for
           Project
                                           prepared
                                                                                                                                                                                                                                                                                                                                            /organ1sm="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="4933403B08"
/note="Site_1: Sall; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riker
                                                                                                                                                        /tissue_type="testis"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                              /sex="male"
                                                                                                                                                                                                                                                                                 (DHIOB)
                                                                                                                                                                                                                                                                                                                 /clone_lib="RIKEN full-length enriched,
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2535 caggcetecatecaggaetacaeggaggegetgeggeaetacetgatecaetggaaaggtg 2594
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                                                                                    This clone is available royalty-free through LLNL; IMAGE Consortium (info@image.llnl.gov) for further i Insert Length; 1252 Std Error: 0.00 Seq primer: -40m13 fwd. ET from Amersham High quality sequence stop: 398.
                                                                                                                                                                                                    Tumor Gene Index
Unpublished (1997)
On Jan 19, 1998 this sequence version
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 464)
                                                                                                                                                                                                                                                                                                                                                NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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/organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                   ocation/Qualifiers
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Pred. No. 2.6
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                                                     Unpublished (1997)
On Dec 20, 1995 this sequence version Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                       AW051287 498 bp mRNA EST 20-SEP-1999 wy83912.x1 Soares.NSF_F8.9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2555206 3' similar to SW:CASR_HUMAN P41180 EXTRACELLULAR CALCIUM-SENSING RECEPTOR PRECURSOR ; mRNA sequence.

AW051287
Email: Robert_Strausberg@nih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
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National Cancer Institute, Cancer Genome Anatomy
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109384-310919, 323208-325895 Soares NbHSF pool 1:
145032-147335, 147720-148103, 148872-149255, 15002 -
150407, 151176-152327 Soares NbHFR pool 1:
758280-760583, 772104-774407 Soares NbHFR pool 1:
304776-306311, 320136-322823, 326280-32663 Soares NbHOT pool 1: 723720-726407, 739080-740999 Subtraction by Bento Soares and M. Fatima Bonaldo."
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/clone_1ib="Soares_NSE_F8_9W_OT_PA_P_S1"
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Pred. No. 7.7e
0; Mismatches
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7.7e-10;
hes 111;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCATCGACTTCAGTGAACTCAT
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                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 514)

Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman, Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.
                                                                                                                                                                                                                                                                                  genomic o
                                                                                                                                                                                                                                                                                                AQ615201 514 bp DNA GSS 15-JUN-1999
HS_5138_B2_C04_SP6E RPCI-11 Human Male BAC Library Homo sapiens
genomic clone Plate=714 Col=8 Row=F, genomic survey sequence.
scanning the human genome Proc. Natl. Acad. Sci. U.
                                                                                                                                                                                               Homo sapiens
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Location/Qualifiers
                                             Sequence-tagged connectors: A sequence approach to mapping
                                                                   Hood
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     libraries and clonells: Soares NbHSF pool 1: 309384-310919, 323208-325995 Soares Nb2HP pool 1: 145032-147335, 147720-148103, 148872-149255, 15002 - 150407, 151176-152327 Soares Nb2HF8-9W pool 1: 758280-760583, 772104-774407 Soares NbHPA pool 1: 304776-305311, 320136-322823, 326280-326663 Soares NbHOT pool 1: 723720-726407, 739080-74099 Subtraction by Bent Soares and M. Fatima Bonaldo." 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note-*Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from five normalized libraries were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 5 libraries. The pools consisted of the following
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /lab_host="DH10B"
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/db_xref="taxon:9606"
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57.6%;
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Pred. No. 8e-10;
0; Mismatches 111;
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96 (17),
    9739-9744
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                                                                                       Holzman, T., Adams, M.D.
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Best Local Sim
Matches 129;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1568 ccacagggttgttgtgggttcccaccac-tgctgctttgagtgtgtgtgccctgcgaagctg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCAGCGAGTGGTAACGGGTTTCCATCACATGCTGCTTTGAGTGTGCCCTGTGGGGGCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                library availability, please contact Pieter de Jong pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Resear h Genetics (info@resgen.com). BAC end Web Server: http://www.htsc.washington.edu plate: 714 row: F column: 8 Seg primer: SP6 Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Mahairas GG, Wallace JC,
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seatt
Tel: (206) 616-3618
                                                                                                                                                                                                                                                                                                                                                                                                                            AL040113 732 bp mRNA EST 2
DKFZp434C2213_r1 434 (synonym: htes3) Homo sapiens
DKFZp434C2213 5', mRNA sequence.
AL040113
AL040113 GI:5935280
Am Klopferspitz 18a D-82152 Martinsried, Germany This is the 5' sequence of the clone insert Clone from S. Wiemann, Molecular Genome Analysis, Research Center (DKFZ); Email s.wiemann@dkfz-hei
                                                                                                                                                     Koehrer, K., Beyer, A., Mewes, H.W., Gas
EST (Koehrer, et al.)
Unpublished (1999)
Unpublished (1999)
On Jul 7, 1999 this sequence version
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Clones are derived from the human BAC library RPCI-11.
Clones are derived from the human BAC library RPCI-11.
                                                                                                                                       Contact: Koehrer
                                                                                                                                                                                                                                                                 Eutheria; Primates; Catarrhini; 1 (bases 1 to 732)
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(206) 616-3887
(207) Wallaceeu washington edu
1: jwallaceeu washington edu
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quality sequence stop: 514.
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/db_xref="taxon:9606"
/clone="plate=714 Col=8 Row=F"
/clone_1ib="RPCI-11 Human Male BAC Library"
/clone_Tib="RPCI-11 Human Male BAC Library"
/sex="male"
/note="Vector: pBACe3 6; Genomic sequence of the sequence of th
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/db_xref="taxon:9606"
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Pred. No. 8.1e-08;
0; Mismatches 71;
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Matches 275;
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Best Local :
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                                                                                                                                                                                                                                                              CATGTACACCACCTGCATCATCTGGCTGGCATTCCTGCCCAT
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                                                    AW015382 442 bp mRNA
UI-H-BIO-aat-d-06-0-UI.sl NCI_CGAP_Sub1
IMAGE:5710331 3', mRNA sequence.
AW015382
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Location/Qualifiers
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This clone is available at the RZPD in Berl:
Please contact the RZPD: Ressourcenzentrum,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequenced by BMFZ within the cDNA sequencing German Genome Project.
     AW015382.1
EST.
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/clone_lib="434 (synonym: h
/tissue_type="testis"
/dev_stage="adult"
/lab_host="DH10B"
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245 c 191 g 169 t 2 others
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/db_xref="taxon:9606"
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TITLE
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  534 cctttcctgatgcccctggtcagctatgaggcaagcagcgtggtactcagtgccaagcgc 593
                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: Robert_Strausberg@nih.gov
Oligo-dT track not found, Not I site shown in beginning of sequence is likely internal to the message. cDNA Library Preparation: M.B. Soares Lab Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/Lini at:
www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             on May 18, 1998 this sequence version replaced Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1997)
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National Cancer Institute, Cancer Genome Anatomy
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 442)
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                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                   /lab_host="Public Corrections of the Public Corrections of the Publisher (Pharmacia) with a modified polylinker; Site_1: Not 1; Site_2: Ecc RI; The NCI_CGAP_Sub1 library is a subtracted library derived from BI CONSTITUTE of 21 normalized or subtracted NCI_CGAP_Sub1 library is a NCI_CGAP_CO4, NCI_CGAP_CO4, NCI_CGAP_CO4, NCI_CGAP_CO4, NCI_CGAP_CO4, NCI_CGAP_CO5, NCI_CGAP_CO5, NCI_CGAP_CO5, NCI_CGAP_CO5, NCI_CGAP_CO5, NCI_CGAP_CO5, NCI_CGAP_CO5, NCI_CGAP_LU3, NCI_CGAP_LU4, NCI_CGAP_LU19, NCI_CGAP_LU19, NCI_CGAP_CO4, NCI_CGAP_CO5, NCI_CGAP_LU19, NCI_CGAP_LU19, NCI_CGAP_CO5, NCI_CGAP_CO5, NCI_CGAP_CO5, NCI_CGAP_CO5, NCI_CGAP_CO5, NCI_CGAP_LU19, NCI_CGAP_LU19, NCI_CGAP_CO5, NCI_CGAP_CO5, NCI_CGAP_CO5, NCI_CGAP_CO5, NCI_CGAP_CU1, NCI_CGAP_LU24, NCI_CGAP_LU19, NCI_CGAP_CO5, NCI_CGAP_CO5, NCI_CGAP_CO5, NCI
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TAG_LIB-NCI_CGAP_Lei2
TAG_TISSUE=leiomyosarcoma
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/clone_lib="NCI_CGAP_Sub1"
/lab_host="DH10B_(Life Ted
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/clone_lib="Zebrafish WashU MPIMG
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Clark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M., Clark, M., Johnson, S.L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Eddy, S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R. Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R. Waterston, R. and Wilson, R. Washu Zebrafish EST Project 1998
Unpublished (1998)
On Jun 5, 1998 this sequence version replaced gi:3189643.
Other ESTs: £14406.X1
                                                                                                                                                                                                                                                                                  cDNA Library Preparation: Matthew Clark. cDNA Library Arrayed by: Matthew Clark. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: Genome Systems. St. Louis, Missouri (web address: www.genomesystems.com) (email contact: info@genomesystems.com) and Research Genetics, Huntsville, Alabama (web address: www.resgen.com) (email contact: info@resgen.com) and Research Genetics; Huntsville, Alabama (web address: www.resgen.com) (email contact: info@resgen.com) and Research Genetics: info@resgen.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Stephen L. Johnson Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. I Tel: 314 286 1810
Email: zbrafish@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazca; Chordata; Craniata; Vertebrata;
Neopterygii; Teleostei; Euteleostei; Ostariophysi; (
Cyprinoidea; Cyprinidae; Rasborinae; Danio.
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                                                                                                               quality sequence stop:
Location/Qualifiers
/organism="Danio rerio"
/db_xref="taxon:7955"
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GSS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FR0044372 615
Fugu rubripes GSS
                     One pass dye-terminator sequencing
                                                                      V_type: phagemid PRIMER: KS
                                                                                                                         Submitted (11-OCT-1999) MRC Human Genome Mapping Project Resource Centre, Hinxton, Cambridge, CB10 ISB. UK Email: biohelp@homp.mrc.ac.uk Vector: pBluescript II KS
                                                                                                                                                                                                                                                        Umrania, Y., Williams, G. and
                                                                                                                                                                                                                                                                           1 (bases 1 to 615)
Elgar,G., Clark,M.S., Smith,S., Meek,S., Warner,S., Edwards,Y.J.K.,
                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontoidei; Tetraodontidae; Fugu.
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sequence
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53.2%;
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Pred. No. 0.0075;
0; Mismatches 103;
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Matches Best BASE COUNT ORIGIN

RESULT 14 FR0044372

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AUTHORS

SOURCE KEYWORDS VERSION

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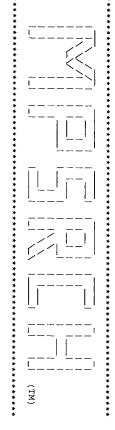
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81 CAGTCTGGGTGGCCNTTGTCNCAGCTTATATCAGCTCTCCAGGGAAATACTCCACGCTCA 140
                                                               AAATGCCAGACNACCTCAACGAGGNCAGACTAATCNCCTTCAGCATGCTCATNTTNTGTG 80
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                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (09-SEP-1997) MRC Human Genome Mapping Project Resource Centre Hinxton, Cambridge, CB10 1SB. Email: biohelp@hgmp.mrc.ac.uk Vector: pBluescript II KS
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AL004753
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Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorpha;
Tetraodontiformes; Tetraodontoidei; Tetraodontidae; Fugu.
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                                                                                                                                                                                                                                                                                                                                                         One pass dye-terminator sequencing of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
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Elgar,G., Clark,M., Smith,S., Meek,S., Warner,S., Umrania,
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/db_xref="taxon:3103"
/clone_lib="cosmid 124A16"
/clone="124A16aA11"
a 70 c 53 g 71 t
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/db_xref="taxon:31033"
/db_ref="toxon:d184F17"
/clone="184F17a68"
/clone="184F17a68"
157 c 136 g 179 t
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Pred. No. 0.018;
0; Mismatches 1
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Search completed: March 18, 2000, 10:28:08 Job time: 2293 sec

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Run on: MPsrch_pp protein - protein database search, using Smith-Waterman algorithm Fri Mar 17 13:05:22 2000: MasPar time 113.50 Seconds 513.137 Million cell updates/sec

Sequence: Description: Perfect Score: >US-09-361-652-1 (1-840) from US09361652.pep 6338 1 MLFWAAHLLLSLQLVYCWAF.....NNTEHFQASIQDYTRRCGTT 840

Tabular output not generated.

Searched: PAM 150 Gap 11 225878 seqs, 69334122 residues

Scoring table:

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

sptrembl12
1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human
5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle
9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified
13:sp_vertebrate 14:sp_virus

Statistics: Mean 52.670; Variance 98.786; scale 0.533

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

212443211 20987654321 20987654321	Result
2083 2083 1455 1422 1385 1371 1371 1218 1218 1170 1170 1177 878 878 878 828 799	score
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                                                                                                                                                                                        SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                       MEDLINE; 99159821.
                                                                                                                                                                                                                                                                                                                                                                           STRAIN-WISTAR;
                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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Eukaryota; Metazoa; Chor
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01-MAY-1999 (TrEMBLrel 10,
01-MAY-1999 (TrEMBLrel 10,
PUTATIVE TASTE RECEPTOR TR2
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Q9Z0R7;
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Sciurognathi; Muridae; Murinae;
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Pred. No. 0.00e+00;
188; Mismatches 286
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Rattus.
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95:5178-5181(1998).

related to the Ca2+-sensing receptor

in

NOZAKI Y.,

TOMURA K.,

HAZAMA

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RESULT 3
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DT 01-AUG-1998 (TIEMBLIEL 07, Cr 07 140G-1998 (TIEMBLIEL 107, La DI 01-AUG-1998 (TIEMBLIEL 112, La DI 01-NOV-1999 (TIEMBLIEL 112, LA DI 112, LA D
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                              SEQUENCE FROM N.A.
MEDLINE; 98225788.
NAITO T., SAITO Y., YAMAMOTO J., N.
NAKANISHI S., ERENNER S.;
"Putative pheromone receptors relat
Fugu.";
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                                                                                                                                                                         Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
Neopterygii; Teleostei; Buteleostei; Acanthopterygii; Percomorpha;
Tetraodontiformes; Tetraodontoidei; Tetraodontidae; Fugu.
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                                                                                                            FTVAVEIFAILASSFGLILCIFAPKCFIILFKPEKNSKKHL
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                                                                                                                                                                                                                                                                              FSLTLCFLCSL-TFIGAPSHLSCMLRHTAFGITFVLCISCVLGKT--VVVLMAFRATLPG
                                                                                                                                                                                                                                                                                                                  TTCFPRTVEFLAWHEPISLVLIAANTLLLLLLVGTAGLFAWHFHTPVVRSAGGRLCFLML
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                                                                                                                                                   FLLAFTHNILLSISTFVCSYLGKELPENYNEAKCVTFSLLLNFVS-WIAFFTMASIYQGS
                                                                                                                                                                             FWAVLGYIGLLAAVCLVLAVLARKLPDNFNEAKMITFSMLI-FCAVWITFIPAYVSSPGK
                                                                                                                                                                                                        FY-RTWAQNHGAGLFVIVSSTVHLLICLTWLVMWTPRPTREYQRFPHLVILECTEVNSVG
                                                                                                                                                                                                                                  SNVMKWFGPPQQRMTVVTFTSIQVLICIVWLVVNPPFPVRNLTTYKERIILECALGSSVG
                                                                                                                                                                                                                                                                                                                                            NACFPKPVEFLSFNEVLGIILAVFSVGGACLAVITAAVFFHHRTSPIVRANNSELSFLLL
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Proc. Natl. Acad. Sci. U.S.A. 95:11987-11992(1998).
EMBL; AF083081; AAC64076.1; ...
PFAM; PF00003; 7tm_3; 1.
PFAM; PF00003; 7tm_3; 1.
PFAM; PF000048; GFCRMGR.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Neopterygii; Teleostei; Buteleostei; Ostariophysi; (
Cyprinoidea; Cyprinidae; Cyprininae; Carassius.
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Local Similarity 31.1%;
nes 254; Conservative
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RTWAQNHGAGLFVIVSSTVHLLICLTWLVMWTPRPTREYQRFPHLVILECTEVNSVGFLL
                          MKWFGPPQQRLSVFSFTLIQVIICVLWLTIYPPFPFKNLNYFKEKIILECNVGSVVGFWA
                                                                  CFPRTVEFLAWHEPISLVLIAANTLLLLLLVGTAGLFAWHFHTPVVRSAGGRLCFLMLGS
                                                                                                                                        CVKKETEFLSYEEIMGILLTTISLVGAFITIIIAVIFFRYKNTPIVKANNSELSFLLLFS
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3.57e-275;
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RESULT 5
ID 073637;
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MEDLINE; 98226788.
NAITO T., SAITO Y., YAMAMOTO J.,
NAKANISHI S., BRENNER S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
Eukaryota; Metazoa; Chordata; Caraniata; Vertebrata; Actinopterygii;
Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorpha;
Tetraodontiformes; Tetraodontoidei; Tetraodontidae; Fugu.
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                     FWNFESNKPPHSVCSESCPPGTRMSRKKGQPVCCFDCLLCSEGKISNTTDSMECTSCPED
                                                    NFLLH-ENTVAFDDNGDTLGYYDIIAWDWNGPEWT-FEIIGSASLSPVH---LDINKTKI
                                                                                  NFTTTFGDQVSFDENGDVLPIYDILNWQWLPDGRTQVQNVGEVKRSPSRGEELQIHEDKI
                                                                                                                 - LGAFSMSAAYRVYEAVYAVAHGLHQLLGC-TS-E-ICS-R-GPVY---PWQLLQQIYKV
                                                                                                                                               FLDVSNLRPEYNIYKAVYALAYALDDMLQCEPGRGPFSGGSCADIHKLEPWQFVHYLQHV
                                                                                                                                                                               QVPGLKEFEESYVRAV-TAAPSACP--EGSW----CS-TNQLCRE-CHTF-TTRNMPT-
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Pred. No. 1.55e-266;
227; Mismatches 299;
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Last sequence up
Last annotation
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Matches 25
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EMBL; AB008857; BAA26122.1; -.
PFAM; PF00003; 7tm_3; 1.
PFAM; PF01094; AME_receptor; 1.
PRINTS; PR00248; GPCRWGR.
PRINTS; PR00592; CASENSINGR.
SEQUENCE 940 AA; 105814 MW; (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE; 98226788.
NAITO T., SAITO Y., YAMAMOTO J., NOZAKI Y
NAKANISHI S., BRENNER S.;
"Putative pheromone receptors related to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
Reopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorpha;
Tetraodontiformes; Tetraodontoidei; Tetraodontidae; Fugu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fugu."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
  268
                                                      266
                                                                                                            208
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nes 256; Conser
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                               KVIVVFASGPDIEPLIKEMVRRNITDRIWLASEAWASSSLIAKPEYLDVVEGTIGFVLKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MTGDILLGGLFPIHFG-ISSKDENLAARPESTKCVRFNFRGFRWLQAMVFAIEEINNSSS
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TEVNSVGFLLAFTHNILLSISTFVCSYLGKELPENYNEAKCYTFSLLLNFVS-WIAFFTM
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                                                                                                                                                                                                                                               SAVSTAVANLLSLEYIPQISYASSSRLLSNKNQYKSFMRTIPTDEHQATAMADVIEYFQW
                                                                                                                                                                                                                                                                                                                                                                   LLPNITLGYRIFDTCNTVSKALEATLSFVAQNKIDSLNLDEFCNCTDHIPATIAVVGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                           LPGDFLLAGLFSLHGDCLQVRHRPLVTSCDRPDS--FNGHGYHLFQAMRFTVEEINNSSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ELSFULLVSLKLCFUCSLL-FIGRPRLWTCQLRHAAFGISFVLCVSCILVKTMVVLAVFR 695
                                                                                                            VWISLIGSYGDYGQLGVQALEELAVPRGICVAFKDIVPFSARVGDPRMQSMMQHLAQART
                                                                                                                                        NWVIAVASDDDYGRPGIEKFEKEMEERDICIHLNELI--SQYFEDCEIKALVDRIENSTA
                                                                                                                                                                                                                  TDHAVTTAALLGPFLMPLVSYEASSVVLSAKRKFPSFLRTVPSDRHQVEVMVQLLQSFGW
                                                                                                                                                                                                                                                                                                                              LLPNITLGYELYDVCSESANVY-ATLRVLALQGPRHIEIQK--DLRNHSSKVVAFIGPDN 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FSTKVPTFYRTW-AQNHGAGLFVIVSSTVHLLICLTWLVMWTPRPTREYQRFPHLVILEC
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Llarity 30.8%;
Conservative 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1371; DB 13;
Pred. No. 2.06e-263;
237; Mismatches 284;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
Last sequence update)
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RESULT AND SERVICE SERVICES OF SERVICES OF
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                                                                                  Query Match
Best Local S
Matches 26
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073639;
01-AUG-1998 (TIEMBLIEL 0
01-AUG-1998 (TIEMBLIEL 0
01-NOV-1999 (TIEMBLIEL 0
                                                                                                                                                                 Pheromone.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                   MEDLINE; 9
NAITO T.,
NAKANISHI
                                                                                                                                                                                                                                    Fugu.";
Proc. Natl. Acad. Sci. U.S.A
EMBL; AB008861; BAA26126.1;
PFAM; PF00003: 7tm.3; 1.
PFAM; PF01094; ANF_receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PHEROMONE
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                                                                                                                                                                                                                PRINTS; PR00248; GPCRMGR
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                                                                                                                                                                                                                                                                                                                                                                                                                                    EQUENCE
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                                          53
  35
GDFLLAGLESLHGDCLQVRHRPLVTSCDRPD-S-FNGHGYHLFQAMRFTVEEINNSSALL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  G-VAV-QQ--RQV-P--G-----LKEF-EESYVRAVTAAPS-ACPEGSWCSTNQLCRECH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GNIPGFREFLQQVQPKRGSHNEFVREFWEETFNCYLEDSPRLQESENGSDSFRPLCTSEE
                                      GDIILGGLFSLHDMVVE-PNLPFTSTPPPTQCTRFSFRTFRWMQTMIFAVEEINRNAEIL 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VSWIAFFTMA-SIYQGSYLPAVNVLAGLTTLSGGFSGYFLPKCYVILCRP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DEIIFITCNEGSYMALGFLIGYTC-LLAAICFFF-AFKSRKLPENFTEAKFITFCMLIFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TPVVRSAGGRLCFLMLGSLVAGSCSFYSFFGEPTVPACLLRQPLFSLGFAIFLSCLTIRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HICOPCGTEEWAPKESTTCFPRTVEFLAWHEPISLVLIAANTLLLLLLVGTAGLFAWHFH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SICTKCPNNSWSSGNHTFCFLKEIEFLAWSEPFGIALAICAVLGVLLTAFVMGVFVRFRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HLDINKTKIQWHGKNNQVPVSVCTTDCLAGHHRVVVVGS-HHCCFECVPCEAGTFLNMSEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KLLIDNTKMMWNAYSSEVPFSNCSEDCEPGTRKGIIDSMPTCCFECTECSDGEYSDHKDA
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                                                                                       260;
                                                                                                         Similarity
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                                                                                                                                                                       880
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                                                                                  21.1%;
larity 30.9%;
Conservative 2
                                                                                                                                                                       ΑA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tetraodontoidei; Tetraodontidae;
                                                                                                                                                                                                                                                                                                                                                                                       YAMAMOTO
                                                                                                                                                                       97464 MW;
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07,
12,
                                                                                                                                                                                                                                                                                                     S.A.
                                                                                Score 1339; DB 13;
Pred. No. 2.79e-256;
Pred: Mismatches 299;
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Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                             the Ca2+-sensing
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                                                                                                                           Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fugu.
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Eukeryota; Metazoa; Euteleostei; Ostariophysi; Cypriniformes;
Cyprinoidea; Cyprinidae; Cyprininae; Carassius.
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"Cloning and localization of two multigene receptor goldfish olfactory epithelium.";

Proc. Natl. Acad. Sci. U.S.A. 95:11987-11992(1998).

EMBL. AF083080; AAC64075.1;

PFAM: PF00003; 7tm_3: 1.

PFAM: PF01094; ANF_receptor; 1.

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                                                                                 ILLSISTFVCSYLGKELPENYNEAKCVTFSLLLNFVS-WIAFFTMASIYQGSYLPAVNVL
                                                                                                                                                                -CSFYSFEGEPTVPACLLRQPLFSLGFAIFLSCLTIRSFQLVIIFKFSTKVPTFYRTWAQ
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Pred. No. 1.74e-246;
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SEQUENCE
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Eukaryota; Metazoa; Chordata; Carniata; Vertebrata; Actinopterygii;
Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorpha;
Tetraodontiformes; Tetraodontoidei; Tetraodontidae; Fugu.
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                                                                                                                                                                        WAARLQKRPLSVCSQSCIPGFRQAVIKGKPICCFTCVACAAGEISNSSNSAECLQCPLEF
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GRLCFLMLGSLVAGS-CSFYSFFGEPTVPACLLRQPLFSLGFAIFLSCLTIRSFQLVIIF
                                                                         WAPKESTTCFPRTVEFLAWHEPISLVLIAANTLLLLLLVGTAG
                                                                                              WSNEDHSQCVPKVIEFLSFEETMG-ALLAAVSLFGAALTSLVFCVF-FRFRHTPLVKASN
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Pred. No. 2.25e-229;
227; Mismatches 311;
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NAITO T., SAITO Y., YA
NAKANISHI S., BRENNER
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
Neopterygii, Teleostei; Euteleostei; Acanthopterygii; Percomorpha;
Tetraodontiformes; Tetraodontoidei; Tetraodontidae; Pugu.
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SPSGTSHCTSPKGIKTTELLQHLSKVNFTTPQGKHLYFRGADIPAMYDLINWQ-SGTDGT
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                                                CSTN-QL-
                                                                                            SETSGDLNASLPPCSGAESLEGVOHPFTDTSHLRVTYNVYLAVYAAANALHSLLSCPIHN
                                                                                                                                                                                                                                              VGDPRMQSMMQHLAQARTTVVVVVFS-NRHLARVFFRSVVLANLTGKVWVASEDWAISTYI
                                                                                                                                                                                                                                                                                                                                                                                         SDIYQAQALAQLVLRENWIWIGAVVANNDYGHVAVKVFQEQTQGKGVCLAFVETLQRETI
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                                                                                                                                               TSVTGIQGIGT-VLGVAVQOROVPGLKEF--E-ESYVR-A---VTA--APS-AC-PEGSW
                                                                                                                                                                                                LKDPDTSTVASGVVGVAIASQHIPGFDRFLRGLNPSLRPSDKFLQEFWEEEFGCSPSPPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                875 AA;
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                                                -C-RECHTFTT-RNMP-TLGAFS-MSAAYRVYEAVYAVAHGLHQLLGC----
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. 07, Last sequence. 12, Last annotation.
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Pred. No. 1.31e-223;
221; Mismatches 326;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          J.,
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annotation
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RESULT 11

ID 070410;
AC 070410;
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AC 070410;
DT 01-AUG-1998 (TIEMBLIE1. 07, C1)
DT 01-AUG-1998 (TIEMBLIE1. 12, L2)
DT 01-AUG-1999 (TIEMBLIE1. 12, L2)
DT 01-AUG-1999 (TIEMBLIE1. 12, L2)
DT 01-AUG-1998 (TIEMBLIE1. 12, L2)
DT 01-AUG-1998 (MOUSE).

OC ENARTYOTA: METAZOA: ChOrdata:
OC ENARTYOTA: METAZOA:
RC TISSUE-VOMERONSAL NEURONS;
RA RYBA N.J. P. TIRINDELLI R.;
RA RYBA N.J. P. TIRINDELI R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δÃ
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Best Local S
Matches 24
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SEQUENCE FROM N.A.

TISSUE-VOMERONASAL NEURONS;

RYBA N.J.P., TIRINDELLI R.;

SUBmitted (MAR-1998) to the EMBL/
SMBL/ AF053986; AAC08413.1; -.

EMBL; AF053986; AAC08413.1; -.

EPAM; PF00003; 7tm_3; 1.

PFANT; PF01094; AME_receptor; 1.

PRINTS; PR00248; GPCRWGR.

SEQUENCE 912 AA; 102348 MW; 3
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                                                                                               LGYQIFDSCYTISKAMESSL-VF-LTG--QEEFKPNFRNSTGSTLAALVGSCGSSLSVAA 165
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larity 29.6%;
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                                                                                                                                                                                                                                                       Score 1170; DB 11;
Pred. No. 9.87e-219;
229; Mismatches 300;
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                                               SEQUENCE FROM N.A.
TISSUE-VOMERONASAL NEURONS;
RYBA N.J.P., TIRINDELLI R.;
Submitted (MAR-1998) to the EI
EMBL; AF053985; AAC08412.1;
PPAM; PF000003; 7tm_3:
PFAM; PF01094; ANF_Feceptor;
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O1-AUG-1998 (TrEMBLrel 07,
O1-AUG-1998 (TrEMBLrel 07,
O1-MAY-1999 (TrEMBLrel 10,
PUTATIVE PHEROMONE RECEPTOR
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070409
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RYBA N.J., TIRINDELLI R.;

RYBA N.J. TIRINDELLI R.;

"A new multigene family of putative
Neuron 19:371-379(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-VOMERONASAL NEURONS
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Matches
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035269
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          PUTATIVE PHEROMONE
GO-VN5.
Rattus norvegicus
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 Eukaryota;
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                                                                                                                                                                                     R-FPHLVILECTEVNSVGF--LLAFTHNILLSISTFVCSYLGKELPENYNEAKCVTFSLL
                                                                                                                                                                                                            SEFGQ-IILWCNEGSTLAFYCVLGYL-GFLASLSLLI-AFLARRLPDSFNEAKTITFSML
                                                                                                                                                                                                                                  IRSFQLVIIFKFSTKVPTFYRTWAQNHGAGLFVIVSSTVHLLICLTWLVMWTPRPTREYQ
                                                                                                                                                                                                                                                     AKTFIVVVAFK-AIKPGSILKMGMVTRLSNAIVCCGSIIQVCICAVWLGTYPPFPDVDMH
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3 (TrEMBLrel. 05,
9 (TrEMBLrel. 10,
HEROMONE RECEPTOR.
 Metazoa;
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larity 28.5%;
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 Chordata;
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Pred. No. 2.75e-197;
234; Mismatches 301;
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 Craniata;
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Matches 20
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EMBL: AF016182: AAC53329.1; -.
PFAM: PF00003; 7tm_3; 1.
PFAM: PF01094: ANE-receptor: 1.
SEQUENCE 779 AA: 88096 MW: B89CE4D5 CRC32;
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SEQUENCE FROM N.A.
STRAIN-SPRAGUE-DAWLEY;
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                 .. S
                                                     TFSLLLNFVS-WIAFFTMASIYQGSYLPAVNVLAGLTTLSGGFSGYFLPKCYVILCRPEL
                                                                                AFSMLV-FCSVWVTFLPVYHSTKGKNMVAMEVFSILASSTSLLGIIFAPKCYLILLRPER
                                                                                                            TREYOR-FPHLVILECTEVNSVGFL--LAFTHNILLSISTFVCSYLGKELPENYNEAKCV
                                                                                                                                                                   SCLTIRSFQLVIIFKFSTKVPTFYRTWAQNHGAGLFVI-VSSTVHLLICLTWLVMWTPRP
                                                                                                                                                                                          STVLAKTITVVIAFKITS--PGRIRRWLLISRAPNFIIPLCTLLQVFLSGIWLTTSPPFI
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Pred. No. 4
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No. 4.63e-175;
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Best Local Similarity 31.2%;
Matches 140; Conservative
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygi
Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes;
Cyprinoidea; Cyprinidae; Cyprininae; Carassius.
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CAO Y., OH B.C., STRYER L.;
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SEQUENCE 458 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SISTEVCSYLGKELPENYNEAKCVTESLLLNEVS-WIAFETMASIYQGSYLPAVNVLAGL
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Pred. No. 1.73e-154;
122; Mismatches 172;
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PFAM; PF01094; ANF_receptor; 1.
SEQUENCE 850 AA; 97415 MW;
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MATISURAMI H., BUCK L.B.;

"A multigene family encoding a diverse array of putative pheromone receptors in mammals.";

Cell 90:775-784(1997).

CEMBL: AF011411; AAC53401.1; -.
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Eutheria; Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           132 LRNHSSKVVAFIGPDNTDHAVTTAALLG-PFLMPLVSYEASSVVLSAKRKFPSFLRTVPS
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                        TFSMLV-FCSVWITFLPVYHSTRGRVMVVVEVFSILASSAGLLMCIFVPKCYVILIRPD
                                                                                                                                                                                                                                                                                                                   LVTFVKYKDTPTVKANNRILSYILLISLVFCFLCSLL-FIGPPDQVTCIFQQTTFGVLFT 661
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FVNYFCYLDDSCAIGLIGPSWKTSLKLAMHSSMPLVFFGPFNPNLRDHDRLPHVHQVAPK 188
TFSLLLNEVS-WIAFFTMASIYQGSYLPAVNVLAGLTTLSGGFSGYFLPKCYVILCRPE
                                                                                         RPTREYQR-FPHLVILECTEVNSVGFLLAFTHNILLSISTFVCSYLGRELPENYNEAKCV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KDFT-LNLFHGIITFEHHRFEIPKLNKFMQTMNTAKYPVDISHTILEWNYFNCSISKNSI 365
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YMTRATIYDKHIMTSSAKVVIIYGEMNSTLEASFRRWEELGA-R-RIWITTSQWDVITNK 306
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                                                                                                                                     FIDRDIQSEHGKIVIL-CNKGSVIAFHVVLGYLGSLALGSFTLAFLARNLPDTFNEAKFL 779
                                                                                                                                                                                                                                                                                     AGLEAWHEHTPVVRSAGGRLCFLMLGSLVAGS-CSFYSFFGEPTVPACLLRQPLFSLGFA
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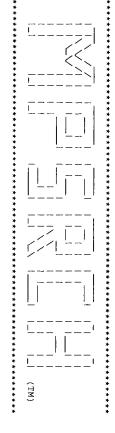
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Search completed: Fri Mar 17 13:09:24 Job time : 242 secs.



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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Mar 17 13:03:18 2000; MasPar time 44.06 Seconds
569.357 Million cell updates/sec

Tabular output not generated.

Title: >US-09-361-652-1
Description: (1-840) from US09361652.pep
Perfect Score: 6338

Sequence: 1 MLFWAAHLLLSLQLVYCWAF.....NNTEHFQASIQDYTRRCGTT 840

Scoring table: PAM 150
Gap 11

rched: 82229 seqs, 29854865 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot38 1:swissprot

Statistics: Mean 54.039; Variance 93.294; scale 0.579

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

22220484321 3221484321	Result
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Tharyota, Thartes; Catarrhini;
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POLLAK M.R., BROWN E.M., CHOU Y.H., HEBERT S.C., STEINMANN B., LEVI T., SEIDMAN C.E., SEIDMAN J.G "Mutations in the human Ca(2+)-sensing receptor hypocalciuric hypercalcemia and neonatal severe hyperparathyroidism."; Cell 75:1297-1303(1993).
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J. Biol. Chem. 270:12919-12925(1995).
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                                                                                                                                                                                                                                                                                                                                                          Commun.
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                                                                                                                                                                                                                                                                             HOLLOSCHI A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata;
                                                                                                                                                                                                                                                                                                                                                          214:524-529(1995)
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                                                                                                                                                                                                                                                                               HAFNER M.,
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                                                                                 1.G.,
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                                                                                     MARX S.
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                                                              cause familial
                                                                                                                                                                                                                                                                                 FLOCKERZI V.,
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HORMONE. SYMPTOMS ARE SEIZURES, TETANY AND CRAMPS.
-!- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.

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-IT FUNCTION: SOUSE CHANGES IN THE EXTRACELLULAR CONCENTRATION OF CALCIUM IONS. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY A G-PROTEIN THAT ACTIVATES A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM.

-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-!- ALTERNATIVE PRODUCTS: TWO ISOFORMS SEEM TO BE PRODUCED BY ALTERNATIVE PRODUCTS: TWO ISOFORMS SEEM TO BE PRODUCED BY ALTERNATIVE SPLICING.
-!- TISSUE SPECIFICITY: FOUND IN KIDNEY, BUT NOT IN BRAIN, LUNG, LIVER, HEART, SKELETAL MUSCLE, OR PLACENTA.
-!- DISEASE: DEFECTS IN CASR ARE A CAUSE OF FAMILIAL HYPOCALCIURIC HYPERCALCEMIA (FHH) AND NEONATAL SEVERE HYPERPARATHYROIDISM (NSHPT), TWO INHERITED CONDITIONS CHARACTERIZED BY ALTERED CALCIUM HOMEOSTASIS: THE MUTATIONS REDUCE THE ACTIVITY OF THE RECEPTOR. FHH AFFECTED INDIVIDUALS EXHIBIT MILD OR MODEST HYPERCALCEMIA, FHAREATIVE HYPOCALCIURIA, AND INAPPROPRIATELY NORMAL PTH LEVELS. IN CONTRAST, NSHPT IS A RARE AUTOSOMAL RECESSIVE LIFE-THREATENING DISORDER CHARACTERIZED BY VERY HIGH SERUM CALCIUM CONCENTRATIONS, SKELETAL DEMINERALIZATION, AND PARATHYROID HYPERPLASIA. IN SOME INSTANCES NSHPT HAS BEEN DEMONSTRATED TO BE THE HOMOZYGOUS FORM OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POLLAK M.R., BROWN E.M., ESTEP H.L., MCLAINE P.N., KIFOR O., HEBERT S.C., SEIDMAN C.E., SEIDMAN J.G.:
"Autosomal dominant hypocalcaemia caused by a Ca(2+)-sensing gene mutation.";
Nat. Genet. 8:303-307/1904\\(\)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE; 97442275.
WARD B.K., STUCKEY B.
RATAJCZAK T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BARON J., WINER K.K., YANOVSKI J.A., CUNNINGHAN ZIMMERMAN D., CUTLER G.B. JR.; "Mutations in the Ca(2+)-sensing receptor gene dominant and sporadic hypoparathyroidism.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AIDA K., KOISHI S., INOUE M., NAKAZATO M., TAWATA M., ONAYA T.; "Familial hypocalciuric hypercalcemia associated with mutation in the human Ca(2+)-sensing receptor gene.":
J. Clin. Endocrinol. Metab. 80:2594-2598(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                associated with familial hyp
Hum. Mutat. 10:233-235(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Mutations in the human Ca(2+)-sensing-receptor gene that cause familial hypocalciuric hypercalcemia."; am. J. Hum. Genet. 56:1075-1079(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHOU Y.-H.W., POLLAK M.R., ATKINSON A.B., PAPAPOULOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VARIANT FHH ARG-174.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VARIANTS ADHP THR-116; HIS-681 AND MEDLINE; 96311554.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VARIANTS FHH MET-62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Calcium-sensing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clin. Invest.
                                                                                                                                                                                                                                                                                                                                                                                                                                                novel mutation (L174R)
CA(2+) LEVELS.

CA(2+) LEVELS.

DISEASE: DEFECTS IN PCAR1 ARE ALSO THE CAUSE OF AUTOS DISEASE: DEFECTS IN PCAR1 ARE ALSO THE CAUSE OF AUTOS HYPOPARATHYROIDISM (ADHP). ADHP IS CHARACTERIZED BY HAVPOPARATHYROIDISM (ADHP). TO INADEQUATE SECRETION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  neonatal hyperparathyroidism.";
Clin. Invest. 96:2683-2692(1995)
                                                                        HYPOCALCEMIA
                                                                                       DISEASE: DEFECTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HEATH
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                                                                       N CASR ARE ALSO
IN WHICH THE RE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , WOODING C., HUGHES I.A.,
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PATERSON C.
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BROWN
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                                                                     OF AUTOSOMAL ACTIVATED AT
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F PARATHYROID
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                                                                       SUBNORMAL
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                                         DOMINANT
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EMBL; X81086; CAA56990.1; --
EMBL; U20759; AAA86504.1; --
EMBL; U20760; AAA86504.1; --
EMBL; D50855; BAA09453.1; --
EMBL; S83176; AAB46873.1; --
EMBL; S68032; AAB29413.1; --
EMBL; S68033; AAB29414.1; --
EMBL; S68033; AAB29415.1; --
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VARSPLIC
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DOMAIN
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PFAM; PF01094; ANF_receptor; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MIM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a c between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformattics Institute. There are no restrict use by non-profit institutions as its content is modified and this statement is not removed. Usage by and fo entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disease mutation; Alternative splicing; SIGNAL 1 19 POTENTIAL.
                                                                            VARIANT
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; 601198; -
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                                                                       /FTId=VAR_003585.

R -> x (IN MILD FHH /
/FTId=VAR_003586.

R -> C (IN FHH).
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EXTRACELLULAR (
VII (POTENTIAL)
CYTOPLASMIC (PO
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CYTOPLASMIC (POTENTIAL).
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-> A (IN FHH).
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l Similarity 32.0%;
273; Conservative
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Pred. No. 4.19e-266;
230; Mismatches 276;
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proc. Na+1 - ---
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RUAT M.,
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RICCARDI D., PARK J., LEE W., GAMBA G., BROWN E.M., "Cloning and functional expression of a rat kidney calcium/polyvalent cation-sensing receptor."; Proc. Natl. Acad. Sci. U.S.A. 92:131-135(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
EXTRACELULAR CALCIUM-SENSING RECEPTOR PRECURSOR (CASR) (PARATHYROID CELL CALCIUM-SENSING RECEPTOR).
                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00979; G_PROTEIN_RECEP_F3_1; PROSITE; PS00980; G_PROTEIN_RECEP_F3_2; PROSITE; PS00981; G_PROTEIN_RECEP_F3_3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-slb.ch/announce/or send an email to license@isb-slb.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           between the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There a use by non-profit institutions as long as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proc. Natl. Acad. Sci. U.S.A. 92:3161-3165(1995).

-:- FUNCTION: SENSE CHANGES IN THE EXTRACELULAR CONCENTRATION OF CALCIUM IONS. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY A G-PROTEIN THAT ACTIVATES A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM.
                                                                                                                                                                                                                                                                                                                     G-protein
SIGNAL
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PFAM; PF01094; ANF_receptor; 1.
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SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS
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SNOWMAN A.M.,
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V (POTENTIAL).
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                                                                                    IILFKPSRNTIEEVRSSTAAHA
                                                                                                             NYNEAKCVTESLLLNEVSWIAFETM- AS IYQGSYLPAVNVLAGLTTLSGGESGYELPKCY
                                                                                                                                                              WLVMWTPRPTREYQRFPHLVILECTEVN--SVGFLLAFTHNILLSISTFVCSYLGKELPE
                                                                                                                                                                                      WLYTAPPSSYRNHELEDEIIFITCHEGSLMALGSLIGYTC-LLAAICFFF-AFKSRKLPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PNITLGYELYDVCSESANVY-ATLRVLALQGPRHIEIQK--DLRNHSSKVVAFIGPDNTD
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d. No. 6.74e-265;
Mismatches 285;
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  01-JUL-1993 (Rel. 26, CT
01-NOV-1995 (Rel. 32, La
15-DEC-1999 (Rel. 39, La
METABOTROPIC GLUTAMATE R
GRM5 OR MGLUR5.
                                                                                                                                                                                                                                                           EMBL; D10891; -; NOT_1
EMBL; S64315; AAB27666
PIR; A42916; A42916.
GCRDB; GCR_0444; -.
TRANSMEM
DOMAIN
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CHAIN
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Multigene
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"A variant of metabotropic glutamate receptor subtype 5: an evolutionally conserved insertion with no termination codon.";

Biochem. Biophys. Res. Commun. 194:522-627(1993).
-!- EUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY A G-PROTEIN THAT ACTIVATES A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM AND GENERATES A CALCIUM-ACTIVATED
                                                                                                                                                                                     PFAM; PF00003; PFAM; PF01094;
                                                                                                                                                                                                          PROSITE; PS00979; G_PROTEIN_RECEP_F3_1; PROSITE; PS00980; G_PROTEIN_RECEP_F3_2; PROSITE; PS00981; G_PROTEIN_RECEP_F3_3;
                                                                                                                                                                                                                                              GCRDB; GCR_0444;
GCRDB; GCR_0760;
                                                                                                                                                                                                                                                                                                                      entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long modified and this statement is not removed
                                                                                                                                                                                                                                                                                                                                                                        the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABE T., SUGIHARA H., NAWA H., SHIGEMOTO R., MIZUNO N., NA "Molecular characterization of a novel metabotropic gluta receptor mGluR5 coupled to inositol phosphate/Ca2+ signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eutheria;
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                                                                          DOMAIN
                                                                                                                           DOMAIN
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MEDLINE; 92317054.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biol. Chem.
                                                                                                                                                                                                                                                                                                                                                          s SWISS-PROT entry is copyright. It is produced through a collab-
ween the Swiss Institute of Bioinformatics and the EMBL outset
European Bioinformatics Institute. There are no restrictions
by non-profit institutions as long as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: BELONGS T
STRONGEST, TO MGLUR1.
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pled receptor; T
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a; Chordata; Craniata; Vertebrata;
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V (POTENTIAL).
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II (POTENTIAL).
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LY 3 OF G-PROTEIN COUPLE
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                                                                                              KESTK-VPTFYRTWAQNHGAGLEV-IVSSTVHLLICLTWLVMWTPRPTREYQREPHLVIL
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                                                                                                                                                 GRLCFLMLGSLVAGS-CSFYSFFGEPTVPACLLRQPLFSLGFAIFLSCLTIRSFQLVIIF
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  TMASIYQGSYLPAVNVLAGLTTLSGGFS:
                                                             ICNTIN-LGVVTPLGYNGLLILSCIF-YAFKTRNVPANFNEAKYIAFTMYITCIIWLAF-
                                                                                                                                                                                                                                                                                                YKVNFL-LHENTVAFDDNGDTLGYYDIIAWDWNGPEWTFEIIGSASLSPVHLDINKTKIQ
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                       -VP-IYFGSNYKIIIMCFSVS-LSATVALGCMFVPKVYIILAKPERNVRSAFTIS
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 -GY-FLPKCYVILCRPELNNTEHFQAS
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No. 2.46e-166
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MGRS_HUMAN STANDARD;
P41594;
01-NOV-1995 (Rel. 32, Cre
01-CCT-1996 (Rel. 34, Las
15-DEC-1999 (Rel. 39, Las
METABOTROPIC GLUTAMATE RI
                                                                                                                                                   GCRDB; GCR_0761
GCRDB; GCR_1002,
GCRDB; GCR_11003,
GCRDB; GCR_11003,
GCRDB; GCR_1317,
MIM; 604102;
PROSITE; PS00980
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PROSITE; PS00980
PFAM; PF00003; 7
PFAM; PF01094; P
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EMBL; D28539;
EMBL; S64316;
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MEDIINE: 94197696.
MINAKAMI R., KATSUKI F., YAMAMOTO T., NAKAMURA K., S
MINAKAMI R., KATSUKI F., YAMAMOTO T., NAKAMURA K., S
MINAKAMI R., KATSUKI F., YAMAMOTO T., NAKAMURA K., S
MINAKAMI R., KATSUKI F., YAMAMOTO T., NAKAMURA K., S
MINAKAMI R., S
MINAKAMI R.
SIGNAL
CHAIN
DOMAIN
TRANSMEM
DOMAIN
TRANSMEM
                                                                                                                   G-protein
Multigene
                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Variant of metabotropic glutamate receptor subtype 5: an lutionally conserved insertion with no termination codon."; them. Biophys. Res. Commun. 194:622-627(1993).

FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY A G-PROTEIN THAT ACTIVATES A PHOSPHATIDYLINOSITOL-MEDIATED BY A G-PROTEIN THAT ACTIVATES A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM AND GENERATES A CALCIUM-ACTIVATED
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sapiens (Human).
iryota; Metazoa; Chordata; Craniata; Vertebrata;
reria; Primates; Catarrhini; Hominidae; Homo.
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GCR_1003;
GCR_1317;
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PS00980; G_PROTEIN_RECEP_F3_2;
PS00981; G_PROTEIN_RECEP_F3_3;
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                                                                                                                                                                                                                                                                                                                                                     BAA05891.1;
BAA05892.1;
AAD13954.1;
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                                                                                                                        EWAPKESTTCFPRTVEFLAW-H-EPISLVLIAANTLLLLLLVGTAGLFAWHFHTPVVRSA
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                                              LAGSKKKICTK-KPREMSACAQLVIAFILICIQLGIIVALFIMEPPDIMHDYPSIRE-VY
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Pred. No. 1.25e-165;
214; Mismatches 326;
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"A family of metabotropic glutamate receptors.";

Neuron 8:169-179(1992).

-i- function: receptor for glutamate. The activity of this is mediated by a G-protein that inhibits adenylate cyclase may mediate suppression of neurotransmission or may be instanced by a G-protein that inhibits adenylate cyclase may mediate suppression of neurotransmission or may be instanced by a G-protein.

-i- SYMALPTOGENESIS OR SYMAPTIC STABILIZATION.

-i- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

-i- TISSUE SPECIFICITY: IS WIDELY DISTRIBUTED IN THE CNS ANI EXPRESSION IS SEEN IN GOLGI CELLS OF THE CEREBELLUM AND PARTICULAR NEURONAL CELLS IN OTHER BRAIN REGIONS.

-i- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED REC.

-i- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED REC.
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RESULT

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01-JUL-1993
01-JUL-1993
15-JUL-1999
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CARBOHYD
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TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           O'HARA P.J., SHEPPARD P.O., THOGERSEN H., VENEZIA D., HALDEMAN B. MCGRANE V., HOUAMED K.M., THOMSEN C., GILBERT T.L., MULVHHILL E.R. "The ligand-binding domain in metabotropic glutamate receptors is related to bacterial periplasmic binding proteins.";
Neuron 11:41-52(1993).

-i- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPT IS MEDIATED BY A G-PROTEIN THAT INHIBITS ADENYLATE CYCLASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TANABE Y., MASU M., ISHII
"A family of metabotropic
Neuron 8:169-179(1992).
[2]
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                                                                                                                                                                                                                                                                                                                 EMBL; M92077; -; NOT_ANNOTATED_CDS.
EMBL; M90518; AAA93190.1; -.
PIR; JH0563; JH0563.
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GRM4 OR MGLUR4.
                                                                                                                                                                                                                                                                                           GCRDB;
                                                                                                                                                                                                            Multigene family.
                                                                                                                                                                                                                        G-protein coupl
                                                                                                                                                                                                                                  PFAM; PF00003;
PFAM; PF01094;
                                                                                                                                                                                                                                                                                                        GCRDB;
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SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

TISSUE SPECIFICITY: IS WIDELY DISTRIBUTED IN THE CREBELLUM.

EXPRESSION IS SEEN IN THE GRANULE CELLS OF THE CEREBELLUM.

SIMILARITY: BELLONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                            GCR_0363;
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                                                                                                                                                                                                                                                                                                                                                             requires a license agreement (S an email to license@isb-sib.ch).
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(Rel. 26, Last sequence u)
(Rel. 38, Last annotation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    T., SHIGEMOTO R., NAKA
glutamate receptors.";
                    CYTOPLASMIC (PO
VI (POTENTIAL).
EXTRACELLULAR (
VII (POTENTIAL)
                                                                                                                                                                                                                       Transmembrane; Glycoprotein;
                                                                                          III (POTENTIAL)
CYTOPLASMIC (P
IV (POTENTIAL)
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                                                        (POTENTIAL).
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                                                                                         FLPKCYVILCRPELN
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Q -> R (IN REF. 2).
MW; 95F3E7D6 CRC32;
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Pred.
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No. 3.01e-159
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  MEDLINE: 95342351.
FLOR P.J., LUKIC S., I
"Molecular cloning, fi
characterization of ti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE; 9814
WU S., WRIGHT
ROSTECK P.R.
 DOMAIN
TRANSMEM
DOMAIN
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DOMAIN
                                                                                                                                                                                       PROSITE; PS00979; G_PROTEIN_RECEP_F3_1; PROSITE; PS00980; G_PROTEIN_RECEP_F3_2; PROSITE; PS00981; G_PROTEIN_RECEP_F3_3;
                                                                                                                                                                                                                                                                      EMBL;
                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restruct by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WU S., WRIGHT R.A., ROCKEY P.K., BURGETT S.G., ARNOLD J.S ROSTBCK P.R. JR., JOHNSON B.G., SCHOEPP D.D., BELAGAJE R. "Group III human metabotropic glutamate receptors 4, 7 an molecular cloning, functional expression, and comparison pharmacological properties in RGT cells.";
Brain Res. Mol. Brain Res. 53:88-97(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Brain
[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MAKOFF A., LELCHUK R., OXER "Molecular characterization glutamate receptor type 4.", Brain Res. Mol. Brain Res. 3
                                                                                                                                          G-protein
Multigene
                                                                                                                                                                PFAM; PF01094;
                                                                                                                                                                                                                                            GCRDB;
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-!- FUNCTION: RECEPTOR FOR GLUTAMATE.
S MEDIATED BY A G-PROTEIN THAT I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=BRAIN;
MEDLINE; 96346635
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METABOTROPIC GLUTAMATE
                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
TISSUE SPECIFICITY: STRONGLY EXPRESSED IN THE CEREBEI
EXPRESSED AT LOW LEVELS IN HIPPOCAMPUS, HYPOTHALAMUS
THALAMUS. NO EXPRESSION DETECTED IN LIVER.
SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED
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                                                                                                                                                                                                                                                                    X80818; CAA56784.1;
U92457; AAB51762.1;
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                       LYMPKVYIILFHPEQN
                                                            VPETFNEAKPIGETMYTTCIVMLAFIPIFFGTSQSADKLYIQTTLTVSVSLSASVSLGM
                                                                                          LVMWTPRPTREYQ--R-F-PHLV--ILECTEVNSVGFLLAFTHNILLSISTFVCSYLGKE
                                                                                                                FVVDPSHSVVDFQDQRTLDPRFARGVLKC-DISDLSLICLLGYSMLLMVTCTVYAIKTRG
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YFLPKCYVILCRPELN
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The tipocampus on the control of litamate receptors in inducing different patterns of calcium release in xenopus oocytes.";

Lipoc. Natl. Acad. Sci. U.S.A. 89:1031-1035(1992).

C. I- FUNCTION. RECEPTOR FOR GUITAMATE. THE ACTIVITY OF THIS RECEPTOR IS CONCINCIAN. RECEPTOR FOR GUITAMATE. THE ACTIVITY OF THIS RECEPTOR IS CONCIONED MESSENGER SYSTEM. MAY PARTICIPATE IN THE CENTRAL CALCIUM SECOND MESSENGER SYSTEM. MAY PARTICIPATE IN THE CENTRAL COATION OF GUITAMATE IN THE CAS. SUCH AS LONG-TERM DOTENTIATION IN COMPANIES AND LONG-TERM DEPRESSION IN THE CEREBELLUM.

C. I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

C. I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

C. I- ALTERNATIVE PRODUCTS: THREE ISOFORMS; IA (SHOWN HERE), 1B AND 1C: ARE PRODUCED BY ALTERNATIVE SPLICING. 1B AND 1C ARE C-TERMINALLY TISSUE SPECIFICITY: IS PREDOMINANTLY EXPRESSED IN CEREBELLAR COLORS OF THE HIPPOCAMPUS, AND ALTERNATIVE OF THE OF THE OFFICE OF THE HIPPOCAMPUS, AND ALTERNATIVE OF THE OFFICE OF THE HIPPOCAMPUS.
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01-NOV-1991 (Rel. 20, Las
15-DEC-1999 (Rel. 39, Las
METABOTROPIC GUUTANATE R
                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entre the European Bioinformatics Institute. There are no restricted the European Bioinformatics Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Cloning, expression, and gene structure glutamate receptor from rat brain."; Science 252:1318-1321(1991).
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MASU M., TANABE Y., TSUCHIDA K.,
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MULVIHILL E.R., ALMERS W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Sequence and expression Nature 349:760-765(1991).
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Eukaryota; Metazoa; Cho
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MISCELLANEOUS: ACTIVATED BY QUISQUALATE > GLOTAMATE TRANS-1- AMINOCYCLOPENTY1-1,3-DICARBOXYLATE; INHIBI
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SIMILARITY: BELONGS TO FAMILY
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GLN/PRO-RICH.
ASP/GLU-RICH (A)
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Pred. No. 4.63e-154;
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AQL (IN ISOFORM 1B).
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MISSING (IN ISOFORM 1C).
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2.";
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Homo sapiens (
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-!- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF TH MEDIATED BY A G-PROTEIN THAT INHIBITS ADENVLATE CYCL. MAY MEDIATE BY A G-PROTEIN THAT INHIBITS ADENVLATE CYCL. MAY MEDIATE SUPPRESSION OF NEUROTRANSMISSION OR MAY I SYNAPTOGENESIS OR SYNAPTIC STABILIZATION.

-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-!- TISSUE SPECIFICITY: WIDELY EXPRESSED IN DIFFERENT RECADULI BRAIN AS WELL AS IN FETAL BRAIN.
-!- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED STRONGEST, TO MGLUR3.
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                                                                                                                                                                                                                                                                                           s SWISS-PROT entry is copyright. It is produced ween the Swiss Institute of Bioinformatics and European Bioinformatics Institute. There are repy hymno-profit institutions as long as its or the swiss and the swiss are represented by non-profit institutions as long as its or the swiss are represented by non-profit institutions as long as its or the swiss are represented by non-profit institutions as long as its or the swiss are represented by non-profit institutions as long as its or the swiss are represented by non-profit institutions as long as its or the swiss are represented by non-profit institutions as long as its or the swiss are represented by non-profit institutions as long as its or the swiss and the swiss are represented by non-profit institutions as long as its or the swiss are represented by non-profit institutions as long as its or the swiss are represented by non-profit institutions as long as its or the swiss are represented by non-profit institutions as long as its or the swiss are represented by non-profit institutions as long as its or the swiss and the swiss are represented by non-profit institutions as long as its or the swiss are represented by non-profit institutions as long as its or the swiss are represented by non-profit institutions as long as its or the swiss are represented by non-profit institutions as long as its order by non-profit institutions as a long as its order by non-profit institutions as a long as its order by non-profit institutions as a long as its orde
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IV (POTENTIAL).
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GCR_1826; GCR_1982; GCR_1825;

U31215; AAA87844.1; U31216; AAA87844.1; L76627; AAB05337.1; L76631; AAB05338.1;

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PROTECTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR MEDIATED BY A G-PROTEIN THAT ACTIVATES A PHOSPHATIDYLINOSITOLOGICAL GUIM SECOND MESSENGER SYSTEM. MAY PARTICIPATE IN THE CENTRAL ACTION OF GLUTAMATE IN THE CNS, SUCH AS LONG-TERM POTENTIATION I THE HIPPOCAMPUS AND LONG-TERM DEPRESSION IN THE CEREBELLUM.

PROTECTION: INTEGRAL MEMBRANE PROTEIN.

ARE PRODUCED BY ALTERNATIVE SPLICING.

ARE PRODUCED BY ALTERNATIVE SPLICING.

ARE PRODUCED BY ALTERNATIVE SPLICING.
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"Cloning and expression of a human metabotropic glutamate receptor 1 alpha: enhanced coupling on co-transfection with a glutamate transporter.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MGR1_HUMAN STANDARD; PRT; 1:
Q13255; Q13256; Q14757; Q14758;
Q1-NOV-1997 (Rel. 35, Created)
Q1-NOV-997 (Rel. 35, Last sequence up
15-DEC-1999 (Rel. 39, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                   This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STEPHAN D., BON C., HOLZWARTH J.A., GALVAN M., PRUSS R.M.; "Human metabotropic glutamate receptor 1: mRNA distribution, chromosome localization and functional expression of two splice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
Eukaryota; M
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Catarrhini;
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i; Hominidae;
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PFAM; PF01094; ANF_receptor; 1.

G-protein coupled receptor; Transmembrane; Multigene family; Alternative splicing.
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 SEI--C-SRGPYYPWQLLQQIYKVNFL-LHENTVAFDDNGDTLGYYDIIAWDWNGPEWTF
                   GHVGLCDAMKPIDGSKLLDFLIKSSFIGVSGEEVWFDEKGDAPGRYDIMNLQYTEANR-Y
                                                                                                                                                                                                                    CLPDGQSLPPGRTKKPIAGVIGPGSSSVAIQVQNLLQLFDIPQIAYSATSIDLSDKTLYK 199
                                                                                                                                                                                                                                         QAMRETVEEINNSSALLPNITLGYELYDVCSESA-NVY-AT--LR-VL-ALQGPRH-IE- 127
                                                          RFQ-CRLPGHLLENPNFKRICTGNESLEENYVQDSKMGFVINAIYAMAHGLQNMHHALCP
                                                                             EDWAISTYITSVTGIQGIGTVLGVAVQQRQVPGLKEFEESYVRAVTAAPSA-CPEGSWCS
                                                                                                                    IVPFSARVGDPRMQSMMQHL-AQ-ARTTVVVVVFSNRHLARVFFRSVVLANLTGKVW-VAS
                                                                                                                                     KI-YSN-AGEKSFDRLLRKLRERLPKARVVVCFCEGMTVRGLLSAMRRLGVVGEFSLIGS
                                                                                                                                                           SFLRTVPSDRHQVEVMVQLLQSFGWVWISLIGSYGDYGQLGVQALEELAVPRGICVAFKD
                                                                                                                                                                              YFLRVVPSDTLQARAMLDIVKRYNWTYVSAVHTEGNYGESGMDAFKELAAQEGLCIAHSD
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CYTOPLASMIC (POTENTICH:
GLN/PRO-RICH:
GLN/PRO-RICH:
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VQL (IN ISOFORM BETA, REF.
P -> S (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                            NSNGKSVSWSEPGGGQVPKG -> KKROPEFSPSSQCPSAH
AQL (IN ISOFORM BETA).
MISSING (IN ISOFORM BETA).
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SER-RICH.
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V (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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No. 6.10e-152;
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                                       -EAVYAVAHGLHQLL-G
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GCRDB; GCR_2070; -.

MIM; 601115; -.

PROSITE; PS00979; G_PROTEIN_RECEP_F3_2; 1.

PROSITE; PS00980; G_PROTEIN_RECEP_F3_2; 1.

PROSITE; PS00981; G_PROTEIN_RECEP_F3_3; 1.

PFAM; PF010903; 7±m_3; 1.

PFAM; PF01094; ANY_receptor; 1.

G-protein coupled receptor; Transmembrane; Multigene family.
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014832;
01-NOV-1997 (Rel. 3
01-NOV-1997 (Rel. 3
01-NOV-1997 (Rel. 3
METABOTROPIC GLUTAN
                                                                                                                                                                                                                                                                                                                                                                    MAKOFF A., VOLPE F., LELCHUK R., HARRINGTON K., EMSON "Molecular characterization and localization of human glutamete receptor type 3.",

Brain Res. Mol. Brain Res. 40:55-63(1996).

-I- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF IS MEDIATED BY A G-PROTEIN THAT INHIBITS ADENYLATE
                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no was modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GRM3 OR MGLUR3
                                                                                                                                                  EMBL; X77748;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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- SUBCELLULAR LOCATION: I
- SIMILARITY: BELONGS TO
- SIMILARITY TO MGLUR2.
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LGFAIFLSCLTIRSFQLVIIFKFSTKVPTFYRTWAQNHGAGLFVIVSST-VHLLICLTWL
                                                                       SSFAICYSALLTKTNCIARIFD-GVKNGA-QRPKFISPSSQVFICLGLILVQIVMVSVWL
                                                                                                     LVGTAGLFAWHFHTPVVRSAGGRLCFLMLGSLVAGSC-SEYSFFGEPTVPACLLRQPLFS
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                                                                                                                                                                PCEAGTFLNMSELHICQPCGTEEWAPKESTTCFPRTVEFLAWHEPISLVLIAANTLLLLL
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                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE: PS00979; G_PROTEIN_RECEP_F3_1; PROSITE: PS00980; G_PROTEIN_RECEP_F3_2; PROSITE: PS00981; G_PROTEIN_RECEP_F3_3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WESTBROOK G.L.;
"Cloning and expression of rat metabotropic glutamate receptor reveals a distinct pharmacological profile.";
MO1. Pharmacol. 51:119-125(1997).

-:- FUNCTION: RECEPTOR FOR GLUTAWATE. THE ACTIVITY OF THIS RECIPION FOR GLUTAWATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE; 97168760. SAUGSTAD J.A., KINZIE
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Rattus norvegicus (Rat).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;

Eukaryota; Metazoa; Chiuroqnathi; Muridae; Murinae;
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01-NOV-1997 (Rel.
15-JUL-1998 (Rel.
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TISSUE SPECIFICITY: PROMINENT EXPRESSION IN OLFACTORY BULB,
PONTINE GRAY, LATERAL RETICULAR NUCLESS OF THE THALAMUS, AND
PIRIFORM CORTEX. LESS ABUNDANT EXPRESSION INCEREBRAL CORTEX,
HIPPOCAMPUS, CEREBELLUM, AND MAMMILLARY BODY.
SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR MEDIATED BY A G-PROTEIN THAT INHIBITS ADENYLATE CYCLASE
                                                                                                                                                                                                                                                                                                                                                         1094; ANF_receptor;
coupled receptor;
    (Rel. 35, Created)
(Rel. 35, Last sequence update)
(Rel. 36, Last annotation update)
GLUTAMATE RECEPTOR 8 PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
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V (POTENTIAL).
CYTOPLASMIC (POT
VI (POTENTIAL).
EXTRACELLULAR (P
VII (POTENTIAL).
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EXTRACELLULAR (P
III (POTENTIAL).
CYTOPLASMIC (POT
IV (POTENTIAL).
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I (POTENTIAL).
                                                                                                                                                                                                                                                                                                                    POTENTIAL.
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Best Local S
Matches 20
MGR8_MOUSE
P47743;
01-FEB-1996
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                                                                                                           MPKVYIIIFHPEQN
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                                                                                 LPKCYVILCRPELN
                                                                                                                                      NYNEAKCYTESLLLNEVSWIAFETMA-SIYQGS---YLPAVNVLAGLTTLSGGES-G-YE
                                                                                                                                                                TENEAKPIGETMYTTCIIWLAFIPIFEGTAQSAEKMYIQTTTLTVSMS-LSASVSLGMLY
                                                                                                                                                                                             WIPRPIREY
                                                                                                                                                                                                                     DPPHTIIDYGEQRTLDPENARGYLKC-DISDLSLICSLGYSILLMYTCTVYAIKTRGVPE
                                                                                                                                                                                                                                                                          MCFSYAALLTKTNRIHRIFEQGKKSVTA-PKFI-SPASQLVITFSLISVQLLGVFVWFVV
                                                                                                                                                                                                                                                                                                       GTAGLFAWHFHTPVVRSAGGRLCFLML-GSLVAGSCSFYSFFGEPTVPACLLRQPLFSLG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FLRTVPSDRHQVEVMVQLLQSFGWVWISLIGSYGDYGQLGVQALEELAVPRG-ICVAFKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EIQK-D--LRNHSSKVVAFIGPDNTDHAVTTAALLGPFLMPLVSYEASSVVLSAKRKFPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KCANGDPPIFTKPDKISGVIGAAASSVSIMVANILRLFKIPQISYASTAPELSDNTRYDF 191
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| Similarity 25.3%;
| 201; Conservative
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Pred. No. 5.33e-151;
228; Mismatches 305;
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                                    Query Match
Best Local S
Matches 21
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CARBOHYD
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PFAM; PF01094; ANE_receptor; G-protein coupled receptor; TMultigene family; Olfaction.
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DOMAIN
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-!- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY IS MEDIATED BY A G-PROTEIN THAT INHIBITS ADENYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "A novel metabotropic olfactory bulb.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00979; G_PROTEIN_RECEP_F3_1; PROSITE; PS00980; G_PROTEIN_RECEP_F3_2; PROSITE; PS00981; G_PROTEIN_RECEP_F3_3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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DUVOISIN R.M.,
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STRAIN=C57BL/6;
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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SUBSCELLUAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

TISSUE SPECIFICITY: STRONGLY EXPRESSED IN OLFACTORY BULB,

TISSUE SPECIFICITY: SUDD, AND MAMMILLARY BODY. WEAKER EXPRESSION

ACCESSORY OLFACTORY BULD, AND MAMMILLARY BODY. WEAKER EXPRESSION

IN THE RETINA, AND IN SCATTERED CELLS IN THE CORTEX AND HINDBRAIN.

SIMILARITY: BELONGS TO FAMILY 3 OF G-FROTEIN COUPLED RECEPTORS.
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MGI:109500; GRM8.
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HSQEYAHSIRLDGDIILGGLFPVHA---KG-ERG-V-PCG--DLKKEKGIHRLEAMLYAI
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                                        212;
                                                        Similarity
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908
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larity 25.2%;
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     MEDLINE; 98141892.
WU S., WRIGHT R.A.,
                                                                                             Eukaryota;
                                                                           Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NSHIKKCTGLERIARDSSYEQEGKVQFVIDAVYSMAYALHNMHKELCPGYIGLCPRMVTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOSMMQHLAQARTT-VVVVFSNRHLARVFFRSVVLANLTGK-VMVASEDWAISTYITSVT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DQTNKDPDLLSNITLGVRILDTCSRDTYALEQSLTFVQALIEKDASDVKCANGDPPIFTK 143
                                                                                                                                                                                                                                                                                                                                                                           LNEVSWIAFETMA-SIYQGS---YLPAVNYLAGLTTLSGGES-G-YELPKCYVILCRPEL
                                                                                                                                                                                                                                                                                                                                                                                                           TTCIIWLAFIPIFFGTAQSAEKMYIQTTTLTVSMS-LSASVSLGMLYMPKVYIIIFHPEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                             -F-P-HL-VILECTEVNSVGFLLAFTHNILLSISTFVCSYLGKELPENYNEAKCVTFSLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TLDPENARGYLKC-DISDLSLICSLGYSILLMYTCTYYAIKTRGYPETFNEAKPIGFTMY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RIHRIFEQGKKSVTA-PKFI-SPASQLVITFSLISVQLLGVFVWFVVDPPHTIIDYGEQR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CELCPLDORPNINRTGCORIPIIKLEWHSPWAVVPVLIAILGIIATTFVIVTFVRYNDTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LDINKTKIQWHGKNNQVPVSVCTTDCLAGHHRVVVGSHHCCFECVPCEAGTFLNMSELHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LKVED - - MQWANREHTHPASVCSLPCKPGERKKTVKGVPCCWHCGRCEGYNY - QVDELS -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DGKELLGYIRAVNENGSAGTPVTENENGDAPGRYDIFQYQINNKSTEYKIIGHWT-NQLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTR-NMPT-LGAFSMSAAY----RV-Y--EAVYAVAHGLHQLL-G-CTSEI--CSR-GPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GIQGIGTVLGVAVQQRQVPGLKEFEESY-VRAVTAAPSACPEGSWCSTNQLCRE-CH-TF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QQEEIAEG-AVTILPKR-ASIDGFDRYFRSRTLANNRRNVWFAEFSEGNFGCKSGSHGKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEKIIKRLLETPNARAVIMFANEDDIRGILEAAKKLNQSGHFLWIGSDSWG-SK-IAPVY
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                                                                           Primates;
                                                                                                              (Human)
                                                                           Catarrhini;
                                                                                            Chordata;
         ROCKEY
         P.K.,
                                                                                            Craniata;
                                                                           Hominidae;
         BURGETT
                                                                                          Vertebrata;
         S.G.,
                                                                             Homo.
         ARNOLD J.S.,
                                                                                            Mammalia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SCHERER S.W., SODER S., DUVOISIN R.M., HUIZENGA J.J., TSUI L.C.; "The human metabotropic glutamate receptor 8 (GRW8) gene: a disproportionately large gene located at 7q31.3-q32.1."; Genomics 44:232-236(1997).

-1- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY A G-PROTEIN THAT INHIBITS ADENYLATE CYCLASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ROSTECK P.R. JR., JOHNSON B.G., SCHOEPP D.D., BELAGAJE R. "Group III human metabotropic glutamate receptors 4, 7 ar molecular cloning, functional expression, and comparison pharmacological properties in RGT cells.";

Jean Res. Mol. Brain Res. 53:88-97(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PFAM; PF00003; 7tm_3; 1. PFAM; PF01094; ANF_receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00979; G_PROTEIN_RECEP_F3_1; PROSITE; PS00980; G_PROTEIN_RECEP_F3_2; PROSITE; PS00981; G_PROTEIN_RECEP_F3_3;
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EMBL; U95025;
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                                                                                           NYNEAKCVTFSLLLNFVSWIAFFTMA-SIYQGS---YLPAVNVLAGLTTLSGGFS-G-YF 807
                                                                                                                                       TENEAKPIGETMYTTCIIWLAFIPIFFGTAQSAEKMYIQTTTLTVSMS-LSASVSLGMLY 834
                                                                                                                                                                                       WTPRPTREY - - QR - F - PHLV - - ILECTEVNSVGFLLAFTHNILLSISTFVCSYLGKELPE
                                                                                                                                                                                                                                   DPPHIIIDYGEQRTLDPEKARGVLKC-DISDLSLICSLGYSILLMVTCTVYANKTRGVPE 775
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Mar 17 13:02:07 2000; MasPar time 35.36 Seconds 951.981 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: Title:

Sequence: >US-09-361-552-1 (1-840) from US09361652.pep 6338 1 MLFWAAHLLLSLQLVYCWAF......NNTEHFQASIQDYTRRCGTT 840

Searched: PAM 150 Gap 11 122810 segs, 40068593 residues

Scoring table:

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: pir62 1:pir1 2:pir2 3:pir3 4:pir4

Statistics: Mean 52.607; Variance 107.685; scale 0.489

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

222108876543 222108876543 222108876543	Result No.
1311 1293 1290 1286 1198 873 873 870 870 844 844 845 844 847 844 847 844 793 775 844 793 775 755 755 755 755 166	Score
20.44.7 20.44.7 113.77.113.7 113.77.113.7 112.77.113.7 2.6.6.6.113.7	% Query Match
1085 1078 1078 1079 1079 1180 1180 11180 1212 912 912 912 912 912 912 912 912 91	Length
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Ca(2+)-sensing recept calcium-sensing recept calcium receptor (clo calcium receptor) (clo metabotropic glutamat metabotropic glutamat metabotropic glutamat metabotropic glutamat metabotropic glutamat metabotropic glutamat glutamat erceptor ho g protein coupled glu metabotropic glutamat probable ligand-gated guanylate cyclase (EC probable ligand-gated hypothetical protein gamma-aminobutyric ac N-methyl-D-aspartate	Description
3.22e-229 1.51e-225 6.44e-225 6.44e-226 6.42e-206 1.21e-140 4.82e-140 4.82e-140 4.82e-140 1.89e-134 2.97e-134 2.97e-134 2.78e-127 7.759e-15 6.63e-117 7.59e-15 6.63e-108 9.97e-08	Pred. No.

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I49704	A43274	S29159	178557	S47555	C45219	S27224	OYURGA	OYURCP	S21104	B45219	I49705	I55466	S33754	C43274	S19710	A46612	ZN0338	JN0337	JN0339	A47551	
glutamate receptor ch	N-methyl D-aspartate	glutamate receptor, N	N-methyl-D-aspartate	N-methyl-D-aspartate	N-methyl-D-aspartate	l-D-aspart	speract receptor prec	speract receptor prec	N-methyl-D-aspartate	N-methyl-D-aspartate	glutamate receptor ch	N-methyl-D-aspartate	glutamate receptor -	N-methyl D-aspartate	N-methyl-D-aspartate	N-methyl-D-aspartate	N-methyl-D-aspartate	N-methyl-D-aspartate	N-methyl-D-aspartate	N-methyl-D-aspartate	
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ALIGNMENTS

Db 327 QIPGFREFLQKVHPRKSVHNGFAKEFWEETFNCHLQEGAKGPLPVDTFLRGHEEGGARLS 386 : : : : : : : : : : : : : : :
Qy 270 VVVFSN-RHLARVFFRSVVLANLTGKVWVASEDWAIS-T-YITSVTG-IQ-GIG 318
Db 268 IVVESSGEDLEPLI-KEIVRRNITGRIMLASEAWASSSLIAMPEYFHVVGGTIGFGLKAG 326
Qy 210 ISLIGSYGDYGQLGVQALEELAVPRGICVAFKDIVPFSARVGDPRMQSMMQHLAQARTTV 269
Db 210 VGTIAADDDYGRPGIEKFREEAEERDICIDFSELISQYSDEEKIQQVVEVIQNSTAKV 257
Qy 150 HAVITAALLGPFLMPLVSYEASSVVLSAKRKFPSFLRTVPSDRHQVEVMVQLLQSFGWVW 209
Db 150 ISTAVANLLGLEYIPQVSYASSSRLLSNKNQFKSFLRTIPNDEHQATAMADIIEYFRWNW 209
Qy 93 PNITLGYELYDVCSESANVY-ATLRVLALQGPRHIEIQXDLRNHSSKVVAFIGPDNTD 149
Db 90 PNMTLGYRIFDTCNTVSKALEATLSFVAQNKIDSLNLDEFCNCSEHIPSTIAVVGATGSG 149
Qy 35 GDFLLAGLFSL4GDCLQVRHRPLVTSCDRPDSFNGHGYHLFQAMRFTVEEINNSSALL 92
Db 31 GDIILGGLF?IHFG-VAVKDQDLKSRPESVECIRYNFRGFRWLQAMIFAIEEINSSPALL 89
Query Match 20.7%; Score 1311; DB 2; Length 1085; Best Local Similarity 31.9%; Pred. No. 3.22e-229; Matches 272; Conservative 232; Mismatches 275; Indels 73; Gaps 50;
##molecule_type mRNA ##residues 1-1085 ##label BRO \$SUMMARY #length 1085 #molecular-weight 121170 #checksum 5738
#accession \$40476
(2+)-sensing receptor from bovine paratnyroid. #cross-references MUID:94077182
Cloning and characterization of an e
#journal Nature (1993) 365:575-580
#authors Brown, E.M.; Gamba, G.; Riccarci, D.; Lombardi, M.; Butters, R.; Kifor, O.; Sun, A.; Hediger, M.A.; Lytton, J.; Hebert,
540476
NISM #formal_name Bos primigenius taurus #common_name
ENTRY \$40476 #tvpe complete
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                                                                                                                                                          #authors Pollak, M.R.; Brown, E.M.; Chou, Y.H.; Hebert, S.C.; S.J.; Steinmann, B.; Levi, T.; Seidman, C.E.; Seid #journal Cell (1993) 75:1297-1303
#title Mutations in the human Ca(2+)-sensing receptor gene familial hypocalciuric hypercalcemia and neonatal hyperparathyroidism.
#cross-references_MUID:94094324
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FSLGFAIFLSCLTIRSFQLVIIFKFSTKVPT-FYRTWAQNHGAGLFVIVSSTVHLLICLT
                           FGISFVLCISCILVKTNRVLLVFE--AKIPTSFHRKWWGLNLQFLLVFLCTFWQIVICVI
                                                                                          LLVGTAGLFAWHFH-TPVVRSAGGRLCFLMLGSLVAG-SCSFYSFFGEPTVPACLLRQPL
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                                                                                                                    LTAFVLGVFI-KFRNTPIVKATNRELSYLLLFSLLCCFSSSLF-FIGEPQDWTCRLRQPA
                                                                                                                                                                                          VPCEAGTFLNMSELHICQPCGTEEWAPKESTTCFPRTVEFLAWHEPISLVLIAANTLLLL
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NDS glycoprotein; receptor; transmembrane protein
% #length 1078 #molecular-weight 120573 #chec
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KEVGYYNVYAKKGERLFINEEKILWSGFSREVPFSNCSRDCLAGTRKGIIEGEPTCCFEC
                                                  SEICS-RGPVYPWQLLQQIYKVNFLLH-ENTVAFDDNGDTLGYYDIIAWDWNGPE-WT-F
                                                                                                     NGSCADIKKVEAWQVLKHLRHLNETNNMGEQVTFDECGDLVGNYSIINWHLSPEDGSIVF
                                                                                                                                                                                                                                                                                                                                                                            VVVFSN-RHLARVFFRSVVLANLTGKVWVASEDWA----IS-T-YITSVTG-IQ-GI--G
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Similarity 32.0%;
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Molecular cloning and functional expression parathyroid calcium receptor cDNAS.
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calcium receptor (clone phPCaR-4.0) - human
#formal_name Homo sapiens #common_name man
19-Oct-1995 #sequence_revision 19-Oct-1995;
17-Mar-1999
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Pred. No. 6.16e-225;
230; Mismatches 276;
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Nemeth, E.F.; Fuller,
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FEATURE
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613-635
650-670
683-700
775-744
770-790
806-828
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REFERENCE
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#title Cloning and functional expression of a rat kidney
extracellular calcium/poly/valent cation-sensing
#cross-references_MUID:95116508
#accession_A55594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #authors Ruat, M.; Molliver, M.E.; Snowman, A.M.; Snyder, if the Proc. Natl. Acad. Sci. U.S.A. (1995) 92:3161-3165 etile Calcium sensing receptor: molecular cloning in ratification to nerve terminals.
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##experimental_source kidney
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                                                                                                                                                                                                                                                                                                                                                 Riccardi, D.; Park,
Hebert, S.C.
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                                                                                                         NENEAKFITESMLIFFIVWISFIPAYASTY-GKEVSAVEVIAILAASFGLLACIFENKVY
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Brown, E.M.; Hebert, S.C.; Nemeth, E.
#journal J. Biol. Chem. (1995) 270:12919-12925
#title Molecular cioning and functional express
parathyroid calcium receptor cDNAs.
#cross-references.MUID:95279439
#accession B56715
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30S glycoprotein; receptor; transmembrane protein
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##experimental_source brain
##note sequence extracted from NCBI backbone (NCBIN-1077/0
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 YKVNFL-LHENTVAFDDNGDTLGYYDIIAWDWNGPEWTFEIIGSASLSPVHLDINKTKIQ
                                  MKTNFTGVSGDMILFDENGDSPGRYEIMNFKEMGKDY-FDYINVGSWDNGELKMDDDEV-
                                                                                                                                            LGVAVQQRQVPGLKEFEESYV--RAVTAAPSACPEGSW-----CSTNQLCRECHTFT-TR
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                                                                      NMP-TLGAFSMSAAYRVY--EAVYAVAHGLHQL-LG-CTS-E-IC-SRGPVYPWQLLQQI
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Similarity 27.7%;
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#formal_name Rattus norvegicus #common_name Norway rat
04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change
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Nakanishi, S.
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Pred. No. 1.21e-140;
215; Mismatches 325;
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 IGPDNTDHAVTTAALLGPFLMPLVSYEASSVVLSAKRKFPSFLRTVPSDRHQVEVMVQLL
                                 IGPGSSSVAIQVQNLLQLFNIPQIAYSATSMDLSDKTLFKYFMRVVPSDAQQARAMVDIV 206
                                                                                                       PNITLGCEIRDSCWHSAVALEQSIEFIRDSLISSEEEEGLVRCVDGSSSSFRSKKPIVGV 146
                                                                                                                                          LPGDFLLAGLFSLHGDCLQVRHRPLVTSCDRPDSFNGHGYHLFQAMRFTVEEINNSSALL
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                                                                       PNITLGYELYDVCSESANVYA-TLR-VL-ALQGPRHIE--IQ-KDLRNHS--SK--VVAF
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Biophys. Res. Commun. (1994) 199:1126-1143
Molecular cloning and the functional expression of two
isoforms of human metabotropic glutamate receptor subtype
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Pred. No. 4.82e-140;
214; Mismatches 326;
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Biochem. Biophys. Res. Commun. (1994) 199:1136-1143

Molecular cloning and the functional expression of two
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#formal_name Rattus norvegicus #common_name Norway
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#title A family of metabotropic
#cross-references MUID:92110002
#accession JH0561
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##experimental_source brain
## This protein is coupled to a G protein and evokes a variety of
functions by mediating intracellular signal transduction.
##superiamily metabotropic glutamate receptor 4
RDS G protein-coupled receptor; glycoprotein; phosphoprotein;
transmembrane protein
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TFEIIGSASLSPVHLDINKTKIQWHG-KNNQVPVSVCTTDCLAGHHRVVVVGSHHCCFECV
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870
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#title A family of metabotropic glutamate receptors.
#cross-references_MUID:92110002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #accession
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This protein is coupled to a G protein and evokes a variety functions by mediating intracellular signal transduction.
IFICATION #superfamily metabotropic glutamate receptor 4
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metabotropic glutamate receptor 4 precursor
#formal_name Rattus norvegicus #common_name
30-Jun-1992 #sequence_revision 30-Jun-1992 #
                                                                                                                          #length 912 #molecular-weight 101818
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                                                                                                                                                                                                                                                                                                                                                                                                                 transmembrane protein
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                                                             Score 843; DB
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                                                                #authors O'Hara, P.J.; Sheppard, P.O.; Thogersen, H.; V
Haldeman, B.A.; McGrane, V.; Houamed, K.M.;
Gilbert, T.L.; Mulvihill, E.R.
#journal Neuron (1993) 11:41-52
#title is related to bacterial periplasmic binding
#cross-references MUID:93332699
                                                          #accession
                     ##molecule_type mRNA
##restdnoc
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                                                                                                                                                                                                                                                                                                                                YMPKVYIILFHPEQN
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                                                                                                                                                                                                                                                                                                                                                                             PETFNEAKPIGFTMYTTCIVMLAFIPIFFGTSQSADKLYIQTTTLTVSVSLSASVSLGML 837
                                                                                                                                                                                                                                                                                                                                                                                                        VMWTDRPTREYQ--R-F-PHLV--ILECTEVNSVGFLLAFTHNILLSISTFVCSYLGKEL
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                                                                                                                                                                     I58149
I58149
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metabotropic glutamate receptor - rat
#formal_name Rattus norvegicus #common_name Norway
26-Jul-1996 #sequence_revision 26-Jul-1996 #text_ct
13-Sep-1998
                                                         I58149
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    GB:M90518;
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NID: g205400;
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K.M.; Thomsen,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GIHRLEAMLFALDRINNDPDLLPNITLGARILDTCSRDTHALEQSLTFVRALIEKDGTEV 134
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\$71376 #type complete
glutamate receptor homolog - cherry salmon
#formal_name Oncorhynchus masou #common_name cherry saln
11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change
01-May-1998

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KEYWORDS
FEATURE
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Best Local Similarity 27.5%;
Matches 198; Conservative
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#accession S71376
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RILAGSKKKICTRKPRFMSAWAQLVIAGL--LVS--VQLTLEVTLIILEPPMPVKSYPSI
                                                         SAGGRICFLMIGSIVAG-SCSFYSFFGEPTVPACILRQPLFSIGFAIFISCLTIRSFQLV
                                                                                                            SSSRELCYIILAGIFLGYICPF-TLIAQPTVASCYLQRLLVGLSATMCYSALVTKTNRIA
                                                                                                                                                                        CGTEEWAPKESTTCFPRTVEFLAWHEPISLVLIAANTLLLLLLLVGTAGLFAWHFHTPVVR
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$71376
$Kubokawa, K.; Miyashita, T.; Nagasawa, H.; Kubo, Y.
FEBS Lett. (1996) 392:71-76
Cloning and characterization of a bifunctional metabotropic
receptor activated by both extracellular calcium and
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*binding_site phosphate (Ser) (covalent) (l
CAMP-dependent kinase) **status predicted
rth 1218 *molecular-weight 136838 *checks
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O'Hara, P.J.; Milvihill, E.R.; Almers, W.;

#journal Science (1991) 252:1318-1321

#title Cloning, expression, and gene structure of a

protein-coupled glutamate receptor from rat

#cross-references MUID:92022526

#accession A41939
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               REQ-CRLPGHLLENPNEKKVCTGNESLEENYVQDSKMGFVINAIYAMAHGLQNMHHALCP
                                                                                  DGWADRDEVIEGYEVEANGGI-TIKLQSPEVRSFDDYFLK-LRLDTNTRNPWFPE-FWQH
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Similarity 25.9%;
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209; Mismatches 314;
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                                                                                                                                                                                                                                                   ##molecule_type mRNA
##residues 1-908 ##label RES
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                                                                                                HSQEYAHSIRLDGDIILGGLFPVHA---KG-ERG-V-PCG--DLKKEKGIHRLEAMLYAI 83
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             PDKISGVIGAAASSVSIMVANILRLFKIPQISYASTAPELSDNTRYDFFSRVVPPDSYQA
                                   EEINNSSALLPNITLGYELYDVCS-ESANVYATLR-VLAL-Q-GPRHIEIQK-D--LRNH
                                                         DQTNKDPDLLSNITLGVRILDTCSRDTYALEQSLTFVQALIEKDASDVKCANGDPPIFTK 143
                                                                                   QRTESSPGFSLPGDFLLAGLFSLHGDCLQVRHRPLVTSCDRPDSFNGHGYHLFQAMRFTV
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                                                                                                                                              Similarity
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neurotransmitter receptor
#length 908 #molecular-weight 101413 #checksum
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metabotroppic glutamate receptor 8 - mouse
#formal_name Mus musculus #common_name hous
02-Jul-1996 #sequence_revision 02-Jul-1996
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CLASSIFICATION KEYWORDS
                                                                                                                                                                                                    PERENCE JH0561
#authors Tanabe, Y.; Masu, M.; Ishii,
#journal Neuron (1992) 8:169-179
#title A family of metabotropic glu
#cross-references MUID:92110002
#accession JH0562
                                                                                                                           ##experimental_source brain
                                                                                                                                                ##residues
                                                                                                                                                                         ##molecule_type mRNA
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                This protein is coupled to a G protein and evokes a variety of functions by mediating intracellular signal transduction.

**Superfamily metabotropic glutamate receptor 4

G protein coupled receptor; glycoprotein; phosphoprotein;
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#formal_name Rattus norvegicus #common_name Norway rat
30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change
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Best Local Similarity 25.5%;
Matches 202; Conservative
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                                                                                                                                                                                                 LGFAIFLSCLTIRSFQLVIIFKFSTKVPTFYRTWAQNHGAGLFVIVSST-VHLLICLTWL
                                                                                                                                                                                                                                                                                                                                      TSFAICYSALLTKTNCIARIFD-GVKNGA-QRPKFISPSSQVFICLGLILVQIVMVSVWL
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                                                NEAKCVTFSLLLNFVSWIAFFTMASIYQGSYLPAVNVLAGLTTLSGGFS-GY-FLPKCYV
                                                                                                         NEAKFIGFTMYTTCIIWLAFLPIFYVTSSDYRVQTTTMCISVSLSGFVVLGCLFAPKVHI
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predicted #label MET\
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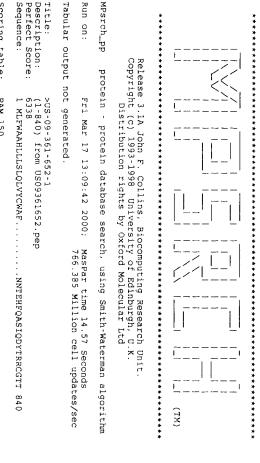
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Search completed: Fri Mar 17 Job time : 50 secs. 13:02:57

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Tabular output not generated

Scoring table: Sequence: PAM 150 Gap 11

134018 seqs, 13297625 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

a-issued 1:5A_COMB 2:5B_COMB 3:5_COMB 4:PCT9_COMB 5:backfiles1

Statistics: Mean 36.328; Variance 178.464; scale 0.204

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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1311 1311 1311 1311 1311 1290 1290 1290 1290 1285 1285 1285 1285 1285 1285 1285 1285	Score
20.77 20.77 20.77 20.77 20.44 20.44 20.33 20.34 20.34 20.33 20.34 20.33 20.34 20.33 20.34 20.33 20.34 20.33 20.34 20.33 20.34 20.33 20.33 20.34 20.33	% Query Match
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ALIGNMENTS

RESULT ID US XX XXXXXX US-08-484-565-5 Sequence 5, Application US/08484565 Sequence 5, Application US/08484565 Patent No. 5763569 GENERAL INFORMATION: PRIOR APPLICATION DATA: including application PRIOR APPLICATION DATA: described below: 9 APPLICATION NUMBER: 08,253,784 FILING DATE: 9 December; 1994 APPLICATION NUMBER: PCI/US/94/12117 FILING DATE: 21 October; 1994 APPLICATION NUMBER: U.S. 08/292,827 FILING DATE: 23 August, 1994 APPLICATION NUMBER: U.S. 08/292,827 FILING DATE: 23 August, 1994 APPLICATION NUMBER: U.S. 08/141,248 FILING DATE: 22 October, 1993 OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: FASTSEQ CURRENT APPLICATION DATA: COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette,
COMPUTER: IBM PC compatible APPLICANT: Edward M. Brown
APPLICANT: Steven C. Hebert
APPLICANT: James E. Garrett, Jr.
TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
TITLE OF INVENTION: MOLECULES PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA: CORRESPONDENCE ADDRESS: NUMBER OF SEQUENCES: ADDRESSEE: Lyon & Lyon
STREET: First Interstate World Center
STREET: Suite 4700
STREET: 633 West Fifth Street CLASSIFICATION: 435 STREET: 633 West F CITY: Los Angeles STATE: California COUNTRY: APPLICATION NUMBER: US/08/484,565 ZIP: 90071 USA STANDARD; Diskette, 1.44 Mb storage 20 PRT; 1085 AA

695

753 800

812

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FILING DATE: 21 August, 1992
APPLICATION NUMBER: U.S. 07/834,
FILING DATE: 11 February, 1992
APPLICATION NUMBER: U.S. 07/749,
FILING DATE: 23 August, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Heber, Sheldon O.
REGISTRATION NUMBER: 38.179
REFERENCE/DOCKET NUMBER: 213/006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
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                                                                                             VECPDGEYSDETDASACDKCPDDFWSNENHTSCIAKEIEFLSWTEPFGIALTLFAVLGIF
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     LLVGTAGLFAWHFH-TPVVRSAGGRLCFLMLGSLVAG-SCSFYSFFGEPTVPACLLRQPL
                     LTAFVLGVFI-KFRNTPIVKATNRELSYLLLFSLLCCFSSSLF-FIGEPQDWTCRLRQPA
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                                                                         VPCEAGTFLNMSELHICQPCGTEEWAPKESTTCFPRTVEFLAWHEPISLVLIAANTLLLL
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FILING DATE: 23 February, 1993
APPLICATION NUMBER: U.S. 08/017,127
FILING DATE: 12 February, 1993
APPLICATION NUMBER: U.S. 07/934,161
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Similarity 31.9%;
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MBER: U.S. 07/834,044
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Pred. No. 3.70e-99;
232; Mismatches 275;
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                                                                                                                                         PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA: including application party described below application NUMBER: 08/353,784

FILING DATE: 9 December, 1994
APPLICATION NUMBER: PCT/US/94/12117

FILING DATE: 21 October, 1994
APPLICATION NUMBER: U.S. 08/292,827
FILING DATE: 23 August, 1994
APPLICATION NUMBER: U.S. 08/2141,248

APPLICATION NUMBER: U.S. 08/141,248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                Z1F: 3007.2
COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
COMPUTER: 1.8M PC compatible
COMPUTER: IBM PC compatible
COMPUTER: FC-DOS/MS-DOS
FILING DATE: 22 October, 1993
APPLICATION NUMBER: U.S. 08/009,389
FILING DATE: 23 February, 1993
APPLICATION NUMBER: U.S. 08/017,127
FILING DATE: 12 February, 1993
APPLICATION NUMBER: U.S. 07/934,161
FILING DATE: 21 August, 1992
APPLICATION NUMBER: U.S. 07/834,044
                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: FASTSEQ CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET:
CITY: I
                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE: 7 Jun. CLASSIFICATION: 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90071
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      633 West Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        First Interstate World Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
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Steven C. Hebert
Forrest H. Fuller
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               James E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lyon & Lyon
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N: 435
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CALCIUM RECEPTOR-ACTIVE
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: described below: 9
08/353,784
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TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 1085 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 11 February, 1992
APPLICATION NUMBER: U.S. 07/74',
FILING DATE: 23 August, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Heber, Sheldon O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TVLG----VA-VQQRQ-VP-GL-KEF-EESY---VR-AVTAA-P--S---ACPEG-SW-C
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              WLNTAPPSSYRNHELEDEIIFITCHEGSLMALGFLIGYTC-LLAAICFFF-AFKSRKLPE
                                                                                                                                                                                                                                                                                                                        ---CS-RGPVYPWQLLQQIYKVNFLLH-ENTVAFDDNGDTLGYYDIIAWDWNGPE-WT-F
                                                                                                                                                                                                                                                                                                                                                                                       -S-TN-Q-LCRECHTFTTRNMPTLGAFSMSAAYRVYEAVYAVAHGLHQLLGCTSE--I--
                                                                                                                                                                                                                                                                                                                                                                                                                       NSPTAFRPLCTGEENISSVETPYMDYTHLRISYNVYLAVYSIAHALQDIYTCIPGRGLFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QIPGFREFLQKVHPRKSVHNGFAKEFWEETFNCHLQEGAKGPLPVDTFLRGHEEGGARLS
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                                               FSLGFAIFLSCLTIRSFQLVIIFKFSTKVPT-FYRTWAQNHGAGLFVIVSSTVHLLICLT
                                                                               FGISFVLCISCILVKTNRVLLVFE--AKIPTSFHRKWWGLNLQFLLVFLCTFMQIVICAI 742
                                                                                                                  LLVGTAGLFAWHFH-TPVVRSAGGRLCFLMLGSLVAG-SCSFYSFFGEPTVPACLLRQPL
                                                                                                                                                LTAFVLGVFI-KERNTPIVKATNRELSYLLLESLLCCESSSLF-FIGEPQDWTCRLRQPA
                                                                                                                                                                                   VPCEAGTFLNMSELHICOPCGTEEWAPKESTTCFPRTVEFLAWHEPISLVLIAANTLLLL
                                                                                                                                                                                                                 VECPDGEYSDETDASACDKCPDDFWSNENHTSCIAKEIEFLSWTEPFGIALTLFAVLGIF
                                                                                                                                                                                                                                                   EIIG--SA-SLSPVHLDINKTKIQWHGKNNQVPVSVCTTDCLAGHHRVVV-GSHHCCFEC
                                                                                                                                                                                                                                                                                    KEVGYYNVYAKKGERLFINDEKILWSGFSREVPFSNCSRDCLAGTRKGIIEGEPTCCFEC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VVVFSN-RHLARVFFRSVVLANLTGKVWVASEDWA----IS-T-YITSVTG-IQ-GI--G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PNMTLGYRIFDTCNTVSKALEATLSFVAQNKIDSLNLDEFCNCSEHIPSTIAVVGATGSG 149
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LLECULE TYPE: protein
NCE 1085 AA; 121170 MW; 5189757 CN;
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REFERENCE/DOCKET NUMBER: 21:
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Similarity 31.9%;
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                                                                                                                                                                                              APPLICATION NUMBER: PCT/US/94/12117
FILING DATE: 21 October, 1994
APPLICATION NUMBER: U.S. 08/292,827
FILING DATE: 23 August, 1994
APPLICATION NUMBER: U.S. 08/141,248
FILING DATE: 2 October, 1933
APPLICATION NUMBER: U.S. 08/09,389
                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 7 June, 1
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FASTSEO
                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA: PRIOR APPLICATION DATA: PRIOR APPLICATION DATA:
               ATTORNEY/AGENT
NAME: Heber
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
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STREET: 533 West Fifth Street
CITY: Los Angeles
STATE: California
          APPLICATION NUMBER: U.S. 07/
FILING DATE: 23 August, 1991
CTORNEY/AGENT INFORMATION:
NAME: Heber, Sheldon 0.
                                                           PEILING DATE: 21 August, 1992
APPLICATION NUMBER: U.S. 07,834,044
FILING DATE: 11 February, 1992
APPLICATION NUMBER: U.S. 07,749,451
                                                                                                                         FILING DATE: 23 February, 1993
APPLICATION NUMBER: U.S. 08/017,127
FILING DATE: 12 February, 1993
APPLICATION NUMBER: U.S. 07/934,151
                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 08/3: FILING DATE: 9 December,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
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5858684
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IVENTION: CALCIUM RECEPTOR-ACTIVE
AVENTION: MOLECULES
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Edward M. Brown
Steven C. Hebert
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REFERENCE/DOCKET NUMBER: 213/
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1085 amino acids

213/004

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31 GDIILGGLFPIHFG-VAVKDQDLKSRPESVECIRYNFRGFRWLQAMIFAIEEINSSPALL 89
                                                                                                                                                                                                                                                                                                                                         EIIG--SA-SLSPVHLDINKTKIQWHGKNNQVPVSVCTTDCLAGHHRVVV-GSHHCCFEC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VVVFSN-RHLARVFFRSVVLANLTGKVWVASEDWA----IS-T-YITSVTG-IQ-GI--G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PNITLGYELYDVCSESANVY-ATLRVLALQGPRHIEIQK--DLRNHSSKVVAFIGPDNTD 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PNMTLGYRIFDTCNTVSKALEATLSFVAQNKIDSLNLDEFCNCSEHIPSTIAVVGATGSG 149
                                                NFNEAKFITFSMLIFFIVWISFIPAYASTY-GKFVSAVEVIAILAASFGLLACIFFNKVY
                                                                                WLVMWTPRPTREYORFPHLVILECTEVN -- SVGFLLAFTHNILLSISTFVCSYLGKELPE
                                                                                                              WLNTAPPSSYRNHELEDEIIFITCHEGSLMALGFLIGYTC-LLAAICFFF-AFKSRKLPE
                                                                                                                                              FSLGFAIFLSCLTIRSFQLVIIFKFSTKVPT-FYRTWAQNHGAGLFVIVSSTVHLLICLT
                                                                                                                                                                            FGISFVLCISCILVKTNRVLLVFE--AKIPTSFHRKWWGLNLQFLLVFLCTFMQIVICAI
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                NYNEAKCYTFSLLLNFVSWIAFFTM-ASIYQGSYLPAVNVLAGLTTLSGGFSGYFLPKCY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     h 20.7%; Score 1311; DB 2; I Similarity 31.9%; Pred. No. 3.70e-99; 272; Conservative 232; Mismatches 275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1085;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                               INFORMATION FOR SEQ ID NO:
                                                                              REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                      FILING DATE: 11 February, 1992
APPLICATION NUMBER: U.S. 07/749,451
FILING DATE: 23 August, 1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 530 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compared operating system: PC-DO SOFTWARE: FASTSEQ CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
                SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
FILING DATE: 7-June-
APPLICATION NUMBER:
FILING DATE: 9 Decem
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VILCRPELNNTE
                                                                                                                                                                                                                               APPLICATION NUMBER: U.S. UB/UL/, 1-APPLICATION NUMBER: U.S. 07/934,161
APPLICATION NUMBER: U.S. 07/934,161
APPLICATION NUMBER: U.S. 07/934,044
                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 21 October, 1994
APPLICATION NUMBER: U.S. 08/292,827
FILING DATE: 23 August, 1994
APPLICATION NUMBER: U.S. 08/141,248
                                                                                                                           NAME: Heber, Sheldon O. REGISTRATION NUMBER: 38,179
                                                                                                                                                                                                                         FILING DATE: 21 AU APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: Suite 4700
STREET: 633 West Fifth
                                                             TELEFAX:
                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET:
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                                              : (213) 955-0440
67-3510
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1085 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PE: 3.5" Diskette, 1.44 Mb storage IBM PC compatible SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Edward M. Brown
Steven C. Hebert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lyon & Lyon
                                                                                                                                                                                                                                                                                                                                                                                                            9 December, 1994
19 December, 1994
1008/94/12117
                                                                                                                                          Sheldon O.
                                                                                                                                                                                                                         21 August, 199.
MMBER: U.S. 07,
                                                                                                                                                                                                                                                                                                                      22 October, 1993
JMBER: U.S. 08/009,389
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CALCIUM RECEPTOR-ACTIVE
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Query Match Best Local S Matches

272;

SEQUENCE

MOLECULE TYPE:

LE TYPE: protein 1085 AA; 121170 MW; 6189757 CN;

TYPE: amino acid TOPOLOGY: linear

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Matches

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US-08-353-784-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
JENCE 1085 AA; 121170 MW; 6189757
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                                                                                   VILCRPELNNTE
                                                                                                                                                                                NFNEAKFITFSMLIFFIVWISFIPAYASTY-GKFVSAVEVIAILAASFGLLACIFFNKVY
                                                                                                                                                                                                                                                                                                                                                                                                                                       VECPDGEYSDEIDASACDKCPDDFWSNENHISCIAKEIEFLSWIEPFGIALILFAVLGIF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QIPGFREFLQKVHPRKSVHNGFAKEFWEETFNCHLQEGAKGPLPVDTFLRGHEEGGARLS
                                                                                                                 IILFKPSRNTIE
                                                                                                                                                                                                                  WLVMWTPRPTREYQREPHLVILECTEVN--SVGFLLAFTHNILLSISTFVCSYLGKELPE
                                                                                                                                                                                                                                                 WLNTAPPSSYRNHELEDEIIFITCHEGSLMALGFLIGYTC-LLAAICFFF-AFKSRKLPE 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EIIG--SA-SLSPVHLDINKTKIQWHGKNNQVPVSVCTTDCLAGHHRVVV-GSHHCCFEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KEVGYYNVYAKKGERLFINDEKILWSGFSREVPFSNCSRDCLAGTRKGIIEGEPTCCFEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---CS-RGPVYPWQLLQQIYKVNFLLH-ENTVAFDDNGDTLGYYDIIAWDWNGPE-WT-F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VVVFSN-RHLARVFFRSVVLANLTGKVWVASEDWA----IS-T-YITSVTG-IQ-GI--G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ISTAVANLLGLFYIPQVSYASSSRLLSNKNQFKSFLRTIPNDEHQATAMADIIEYFRWNW
                                                                                                                                                   NYNEAKCYTESLLLNEVSWIAFETM-ASIYQGSYLPAVNVLAGLTTLSGGFSGYFLPKCY
                                                                                                                                                                                                                                                                                FSLGFAIFLSCLTIRSFQLVIIFKFSTKVPT-FYRTWAQNHGAGLFVIVSSTVHLLICLT
                                                                                                                                                                                                                                                                                                               FGISFVLCISCILVKTNRVLLVFE--AKIPTSFHRKWWGLNLQFLLVFLCTFMQIVICAI 742
                                                                                                                                                                                                                                                                                                                                                   LLVGTAGLFAWHFH-TPVVRSAGGRLCFLMLGSLVAG-SCSFYSFFGEPTVPACLLRQPL
                                                                                                                                                                                                                                                                                                                                                                                LTAFVLGVFI-KFRNTPIVKATNRELSYLLLFSLLCCFSSSLF-FIGEPQDWTCRLRQPA 684
                                                                                                                                                                                                                                                                                                                                                                                                                  VPCEAGTFLNMSELHICOPCGTEEWAPKESTTCFPRTVEFLAWHEPISLVLIAANTLLLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ISLIGSYGDYGQLGVQALEELAVPRGICVAFKDIVPFSARVGDPRMQSMMQHLAQARTTV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  {\tt HAVITAALLGPFLMPLVSYEASSVVLSAKRKFPSFLRTVPSDRHQVEVMVQLLQSFGWVW}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PNMTLGYRIFDTCNTVSKALEATLSFVAQNKIDSLNLDEFCNCSEHIPSTIAVVGATGSG 149
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l Similarity 31.9%;
272; Conserunt;
                    STANDARD;
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Pred. No. 3
                    PRT;
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3.70e-99;
tches 275;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels 73;
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                                                                  Query Match
Best Local S
Matches 27
                                                                  SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 514

PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA: including applic

PRIOR APPLICATION DATA: described below
APPLICATION NUMBER: PCT/US/94/12117

FILING DATE: 21 October, 1994

APPLICATION NUMBER: U.S. 08/292,827

FILING DATE: 23 August, 1994

APPLICATION NUMBER: U.S. 08/11,248

FILING DATE: 22 October, 1993

APPLICATION NUMBER: U.S. 08/09,389

FILING DATE: 22 October, 1993

APPLICATION NUMBER: U.S. 08/09,389
Local Similarity
nes 272; Conser
                                                                                                                                                             TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                           FILING DATE: 23 February, 1993
APPLICATION NUMBER: U.S. 08/017,127
FILING DATE: 12 February, 1993
APPLICATION NUMBER: U.S. 07/934,151
FILING DATE: 21 August, 1992
APPLICATION NUMBER: U.S. 07/834,044
FILING DATE: 11 February, 1992
APPLICATION NUMBER: U.S. 07/7749,451
FILING DATE: 23 August, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: 3.5" Di
                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 1085 amino aci
                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Heber, Sheldon O.
                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                TOPOLOGY: I
                                                                                                                                                                                                                                                                                                                                                                                                        STREET:
                                                                                                                                                                                                                                              REGISTRATION NUMBER: 38, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM:
SOFTWARE: FASTSEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE:
COMPUTER: II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE: 9 Dec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5, Application o. 6011068
                                                               1085 AA; 121170 MW; 6189757 CN;
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 Conservative
                                                                                                                 amino acid
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633 West Fifth
                                                                                                                              1085 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eric G. DelMar, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
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                                                                                              linear
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               20.7%;
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Score 1311; DB 3;
Pred. No. 3.70e-99;
232; Mismatches 275;
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 Sequence 7, Application US/08943986 Patent No. 5962314
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TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1078 amino
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APPLICATION NUMBER: U.S. 08/292,827
FILING DATE: 23 August, 1994
APPLICATION NUMBER: U.S. 08/141,248
APPLICATION DATE: 22 October, 1993
TTIING DATE: 22 October, 1993
TTIING DATE: 22 October, 1993
TTIING DATE: 1993
                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: U.S. V.,
APPLICATION NUMBER: U.S. 0,7017,127
FILING DATE: 23 February, 1993
APPLICATION NUMBER: U.S. 09/017,127
FILING DATE: 12 February, 1993
APPLICATION NUMBER: U.S. 07/934,161
APPLICATION NUMBER: U.S. 07/834,044
TILING DATE: 21 August, 1992
TILING DATE: 1992
TILING DATE: 1992
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APPLICATION NUMBER: U.S. 07/834,044
FILING DATE: 11 February, 1992
APPLICATION NUMBER: U.S. 07/749,451
FILING DATE: 23 August, 1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: FASTSEQ CURRENT APPLICATION DUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
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APPLICANT: Steven C. Hebert
APPLICANT: James E. Garrett, Jr.
TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
TITLE OF INVENTION: MOLECULES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                            MOLECULE TYPE:
ENCE 1078 AA
                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
                                                                         GDIILGGLFPIHFG-VAAKDQDLKSRPESVECIRYNFRGFRWLQAMIFAIEEINSSPALL
                                                         GDFLLAGLFSLHGDCLQVRHRPLVTSCDRPDS--FNGHGYHLFQAMRFTVEEINNSSALL
 PNITLGYELYDVCSESANVY-ATLRVLALQGPRHIEIQK--DLRNHSSKVVAFIGPDNTD
                           PNLTLGYRIFDTCNTVSKALEATLSFVAQNKIDSLNLDEFCNCSEHIPSTIAVVGATGSG 148
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CITY: Los Angeles
STATE: California
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                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                      NAME: Heber, Sheldo REGISTRATION NUMBER:
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633 West Fifth Street
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AA; 120573 MW; 6153012 CN;
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Pred. No. 2.40e-97;
230; Mismatches 276;
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US-08-353-784-7
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                                                                                                                                                                Sequence 7, Application Patent No. 6011068 GENERAL INFORMATION:
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APPLICANT: Edward F. Nemeth, Edward M. APPLICANT: Brown, Steven C. Hebert, APPLICANT: Bradford C. Van Wagenen, Manuel APPLICANT: F. Balandrin, Forrest H. Fuller, APPLICANT: Eric G. Delmar, and Scott T. Moe TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE TITLE OF INVENTION: MOLECULES
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Best Local :
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TELEPHONE: (213) 489-1600
TELEPAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1078 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
       210
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PRIOR APPLICATION DATA: including applic
PRIOR APPLICATION DATA: described below:
PRIOR APPLICATION NUMBER: PCT/US/94/12117
FILING DATE: 21 October, 1994
APPLICATION NUMBER: U.S. 08/20,827
FILING DATE: 23 August, 1994
APPLICATION NUMBER: U.S. 08/141,248
FILING DATE: 22 October, 1993
APPLICATION NUMBER: U.S. 08/00,389
FILING DATE: 23 February, 1993
APPLICATION NUMBER: U.S. 08/017,127
FILING DATE: 23 February, 1993
APPLICATION NUMBER: U.S. 08/017,127
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MEDIUM TYPE: 3.5" Diskette, 1.4/
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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STREET: Suite 4700
STREET: 533 West Fifth Str
CITY: Los Angeles
STATE: California
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                                                                                                                                                                                                                PNLTLGYRIFDTCNTVSKALEATLSFVAQNKIDSLNLDEFCNCSEHIPSTIAVVGATGSG 148
                                                                                                                                                                                                                                                                                                                         GDIILGGLFPIHFG-VAAKDQDLKSRPESVECIRYNFRGFRWLQAMIFAIEEINSSPALL
                                                                                                                                                                                                                                                                              GDFLLAGLFSLHGDCLQVRHRPLVTSCDRPDS--FNGHGYHLFQAMRFTVEEINNSSALL
    ISLIGSYGDYGQLGVQALEELAVPRGICVAFKDIVPFSARVGDPRMQSMVQHLAQARTTV
                                             VGTIAADDDYGRPGIEKFREEAEERDICIDFSELI--SQYSDEEEIQHVVEVIQNSTAKV
                                                                                             HAVTTAALLGPFLMPLVSYEASSVVLSAKRKFPSFLRTVPSDRHQVEVMVQLLQSFGWVW
                                                                                                                     PNITLGYELYDVCSESANVY-ATLRVLALQGPRHIEIQK--DLRNHSSKVVAFIGPDNTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 21 August, 1972
APPLICATION NUMBER: U.S. 07/834, APPLICATION NUMBER: U.S. 07/749, APPL
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ZIP: 900
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FILING DATE: L. APPLIATION NUMBER: U.S. 07/934,161
TWEER: U.S. 07/934,161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Heber, Sheldor REGISTRATION NUMBER:
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1078 AA; 120573 MW; 6153012 CN;
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h: described below: 8
PCT/US/94/12117
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Pred. No. 2.
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                                                                                                                                                                                                                        Patent No. 5688938
GENERAL INFORMATION:
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                                                                                                                             APPLICANT: Edward M. Brown
APPLICANT: Steven C. Hebert
APPLICANT: Forrest H. Fuller
APPLICANT: James E. Garrett, Jr.
TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
TITLE OF INVENTION: MOLECULES
                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VECPDGEYSDETDASACNKCPDDFWSNENHTSCIAKEIEFLSWTEPFGIALTLFAVLGIF 625
                                                                                                                   NUMBER OF SEQUENCES:
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                                                       STREET:
                                                                                      ADDRESSEE:
                        Los Angeles
               California
                                                       E: Lyon & Lyon
First Interstate World
Suite 4700
                                         633 West Fifth Street
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AFLICATION NUMBER: U.S. 1992
FILING DATE: 21 August, 1992
APPLICATION NUMBER: U.S. 07/834,044
FILING DATE: 11 February, 1992
FILING DATE: 11 February, 1992
FILING DATE: 11 February, 1992
FILING DATE: 11 February, 1991
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PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
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PRIOR APPLICATION NUMBER: 08/
FILING DATE: 9 December
APPLICATION NUMBER: PCT
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FASTSEQ
                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: protein
JENCE 1078 AA; 120573 MW; 6153012 CN;
                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 1078 amino aci
                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 23 August, ATTORNEY/AGENT INFORMATION: NAME: Heber, Sheldon O.
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VGTIAADDDYGRPGIEKFREEAEERDICIDFSELI--SQYSDEEEIQHVVEVIQNSTAKV
                                                                                                                                     HAVTTAALLGPFLMPLVSYEASSVVLSAKRKFPSFLRTVPSDRHQVEVMVQLLQSFGWVW
                                                                                                                                                            VSTAVANLLGLEYIPQVSYASSSRLLSNKNQFKSFLRTIPNDEHQATAMADIIEYFRWNW
                                                                                                                                                                                                    PNLTLGYRIFDTCNTVSKALEATLSFVAQNKIDSLNLDEFCNCSEHIPSTIAVVGATGSG 148
                                     VVVFSN-RHLARVFFRSVVLANLTGKVWVASEDWA----IS-T-YITSVTG-IQ-GI--G
                                                  IVVFSSGPDLEPLI-KEIVRRNITGKIWLASEAWASSSLIAMPQYFHVVGGTIGFALKAG
                                                                                                                                                                                       PNITLGYELYDVCSESANVY-ATLRVLALQGPRHIEIQK--DLRNHSSKVVAFIGPDNTD 149
                                                                                                                                                                                                                                      GDFLLAGLFSLHGDCLQVRHRPLVTSCDRPDS--FNGHGYHLFQAMRFTVEEINNSSALL
                                                                                    ISLIGSYGDYGQLGVQALEELAVPRGICVAFKDIVPFSARVGDPRMQSMMQHLAQARTTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 21 October, 1994
APPLICATION NUMBER: U.S. 08/292,827
APPLICATION NUMBER: U.S. 08/292,827
FILING DATE: 23 August, 1994
FILING DATE: U.S. 08/141,248
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APPLICATION NUMBER: U.S. 08/017,127
NUMBER: U.S. 08/017,127
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TELEFAX: (213) 955-0440
TELEX: 67-3510
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                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
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l Similarity 32.0%;
273; Conservative
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UMBER: PCT/US/94/12117
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Pred. No. 2
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2.40e-97;
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STREET: First Interstate World Center STREET: Suite 4700
STREET: Galifornia
CITY: Los Angeles
GOUNTRY: USA
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb st
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FASTSEO
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,565
                                                                                                                                                                                                                                                                                                                                                                Sequence 7, Application US/08484565 Patent No. 5763569
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                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                 APPLICANT: Edward M. Brown
APPLICANT: Steven C. Hebert
APPLICANT: James E. Garrett, Jr.
TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
TITLE OF INVENTION: MOLECULES
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Best Local !
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 7:
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FILING DATE: 9 December.
APPLICATION NUMBER: PCT/US/94/1211/
FILING DATE: 21 October, 1994
APPLICATION NUMBER: U.S. 08/292,827
APPLICATION NUMBER: U.S. 08/292,827
TILING DATE: 23 August, 1994
TILING DATE: U.S. 08/141,248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 21 August, 1992
APPLICATION NUMBER: U.S. 07/834,044
FILING DATE: 11 February, 1992
APPLICATION NUMBER: U.S. 07/749,451
FILING DATE: 23 August, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Heber, Sheldon O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 23 August, 1994
APPLICATION NUMBER: U.S. 08/141,248
FILING DATE: 22 October, 1993
APPLICATION NUMBER: U.S. 08/009,389
FILING DATE: 23 February, 1993
APPLICATION NUMBER: U.S. 08/017,127
FILING DATE: 12 February, 1993
APPLICATION NUMBER: U.S. 08/017,127
FILING DATE: 12 February, 1993
APPLICATION NUMBER: U.S. 07/934,161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein FINCE 1078 AA; 120573 MW; 6153012 CN;
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LENGTH: 1078 amino aci
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PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER:
 NGSCADIKKVEAWQVLKHLRHLNFTNNMGEQVTFDECGDLVGNYSIINWHLSPEDGSIVF
                                                                                                                                         QIPGFREFLKKVHPRKSVHNGFAKEFWEETFNCHLQEGAKGPLPVDTFLRGHEESGDRFS
                                                                                                                                                                        VVVFSN-RHLARVFFRSVVLANLTGKVWVASEDWA----IS-T-YITSVTG-IQ-GI--G
                                                -CSTN-Q-LCRECHTFTTRNMPTLGAFSMSAAYRVYEAVYAVAHGLHQL---L-GC---T
                                                                             NSSTAFRPLCTGDENISSVETPYIDYTHLRISYNVYLAVYSIAHALQDIYTCLPGRGLFT
                                                                                                          TVLG----VA-VQQRQ-VP-GL-KEF-EESY---VR-AVTAA-P--S---ACPE-GSW--
                                                                                                                                                                                                   IVVFSSGPDLEPLI-KEIVRRNITGKIWLASEAWASSSLIAMPQYFHVVGGTIGFALKAG
                                                                                                                                                                                                                                    ISLIGSYGDYGQLGVQALEELAVPRGICVAFKDIVPFSARVGDPRMQSMMQHLAQARTTV
                                                                                                                                                                                                                                                                   VGTIAADDDYGRPGIEKFREEAEERDICIDFSELI--SQYSDEEEIQHVVEVIQNSTAKV
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                                                                                                                                                                                                                                                                                                                                                             PNITLGYELYDVCSESANVY-ATLRVLALQGPRHIEIQK--DLRNHSSKVVAFIGPDNTD 149
                                                                                                                                                                                                                                                                                                                                                                                            PNLTLGYRIFDTCNTVSKALEATLSFVAQNKIDSLNLDEFCNCSEHIPSTIAVVGATGSG
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REGISTRATION NUMBER:
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Pred. No. 2
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92 88 49;

407

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SOTUMARE: FASTISEQ
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,751
FILING DATE: 7 June, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA: including application PRIOR APPLICATION DATA: described below: 9
APPLICATION NUMBER: 08/353,784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 7, Application US/08480751
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                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Di
                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Edward M. Brown
APPLICANT: Steven C. Hebert
APPLICANT: Forrest H. Fuller
APPLICANT: James E. Garrett, Jr.
TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
TITLE OF INVENTION: MOLECULES
                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICATION NUMBER: U.S. 08/292,827
APPLICATION NUMBER: U.S. 08/41,248
APPLICATION NUMBER: U.S. 08/141,248
TILING DATE: 22 October, 1993
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       EIIG--SA-SLSPVHLDINKTKIQWHGKNNQVPVSVCTTDCLAGHHRVVV-GSHHCCFEC
                                  KEVGYYNVYAKKGERLFINEEKILWSGFSREVPFSNCSRDCLAGTRKGIIEGEPTCCFEC
                                                                                                                                                         NSSTAFRPLCTGDENISSVETPYIDYTHLRISYNVYLAVYSIAHALQDIYTCLPGRGLFT
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TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                   NGSCADIKKVEAMQVLKHLRHLNFTNNMGEQVTFDECGDLVGNYSIINWHLSPEDGSIVF: |: || : | : || : | : || : : |
                                                                                                                           -CSTN-Q-LCRECHTFTTRNMPTLGAFSMSAAYRVYEAVYAVAHGLHQL---L-GC---T
                                                                                                                                                                                       TVLG----VA-VQQRQ-VP-GL-KEF-EESY---VR-AVTAA-P--S---ACPE-GSW--
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APPLICATION NUMBER: U.S. 07/749,451
FILING DATE: 23 AUGUST, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Heber, Sheldon O.
REGISTRATION NUMBER: 38,179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 22 October, 1993
APPLICATION NUMBER: U.S. 08/009,389
FILING DATE: 23 February, 1993
APPLICATION NUMBER: U.S. 08/017,127
FILING DATE: 12 February, 1993
APPLICATION NUMBER: U.S. 07/934,161
FILING DATE: 21 August, 1992
APPLICATION NUMBER: U.S. 07/834,044
                                                                  REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                 VVVFSN-RHLARVFFRSVVLANLTGKVWVASEDWA----IS-T-YITSVTG-IQ-GI--G
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TELEX: 67-3510
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Similarity 32.0%;
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1078 AA; 120573 MW; 6153012 CN;
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RESULT

US-08-480-751-7

Patent No. GENERAL I Sequence 7,

INFORMATION:

Edward

5858684

APPLICANT:
APPLICANT:
APPLICANT:

ADDRESSEE: Lyo

STREET:
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STREET:
CITY: LC
STATE: C
COUNTRY:

9007

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Patent No
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                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/O
FILING DATE: 7 June, 199
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA: 11
PRIOR APPLICATION DATA: 11
        APPLICATION NUMBER: 08/353,784
FILING DATE: 9 December, 1994
APPLICATION NUMBER: PCT/US/944/12117
FILING DATE: 21 October, 1994
APPLICATION NUMBER: U.S. 08/292,827
FILING DATE: 23 August, 1994
APPLICATION NUMBER: U.S. 08/141,248
APPLICATION NUMBER: U.S. 08/141,248
APPLICATION NUMBER: 19.5. 08/141,248
APPLICATION NUMBER: 19.5. 08/141,248
                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Edward M. Brown
APPLICANT: Steven C. Hebert
APPLICANT: James E. Garrett, Jr.
TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
TITLE OF INVENTION: MOLECULES
NUMBER OF SEQUENCES: 20
                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44
COMPUTER: IBM PC compatible
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FASTSEO
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FILING DATE:
APPLICATION |
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NUMBER:
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FILING DATE: 11 February, 1992
APPLICATION NUMBER: U.S. 07/749,451
FILING DATE: 23 August, 1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 1079 amino aci
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TELECOMMUNICATION INFORMATION:
          LLVGTAGLFAWHFH-TPVVRSAGGRLCFLMLGSLVAG-SCSFYSFFGEPTVPACLLRQPL
                                LTAFVLGVFI-KFRNTPIVKATNRELSYLLLFSLLCCFSSSLF-FIGEPQDWTCRLRQPA
                                                                           VECPDGEYSGETDASACDKCPDDFWSNENHTSCIAKEIEFLAWTEPFGIALTLFAVLGIF
                                                                                                                             KEVGYYNVYAKKGERLFINEEKILWSGFSREVPFSNCSRDCQAGTRKGIIEGEPTCCFEC
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                                                                                                             EIIG--SA-SLSPVHLDINKTKIQWHGKNNQVPVSVCTTDCLAGHHRVVV-GSHHCCFEC
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                                                            VPCEAGTFLNMSELHICQPCGTEEWAPKESTTCFPRTVEFLAWHEPISLVLIAANTLLLL
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TOPOLOGY:
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FILING DATE: 12 February, 1993
APPLICATION NUMBER: U.S. 07/934,151
FILING DATE: 21 August, 1992
FILING DATE: 21 August, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
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31.6%;
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Pred. No. 6.48e-97;
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                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: PC-DOL SOFTWARE: FASTSEO CURRENT APPLICATION DATA: APPLICATION NUMBER: US/OFILING DATE: 7 June, 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: IBM FC compatible
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APPLICANT:
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CORRESPONDENCE ADDRESS:
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                                                                                                                                     APPLICATION NUMBER: PCT/US/17,
FILING DATE: 21 October, 1994
APPLICATION NUMBER: U.S. 08/292,827
APPLICATION NUMBER: U.S. 08/292,827
FILING DATE: 23 August, 1994
FILING DATE: 123 August, 1994
FILING DATE: 123 August, 1994
FILING DATE: 1993
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CITY: I
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                      FILING DATE: 23 February,
APPLICATION NUMBER: U.S. 08/017,127
FILING DATE: 12 February, 1993

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                                                                                                                  FILING DATE: 22 October, 1993
APPLICATION NUMBER: U.S. 08/009,389
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Edward M. Brown
Steven C. Hebert
Forrest H. Fuller
James E. Garrett, Jr.
VENTION: CALCIUM RECEPTOR-ACTIVE
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BER: U.S.
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: described below: 9
08/353,784
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  07/834,044
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MOLECULE TYPE: protein
JENCE 1079 AA; 120867
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEPAX: (213) 955-0440
TELEX: 67-3510
TELEX: 67-3510
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APPLICATION NUMBER: U.S. 07/74/
FILING DATE: 23 August, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Heber, Sheldon O.
BEGGGTERSTON WILDER
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WLYTAPPSSYRNHELEDEIIFITCHEGSLMALGSLIGYTC-LLAAICFFF-AFKSRKLPE
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                                                                                                                                                                                                                  VPCEAGTFLNMSELHICQPCGTEEWAPKESTTCFPRTVEFLAWHEPISLVLIAANTLLLL
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                                                                                                                                                                            LTAFVLGVFI-KFRNTPIVKATNRELSYLLLFSLLCCFSSSLF-FIGEPQDWTCRLRQPA
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                                                         FSLGFAIFLSCLTIRSEQLVIIFKFSTKVPT-FYRTWAQNHGAGLFVIVSSTVHLLICLT
                                                                                                FGISFVLCISCILVKTNRVLLVFE--AKIPTSFHRKWWGLNLQFLLVFLCTFMQILICII
                                                                                                                                       LLVGTAGLFAWHFH-TPVVRSAGGRLCFLMLGSLVAG-SCSFYSFFGEPTVPACLLRQPL
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larity 31.6%;
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Pred. No. 6
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Patent No
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PRIOR APPLICATION NUMBER: PCT/C/
APPLICATION NUMBER: U.S. 08/292,827
APPLICATION NUMBER: U.S. 08/292,827
FILING DATE: 23 August, 1994
APPLICATION NUMBER: U.S. 08/141,248
APPLICATION NUMBER: U.S. 08/141,248
TTIING DATE: 22 October, 1993
TTIING DATE: 12 OSTOBER: U.S. 08/009,389
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Di
COMPUTER: IBM PC con
                                ATTORNEY/AGENT INFORMATION:
NAME: Heber, Sheldon O.
REGISTRATION NUMBER: 38,
                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 514
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
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                                                                                                                                APPLICATION NUMBER: U.S.
APPLICATION NUMBER: U.S.
APPLICATION TATE: 21 August,
T.S.
T.S.
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                                                                          APPLICATION NUMBER: U.S. 07/834,044
FILING DATE: 11 February, 1992
APPLICATION NUMBER: U.S. 07/749,451
FILING DATE: 23 August, 1991
                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE: 9 Dec
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SOFTWARE: FASTSE
                                                                                                                                                                                       APPLICATION NUMBER:
                     REFERENCE/DOCKET NUMBER:
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633 West Fifth
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Bradford C. Van Wagenen, Manuel
F. Balandrin, Forrest H. Fuller,
Eric G. DelMar, and Scott T. Moe
WENTION: CALCIUM RECEPTOR-ACTIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
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12 February, 1955
11.S. 07/934,161
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UMBER: U.S. 08/017,127
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   INFORMATION:
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TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 1079 amino acids
TYPE: amino acid
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                                              NYNEAKCVTFSLLLNFVSWIAFFTM-ASIYQGSYLPAVNVLAGLTTLSGGFSGYFLPKCY
                                                                 NENEAKFITESMLIFFIVWISFIPAYASTY-GKFVSAVEVIAILAASFGLLACIFFNKVY
                                                                                                                                                                         FSLGFAIFLSCLTIRSFQLVIIFKFSTKVPT-FYRTWAQNHGAGLFVIVSSTVHLLICLT
                                                                                                                                                                                                       FGISFVLCISCILVKTNRVLLVFE--AKIPTSFHRKWWGLNLQFLLVFLCTFMQILICII
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                                                                                                           WLVMWTPRPTREYQRFPHLVILECTEVN--SVGFLLAFTHNILLSISTFVCSYLGKELPE
                                                                                                                                        WLYTAPPSSYRNHELEDEIIFITCHEGSLMALGSLIGYTC-LLAAICSFF-AFKSRKLPE
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APPLICANT: E
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APPLICANT: J
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                               TELECOMMUNICATION INFORMATION: (213) 489-1600
TELEFAX: (213) 955-0440
TELEY: 67-3510
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                               FILING DATE: 11 February, 1992
APPLICATION NUMBER: U.S. 07/749,451
FILING DATE: 23 August, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Heber, Sheldon O.
REGISTRATION NUMBER: 38,179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: CALCIUM RITITLE OF INVENTION: MOLECULES NUMBER OF SEQUENCES: 20
                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 0
FILING DATE: 9 Decemb
APPLICATION NUMBER: P
FILING DATE: 21 Octob
                                                                                                                                                                                  FILING DATE: 23 February, 1993
APPLICATION NUMBER: U.S. 08/017,127
FILING DATE: 12 February, 1993
APPLICATION NUMBER: U.S. 07/934,161
FILING DATE: 21 August, 1992
APPLICATION NUMBER: U.S. 07/834,044
                                                                                                                                                                                                                                                   FILING DATE: 21 October, 1994
APPLICATION NUMBER: U.S. 08/292,827
FILING DATE: 23 August, 1994
APPLICATION NUMBER: U.S. 08/141,248
FILING DATE: 22 October, 1993
APPLICATION NUMBER: U.S. 08/009,389
ETILING DATE: 25 OCTOBER, 1993
APPLICATION NUMBER: U.S. 08/009,389
                                                                                                     REGISTRATION NUMBER: 38, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 08/484,565
FILING DATE: 7-June-1995
                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/0 FILING DATE: 03-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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California
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Suite 4700
633 West Fifth Street
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Steven C. Hebert
James E. Garrett, Jr.
VENTION: CALCIUM RECEPTOR-ACTIVE
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JMBER: U.S. 08/017,127
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JENCE 1079 AA;
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 VILCRPELNNTEHFQASIQDYT
                           IILFKPSRNTIEEVRSSTAAHA
                                                      NYNEAKCYTFSLLLNFVSWIAFFTM-ASIYQGSYLPAVNVLAGLTTLSGGFSGYFLPKCY
                                                                                                            WLVMWTPRPTREYQRFPHLVILECTEVN -- SVGFLLAFTHNILLSISTFVCSYLGKELPE
                                                                                                                                      WLYTAPPSSYRNHELEDEIIFITCHEGSLMALGSLIGYTC-LLAAICFFF-AFKSRKLPE
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272; Conser
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120867 MW; 6054255 CN;
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Query Match
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                                             MOLECULE TYPE: SEQUENCE 1079 AA;
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                                                                                                 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA: including applipation of the prior application data: described below application NUMBER: 08/353,784

FILING DATE: 9 December, 1994

APPLICATION NUMBER: PCT/US/94/12117

FILING DATE: 21 October, 1994

APPLICATION NUMBER: U.S. 08/292,827

FILING DATE: 23 August, 1994

APPLICATION NUMBER: U.S. 08/292,827
                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-D SOFTWARE: FASTSEO CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/485 FILING DATE: 7 June, 1995 CLASSIFICATION: 435
                                                                                                                                                                                                       APPLICATION NUMBER: U.S. 07/934,161
FILING DATE: 21 August, 1992
APPLICATION NUMBER: U.S. 07/834,044
FILING DATE: 11 February, 1992
APPLICATION NUMBER: U.S. 07/749,451
FILING DATE: 23 August, 1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette,
                                                                                                                        REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEEX: 67-3510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
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STREET:
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CITY: Lo
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                                                                                                                                                                                                                                                                                                                FILING DALL.
APPLICATION NUMBER: U.S. 00/11.
FILING DATE: 22 October, 1993
FILING DATE: U.S. 08/009,389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
ZIP: 90
                                                                                                                                                                                 NAME: Heber, Sheldon O. REGISTRATION NUMBER: 38,179
                                                                   TOPOLOGY:
                                                                                         LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
 . Similarity
272; Conser
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Edward M. b..

f: Steven C. Hebert

(T: Forrest H. Fuller

T: James E. Garrett, Jr.

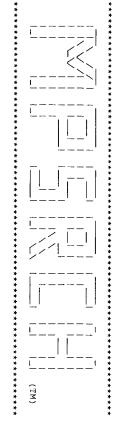
TON: CALCIUM RECEPTOR-ACTIVE

MOLECULES
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                                                                                                                      WLVMWTPRPTREYQRFPHLVILECTEVN -- SVGFLLAFTHNILLSISTFVCSYLGKELPE
                                                                                                                                                                                                     FGISFVLCISCILVKTNRVLLVFE--AKIPTSFHRKWWGLNLQFLLVFLCTFMQILICII
                                                                                                                                                                                                                                                                                                                                                                                                                                                       NGSCADIKKVEAWQVLKHLRHLNFTNNWGEQVTFDECGDLVGNYSIINWHLSPEDGSIVF
VILCRPELNNTEHFQASIQDYT
                            IILFKPSRNTIEEVRSSTAAHA
                                                            NYNEAKCVTFSLLLNFVSWIAFFTM-ASIYQGSYLPAVNVLAGLTTLSGGFSGYFLPKCY
                                                                           NENEAKEITESMLIFEIVWISEIPAYASTY-GKEVSAVEVIAILAASEGLLACIFENKVY
                                                                                                                                                   WLYTAPPSSYRNHELEDEIIFITCHEGSLMALGSLIGYTC-LLAAICFFF-AFKSRKLPE
                                                                                                                                                                                     FSLGFAIFLSCLTIRSFQLVIIFKFSTKVPT-FYRTWAQNHGAGLFVIVSSTVHLLICLT
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                                                                                                                                                                                                                                                                                                          VPCEAGTFLNMSELHICQPCGTEEWAPKESTTCFPRTVEFLAWHEPISLVLIAANTLLLL
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Search completed: Fri Mar 17 13:10:13 2000 Job time: 31 secs.

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm Run on:

Fri Mar 17 13:00:08 2000; MasPar time 39.94 Seconds

Run on: Fri Mar 17 13:00:08 2000; MasPar time 39.94 Seconds
Tabular output not generated.

498.146 Million cell updates/sec

Title: >US-09-361-652-1

Description: (1-840) from US09361652.pep

Perfect Score: 6338

Sequence: 1 MLFWAAHLLLSLQLVYCWAF.....NNTEHFQASIQDYTRRCGTT 840

Scoring table:

PAM 150 Gap 11

earched: 188963 seqs, 23686106 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: a-geneseq36 1:geneseqp

Statistics: Mean 38.602; Variance 175.356; scale 0.220

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Mouse pheromone recept	Human mGluR5c.	Human mGluR5b.		Rat pheromone receptor		Amino acid sequence of	11	Human parathyroid calc	Human parathyroid calc	rathyroid cel	ark ki		yroid cal	Rat kidney calcium rec	Rat kidney extracellul	Human parathyroid cell	Parathyroid calcium re	cal	d cal	Bovine parathyroid cel	thyro	Bovine parathyroid cal	Description	
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Rat pheromone receptor Rat metabotropic gluta	Human mGluR7b.	Human mGluR7a.	Human mGluR7 clone cmR	Metabotropic glutamate	Mouse pheromone recept		Human metabotropic glu	Amino acid sequence of	Human mGluR3.		Rat pheromone receptor	HSmGluR1.	Human mGluR1B.	Metabotropic glutamate	GLU-G-R subtype la.	Amino acid sequence of	GLU-G-R subtype 1b.	Human mGluR4.	Human mGluR4.	Human metabotropic glu
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ALIGNMENTS

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method described above. The compounds identified can be used to treat diseases or disorders characterised by abnormal calcium homeostasis, e hyperparathyroidism, osteoporosis and other bone and mineral-related disorders. They can also be used for the treatment of diseases and disorders associated with disrupted Ca2+ responses, e.g. seizures, stroke, spinal cord injury, hypoxia-induced nerve cell damage such as cardiac arrest or neonatal distress, epilepsy, neurodegenerative diseases such as Alzheimer's disease, Huntington's disease and
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                                                                                                                                                                                                                                                                                             FGISFVLCISCILVKTNRVLLVFE--AKIPTSFHRKWWGLNLQFLLVFLCTFMQIVICAI
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NYNEAKCYTFSLLLNFVSWIAFFTM-ASIYQGSYLPAVNVLAGLTTLSGGFSGYFLPKCY
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272; Conse
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llarity 31.9%;
Conservative
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Pred. No. 1.79e-106;
232; Mismatches 275;
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Best Local :
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07-JUN-1995; US-484565.
23-AUG-1991; US-749451.
11-FBB-1992; US-834044.
21-AUG-1992; US-934161.
12-FBB-1993; US-017127.
23-FBB-1993; US-017127.
23-FBB-1993; US-017127.
23-FBB-1993; US-017127.
21-OCT-1994; US-292827.
21-OCT-1994; US-353784.
(BGHM ) BRIGHAM & WOMENS HOSPITAL.
(NPSP-) NPS PHARM INC.
BIOWN EM, GATREET JE, Hebert SC;
WPI; 98-347412/30.
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W54844 standard; P
W54844;
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Bos sp.
US5763569-A.
09-JUN-1998.
07-JUN-1995; 4845
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Bovine paratl
Calcium ion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antibody production
(Claim 5; Fig 47; 174pp; English.
The bovine parathyroid calcium receptor gene encodes a 1085 amino acid protein. The tissue from which this receptor and receptors from human parathyroid and rat kidney are derived, respond to changes, and control changes, in calcium ion concentration, e.g. parathyroid hormone regulates (22) homeostasis in blood and extracellular fluid, and kidney function alters through changes in Ca2+ levels in juxtaglomerular and proximal tubule cells in the kidney. The purified receptors (produced receptor activity, especially those that can be used to screen for compounds that modulate calcium receptor activity, especially those that can be used to treat diseases associated with the receptors in these tissues. They can also be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Calcium receptor poly:peptide(s) -
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TVLG---
                  IVVFSSGPDLEPLI-KEIVRRNITGRIWLASEAWASSSLIAMPEYFHVVGGTIGFGLKAG
                                                                                                                                ISLIGSYGDYGQLGVQALEELAVPRGICVAFKDIVPFSARVGDPRMQSMMQHLAQARTTV
                                                                                                                                                               VGTIAADDDYGRPGIEKFREEAEERDICIDFSELI--SQYSDEEKIQQVVEVIQNSTAKV
                                                                                                                                                                                                                                ISTAVANLLGLFYIPQVSYASSSRLLSNKNQFKSFLRTIPNDEHQATAMADIIEYFRWNW
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                                                                                                                                                                                                                                                                                              PNMTLGYRIFDTCNTVSKALEATLSFVAQNKIDSLNLDEFCNCSEHIPSTIAVVGATGSG 149
                                                                                                                                                                                                                                                                                                                                GDFLLAGLFSLHGDCLQVRHRPLVTSCDRPDS--FNGHGYHLFQAMRFTVEEINNSSALL
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parathyroid calcium receptor 1 protein 5Kb fragment.
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Similarity 31.9%;
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-VA-VQQRQ-VP-GL-KEF-EESY---VR-AVTAA-P--S---
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                                                                                                                                                                                                                                                                                                                                                                                                 232; Mismatches 275;
                                                                                                                                                                                                                                                                                                                                                                                                                Score 1311; DB 1;
Pred. No. 1.79e-106;
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                                                               IS-T-YITSVTG-IQ-GI--G
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18-NOV-1997.
07-JUN-1995. US-485588.
07-JUN-1995. US-485588.
07-JUN-1995. US-834044.
11-FEB-1992. US-934151.
11-FEB-1992. US-934151.
12-FEB-1993. US-017127.
23-FEB-1993. US-017127.
23-FEB-1993. US-141248.
19-AUG-1994. US-292827.
21-OCT-1994. WG-292827.
21-O
                                                                                       DNA encoding calcium receptor polypeptide(s) therapeutic purposes, e.g. hyperparathyroidism Claim 4; Columns 107-116; 174pp; English.
The present sequence is bovine parathyroid cell receptor 1 (BoPCaR 1).
The specification includes details of molecules that can modulate one or more inorganic ion receptor activities, and antibodies and antibody fragments targetted to inorganic ion receptor proteins. To proteins, nucleic acids and antibodies may be used to treat disorders by modulating one or more inorganic ion receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bovine parathyroid cell calcium receptor 1 (BoPCaR Bovine parathyroid cell calcium receptor 1; BoPCaR calcium homeostasis; hyperparathyroidism; osteoporo
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NPS PHARM INC.

M, Fuller FH, Garrett JE, F
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W54846;
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hyperparathyroidism and osteoporosequence 1085 Ap.
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VILCRPELNITE
                                    IILFKPSRNTIE
                                                                       NYNEAKCVTESLLLNEVSWIAFETM-ASIYQGSYLPAVNVLAGLTTLSGGESGYFLPKCY
                                                                                            NFNEAKFITFSKLIFFIVWISFIPAYASTY-GKFVSAVEVIAILAASFGLLACIFENKVY
                                                                                                                                            WLVMWTPRPTREYQREPHLVILECTEVN--SVGFTLAFTHNILLSISTEVCSYLGRELPE
                                                                                                                                                                                                                     LLVGTAGLFAWHFH-TPVVRSAGGRLCFLMLGSLVAG-SCSFYSFFGEPTVPACLLRQPL
                                                                                                                                                                                                                                                                                                                  LTAFVLGVFI-KFRNTDIVKATNRELSYLLLFSLLCCFSSSLF-FIGEPQDWTCRLRQPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IVVFSSGPDLEPLI-KEIVRRNITGRIWLASEAWASSSLIAMPEYFHVVGGTIGFGLKAG
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                                                                                                                                                                               WLNTAPPSSYRNHELEDEIIFITCHEGSLMALGFLIGYTC-LLAAICFFF-AFKSRKLPE
                                                                                                                                                                                                                                                        FGISFVLCISCILVKTNRVLLVFE--AKIPTSFHRKWWGLNLQFLLVFLCTFMQIVICAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -S-TN-Q-LCRECHTFTTRNMPTLGAFSMSAAYRVYEAVYAVAHGLHQLLGCTSE--I--
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272; Conser
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larity 31.9%;
Conservative
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Pred. No. 1.79e-106;
232; Mismatches 275;
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Best Local S
Matches 27
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21-OCT-1994;
08-DEC-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The tissue from which the human parathyroid calcium receptor and receptors from bovine parathyroid and rat kidney are derived, respond to changes, and control changes, in calcium ion concentration, e.g. parathyroid hormone regulates Ca2+ homeostasis in blood and extracellular fluid, and kidney function alters through changes in Ca2+ levels in juxtaglomerular and proximal tubule cells in the kidney. The purified receptors (produced recombinantly) can be used to screen for compounds that modulate calcium receptor activity, especially those that can be used to treat diseases associated with the receptors in these tissues. They can also be used to raise antibodies for use in detection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapie
US5763569-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; V26964.
Calcium receptor poly:peptide(s) -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 7; Fig 49; 174p
The tissue from which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             claim 7; Fig 49; 174pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (BGHM )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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22-OCT-1993;
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                                                                                                                                          QIPGFREFLKKVHPRKSVHNGFAKEFWEETFNCHLQEGAKGPLPVDTFLRGHEESGDRFS
                                                                                                                                                                    VVVFSN-RHLARVFFRSVVLANLTGKVWVASEDWA----IS-T-YITSVTG-IQ-GI--G
                                                                                                                                                                                      IVVFSSGPDLEPLI-KEIVRRNITGKIWLASEAWASSSLIAMPQYFHVVGGTIGFALKAG
                                                                                                                                                                                                                                                        VGTIAADDDYGRPGIEKFREEAEERDICIDFSELI--SQYSDEEEIQHVVEVIQNSTAKV
                                                                                                                                                                                                                                                                                HAVTTAALLGPELMPLVSYEASSVVLSAKRKEPSELRTVPSDRHQVEVMVQLLQSEGWVW
                                                                                                                                                                                                                                                                                                                                                                                               GDFLLAGLFSLHGDCLQVRHRPLVTSCDRPDS--FNGHGYHLFQAMRFTVEEINNSSALL
                                                                                                                                                                                                                                                                                                                                                                                                                 GDIILGGLFPIHFG-VAAKDQDLKSRPESVECIRYNFRGFRWLQAMIFAIEEINSSPALL 88
                                                                                   NSSTAFRPLCTGDENISSVETPYIDYTHLRISYNVYLAVYSIAHALQDIYTCLPGRGLFT
                                                                                                                                                                                                                                                                                                      VSTAVANILGIFYIPQVSYASSSRILSNKNQFKSFIRTIPNDEHQATAMADIIEYFRWNW
  SEICS-
                           NGSCADIKKVEAWQVLKHLRHLNFTNNMGEQVTFDECGDLVGNYSIINWHLSPEDGSIVF
                                                                                                                                                                                                                             ISLIGSYGDYGQLGVQALEELAVPRGICVAFKDIVPFSARVGDPRMQSMMQHLAQARTTV
                                                                                                                                                                                                                                                                                                                                        PNITLGYELYDVCSESANVY-ATLRVLALQGPRHIEIQK--DLRNHSSKVVAFIGPDNTD
                                                                                                                                                                                                                                                                                                                                                                    PNLTLGYRIFDTCNTVSKALEATLSFVAQNKIDSLNLDEFCNCSEHIPSTIAVVGATGSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   parathyroid calcium
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ch 20.4%;
Similarity 32.0%;
273; Conservative
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 RGPVYPWQLLQQIYKVNFLLH-ENTVAFDDNGDTLGYYDIIAWDWNGPE-WT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GHAM & WOMENS HOSPITAL.
PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-834044.

US-934161.

US-017127.

US-009389.

US-141248.

US-141248.

US-292827.

WO-U12117.

US-353784.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         concentration;
                                                                                                                -VA-VQQRQ-VP-GL-KEF
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US-749451.
                                                        LCRECHTFTTRNMPTLGAFSMSAAYRVYEAVYAVAHGLHQL---L-GC---T
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Pred.
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                                                                                                                -EESY---VR-AVTAA-P--S---ACPE-GSW--
                                                                                                                                                                                                                                                                                                                                                                                                                                                    e 1290; DB 1;
. No. 1.61e-104;
Mismatches 276;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           useful
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hormone; homeostasis;
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12-JAN-1999
07-JUN-1995
07-JUN-1995
US-749451
11-FEB-1992
US-94161
12-FEB-1992
US-94161
12-FEB-1993
US-017127
23-FEB-1993
US-017127
23-FEB-1993
US-017127
23-FEB-1993
US-0171248
19-AUG-1994
US-29827
21-OCT-1994
US-353784
Screening for calcium receptor-active compounds - by recombinant expression of nucleic acid encoding calcium receptor and determin the effect of compounds on calcium receptor activity claim 1; Fig 49; 176pp; English.

A method has been developed of screening for a compound able to a one or more activities of a calcium receptor (CR) comprises: (A) contacting a recombinant cell with a test compound, where the recombinant cell comprises a recombinant nucleic acid expressing provided that the cell does not have functional CR expression froe endogenous nucleic acid; (B) determining the ability of the test compound to affect one or more activities of the calcium receptor (C) comparing the ability with the ability of the test compound to
                                                                                                                                                                                                                                         (BGHM ) BRIGHA (NPSP-) NPS PH Balandrin MF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human parathyroid calcium receptor pHuPCaR 4.0.

Parathyroid calcium receptor; inorganic ion receptor; osteoporosis; calcium homeostasis; hyperparathyroidism; seizure; stroke; epilepsy spinal cord injury; hypoxia-induced nerve cell damage; cardiac arrestinal cord injury; hypoxia-induced nerve cell damage; cardiac arrestinated distress; neurodegenerative disease; Alzheimer's disease; neurodegenerative disease; Alzheimer's disease;
                                                                                                                                                                                                                             Hebert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  depression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Huntington's disease; Parkinson's disease; dementia; muscle
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parathyroid calcium
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NPS PHAF
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PHARM INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            affect the one or more CR activities in a cell not comprising recombinant nucleic acid. The present sequence represents huma parathyroid CR, designated a pHuPCaR 4.0. The nucleic acid see pHuPCaR 4.0 can be used as part of the recombinant nucleic acid
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                            NFNEAKFITFSMLIFFIVWISFIPAYASTY-GKFVSAVEVIAILAASFGLLACIFFNKIY
                                                                                                    WLVMWTPRPTREYQRFPHLVILECTEVN--SVGFLLAFTHNILLSISTFVCSYLGKELPE
                                                                                                                                                                    WLYTAPPSSYRNQELEDEIIFITCHEGSLMALGFLIGYTC-LLAAICFFF-AFKSRKLPE
                                                                                                                                                                                                                                        FSLGFAIFLSCLTIRSFQLVIIFKFSTKVPT
                                                                                                                                                                                                                                                                                                     FGISFVLCISCILVKTNRVLLVFE---AKIPTSFHRKWWGLNLQFLLVFLCTFMQIVICVI
                                                                                                                                                                                                                                                                                                                                                                     LIVGTAGLEAWHEH-TPVVRSAGGRICELMLGSLVAG-SCSFYSEFGEPTVPACLLRQPL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEICS-RGPVYPWQLLQQIYKVNFLLH-ENTVAFDDNGDTLGYYDIIAWDWNGPE-WT-F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -CSTN-Q-LCRECHTFTTRNMPTLGAFSMSAAYRVYEAVYAVAHGLHQL---L-GC---T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NSSTAFRPLCTGDENISSVETPYIDYTHLRISYNVYLAVYSIAHALQDIYTCLPGRGLFT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QIPGFREFLKKVHPRKSVHNGFAKEFWEETFNCHLQEGAKGPLPVDTFLRGHEESGDRFS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VPCEAGTFLNMSELHICQPCGTEEWAPKESTTCFPRTVEFLAWHEPISLVLIAANTLLLL
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Similarity 273; Conser
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Pred. No. 1
Mismatches
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PNLTLGYRIFDTCNTVSKALEATLSFVAQNKIDSLNLDEFCNCSEHIPSTIAVVGATGSG

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                                                                                                                                                                                                                           C gland adenoma tumour using pBoPCRRI as a hybridisation probe. mRNA was consisted from a 39 year old caucasian male diagnosed with primary chyperparathyroidism and two clones of approx. 5 and 4 kb were identified. These cDNA's were injected into Xenopus cocytes which were consisted for the presence of functional calcium receptors. Both clone types gave rise to functional calcium receptors as assessed by the compression of calcium-activated chloride currents upon addition of calcium receptor agonists, e.g. NPS R-467 and NPS R-568. Sequence analysis of the two cDNA clones indicated the existence of at cleast two sequence variants differing in the 3' untranslated region and compression may result from alternative polyadenyiation. Sequence variation also exists in the 5' end of the inserts. These sequence variation compared the calcium receptor variation occur within the coding regions of cDNA clones phupCaR5.2 and phupCaR4.0 demonstrating that they encoded distinct proteins. Sequence variation occur within the coding cregions of cDNA clones phupCaR5.2 and phupCaR4.0 demonstrating that they encoded distinct proteins. Sequence analysis of the human CaR gene concoded by pHupCaR5.2 between residues 536 and 537 of the protein encoded by pHupCaR5.2 between residues 536 and 537 of the protein encoded by pHupCaR5.2 between residues 536 and 537 of the protein encoded by pHupCaR5.2 between residues 536 and 537 of the protein encoded by pHupCaR5.1 between residues 536 and 537 of the protein encoded by pHupCaR5.1 between residues 536 and 537 of the protein encoded by pHupCaR5.1 between residues 536 and 537 of the protein encoded by pHupCaR5.1 between residues 536 and 537 of the protein encoded by pHupCaR5.1 between residues 536 and 537 of the protein encoded by pHupCaR5.1 between residues 536 and 537 of the protein encoded by pHupCaR5.1 between residues 536 and 537 of the protein encoded by pHupCaR5.1 between residues 536 and 537 of the protein encoded by pHupCaR5.2 between residues 536 and 537 of the protein encoded by pHup
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                                                                                                                                            Query Match
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21-OCT-1994; WO-U12117.
08-DEC-1994; US-353784.
(NPSP-) NPS PHARM INC.
Balandrin MF, Delmar EG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-APR-1997 (first entry)

Parathyroid calcium receptor encoded by clone phuPCaR4.0.

Parathyroid calcium receptor; human parathyroid gland adenoma tumour; pBoPCaR1; primary hyperparathyroidism; Xenopus occyte; alternative splicing; calcium-activated coloride current; agonist; NPS R-467; NPS R-568; variant; untranslated region; alternative polyadenylation; probe; variant; untranslated region; alternative polyadenylation; probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; Page 93-100; 231pp; English.
The sequences given in W11888-89 represent functional calcium
The cDNAs encoding these sequences were isolated from human pa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New di:arylalkyl amine cpds. useful for modulating receptor activities - esp. for modulating effect calcium on cell surface calcium receptors, useful
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W11889;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hyperparathyroidism, Paget's disease or osteoporosis Example 1; Page 93-100; 231pp; English.
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Pred. No. 1.61e-104;
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23-AUG-1991.
11-FEB-1992.
21-AUG-1992.
21-FEB-1993.
23-FEB-1993.
                                                                                                                                                                                                                                                      Human parathyroid cell calcium receptor 4.0 (HuPCaR Human parathyroid cell calcium receptor 4.0; HuPCaR calcium homeostasis; hyperparathyroidism; osteoporos
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US-749451.

US-834044.

US-934161.

US-934161.

US-017127.

US-009389.
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19-AUG-1994; US-292827.

21-OCT-1994; US-253784.

08-DEC-1994; US-353784.

(BGHM ) BRIGHAM & WOMENS H

(NPSP-) NPS PHARM INC.

Brown EM, Fuller FH, Garre

WPI; 98-008040/01.
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The specification includes details of molecules that can modulate one or more inorganic ion receptor activities, and antibodies and antibody fragments targetted to inorganic ion receptor proteins. I proteins, nucleic acids and antibodies may be used to treat disorders by modulating one or more inorganic ion receptor activities, preferably disorders of calcium homeostasis, e.g. hyperparathyroidism and osteoporosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA encoding calcium receptor polypeptide(s) - useful therapeutic purposes, e.g. hyperparathyroidism and ost Claim 20; Columns 125-134; 174pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; T95859
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                                                                         VPCEAGTFLNMSELHICQPCGTEEWAPKESTTCFPRTVEFLAWHEPISLVLIAANTLLLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -CSTN-Q-LCRECHTFTTRNMPTLGAFSMSAAYRVYEAVYAVAHGLHQL---L-GC---T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VVVFSN-RHLARVFFRSVVLANLTGKVWVASEDWA----IS-T-YITSVTG-IQ-GI--G
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l Similarity 32.0%;
273; Conservative
                                                                                                                                                                                                                                                                                 -SA-SLSPVHLDINKTKIQWHGKNNQVPVSVCTTDCLAGHHRVVV-GSHHCCFEC
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230; Mismatc
                       -AKIPTSFHRKWWGLNLQFLLVFLCTFMQIVICVI
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1.61e-104;
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Best Local S
Matches 27
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The invention relates to polynucleotide sequences encoding mammalian pheromone receptor polypeptides. The polypeptides are expressed in murine and rat vomeronasal organ. The products can be used for modifying pheromone activity, e.g. for decreasing pheromone receptor mediated signal transduction. They can be used for controlling fertility and behaviour in vertebrates and invertebrates. Compositions comprising the polypeptides are particularly useful in e.g. controlling fertility in livestock and controlling reproduction in rodents or insects by interrupting the normal behaviours of rodents or insects that result in reproduction. The present sequence represents a rat kidney extracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              W94928
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07-JAN-1999.
30-JUN-1998; U13680.
30-JUN-1997; US-051284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rat kidney extracellular calcium/polyvalent cation-sensing receptor. Pheromone receptor: signal transduction; fertility; behaviour;
                                                                                                                                                                                                                                                                                                                                                                                                                                             calcium/polyvalent cation-sensing receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      invertebrates
Disclosure; Page 169-170;
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             QIPGFREFLQKVHPRKSVHNGFAKEFWEETFNCHLQEGAKGPLPVDTFVRSHEEGGNRLL
                                            VVVFSN-RHLARVFFRSVVLANLTGKVWVASEDWA----IS-T-YITSVTG-IQ-GI--G
                                                                            IVVFSSGPDLEPLI-KEIVRRNITGRIWLASEAWASSSLIAMPEYFHVVGGTIGFGLKAG
                                                                                                                                       VGTIAADDDYGRPGIEKFREEAEERDICIDFSELI--SQYSDEEEIQQVVEVIQNSTAKV
                                                                                                                                                                        HAVTTAALLGPFLMPLVSYEASSVVLSAKRKFPSFLRTVPSDRHQVEVMVQLLQSFGWVW
                                                                                                                                                                                            VSTAVANLLGLEYIPQVSYASSSRLLSNKNQYKSFLRTIPNDEHQATAMADIIEYFRWNW
                                                                                                                                                                                                                                     PNITLGYELYDVCSESANVY-ATLRVLALQGPRHIEIQK--DLRNHSSKVVAFIGPDNTD
                                                                                                                                                                                                                                                                     PNMTLGYRIFDTCNTVSKALEATLSFVAQNKIDSLNLDEFCNCSEHIPSTIAVVGATGSG
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                                                                                                           ISLIGSYGDYGQLGVQALEELAVPRGICVAFKDIVPFSARVGDPRMQSMMQHLAQARTTV
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272; Conser
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Pred. No. 4.71e-104;
232; Mismatches 285;
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21-OCT-1994;
08-DEC-1994;
                                                                                                                                                                                                                                       23-AUG-1991;
11-FEB-1992;
21-AUG-1992;
12-FEB-1993;
                                                                                                                                                                                                                                                                                                                                                                                                               W54847
W54847
The tissue from which the rat kidney calcium receptor and receptors from bovine parathyroid and rat kidney are derived, respond to changes, and control changes, in calcium ion concentration, e.g. parathyroid hormone regulates Ca2+ homeostasis in blood and extracellular fluid, and kidney function alters through changes in Ca2+ levels in juxtaglomerular and
                                                    antibody production
Claim 8; Fig 50; 174pp;
The tissue from which t
                                                                                                                                              (BGHM )
(NPSP-)
                                                                                                                                                                                                  22-OCT
19-AUG
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07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                  Rattus sp.
US5763569-A
                                                                                          Calcium receptor poly:peptide(s) -
                                                                                                           N-PSDB; V26965
                                                                                                                                  Brown
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SP-) NPS PHARM INC.
WN EM, Garrett JE, Hebe
98-347412/30.
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US-8340461.
US-934161.
US-009389.
US-0141248.
US-292827.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              KEVGYYNYYAKKGERLFINEEKILWSGFSREVPFSNCSRDCQAGTRKGIIEGEPTCCFEC
                                                                                                           NENEAKFITESMLIFFIVWISFIPAYASTY-GKEVSAVEVIAILAASEGLLACIFENKVY
                                                                                                                                             WLVMWTPRPTREYQRFPHLVILECTEVN -- SVGFLLAFTHNILLSISTFVCSYLGKELPE
                                                                                                                                                                                 WLYTAPPSSYRNHELEDEIIFITCHEGSLMALGSLIGYTC-LLAAICFFF-AFKSRKLPE
                                                                                                                                                                                                                       FSLGFAIFLSCLTIRSFQLVIIFKFSTKVPT-FYRTWAQNHGAGLFVIVSSTVHLLICLT
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                                                                                                                                                                                                                                                                                             LLVGTAGLFAWHFH-TPVVRSAGGRLCFLMLGSLVAG-SCSFYSFFGEPTVPACLLRQPL
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VILCRPELNNTEHFQASIQDYT
                                                                         NYNEAKCYTFSLLLNFVSWIAFFTM-ASIYQGSYLPAVNVLAGLTTLSGGFSGYFLPKCY
                                                                                                                                                                                                                                                                                                                                                                   VPCEAGTFLNMSELHICQPCGTEEWAPKESTTCFPRTVEFLAWHEPISLVLIAANTLLLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PNMTLGYRIFDTCNTVSKALEATLSFVAQNKIDSLNLDEFCNCSEHIPSTIAVVGATGSG 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -CSTN-Q-LCRECHTFTTRNMPTLGAFSMSAAYRVYEAVYAVAHGLHQL---L-GC---T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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31.6%;
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. No. 4.71e-104;
Mismatches 285;
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                                                                                                                                                                                                                                                                                                                                                              contacting a recombinant cell with a test compound, where the recombinant cell comprises a recombinant nucleic acid expressing the CR, provided that the cell does not have functional CR expression from cendogenous nucleic acid; (B) determining the ability of the test compound to affect one or more activities of the calcium receptor; and (C) comparing the ability with the ability of the test compound to affect the one or more activities in a cell not comprising the recombinant nucleic acid. The present sequence represents rat parathyroid CR, designated a pRakCaR 3A. The nucleic acid sequence of pRakCaR 3A can be used as part of the recombinant nucleic acid in the method described above. The compounds identified can be used to treat diseases or disorders characterised by abnormal calcium homeostasis, e.g. typerparathyroidism, osteoporosis and other bone and mineral-related disorders. They can also be used for the treatment of diseases and disorders associated with disrupted Ca2+ responses, e.g. seizures, stroke, spinal cord injury, hypoxia-induced nerve cell damage such as in cardiac arrest or neonatal distress, epilepsy, neurodegenerative diseases such as Alzheimer's disease, Huntington's disease and demontial muscle tension and mineral-related and demontial demonts a muscle tension and apprietred and demontial demonts and apprietred and demontial demonts a muscle tension and apprietred and demontial demonts a muscle tension and apprietred and demonts and apprietred apprietred and demonts and apprietred apprietred and demonts and apprietred apprietred and apprietred apprietred and apprietred apprietred apprietred apprietred and apprietred apprie
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12-VAN-1999
07-JUN-1995; 480751.
07-JUN-1995; US-480751.
11-FEB-1992; US-934064.
11-FEB-1992; US-934161.
12-FEB-1993; US-017127.
23-FEB-1993; US-009389.
22-OCTT1994; US-292827.
21-OCT-1994; WO-UJ2117.
21-OCT-1994; WO-UJ2117.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Screening for calcium receptor-active compounds - by expression of nucleic acid encoding calcium receptor the effect of compounds on calcium receptor activity Claim 1; Fig 50; 176pp; English.

A method has been developed of screening for a compound one or more activities of a calcium receptor (CR) compounds on the compound of the co
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Parathyroid calcium receptor; inorganic ion receptor; osteoporosis;

calcium homeostasis; hyperparathyroidism; seizure; stroke; epilepsy;

spinal cord injury; hypoxia-induced nerve cell damage; cardiac arrest;

neonatal distress; neurodegenerative disease; Alzheimer's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; V82486
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W89566;
19-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                           Parkinson's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hebert SC,
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89
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                                                                                                                                          GDIILGGLFPIHFG-VAAKDQDLKSRPESVECIRYNFRGFRWLQAMIFAIEEINSSPSLL
                                                                     GDFLLAGLFSLHGDCLQVRHRPLVTSCDRPDS--FNGHGYHLFQAMRFTVEEINNSSALL
PNMTLGYRIFDTCNTVSKALEATLSFVAQNKIDSLNLDEFCNCSEHIPSTIAVVGATGSG
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NPS PHARM INC.
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                                                                                                                                                                                                                                                                                                                                                              1079
                                                                                                                                                                                                                                                                                                                                                                                        disease, dementia, muscle tension, depression,
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                                                                                                                                                                                                            Score 1285; DB 1;
Pred. No. 4.71e-104;
232; Mismatches 285;
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18-NOV-1995.
07-JUN-1995.
07-JUN-1995.
23-AUG-1992.
11-FEB-1992.
12-FEB-1993.
12-FEB-1993.
23-FEB-1993.
23-FEB-1993.
23-FEB-1993.
19-AUG-1994.
21-OCT-1994.
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W38275;
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(NPSP-)
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                                                                                                                                                                                                kidney cell calcium receptor 3A (RakC
kidney cell calcium receptor 3A; RakC
cium homeostasis; hyperparathyroidism;
                                                                                                                                                                                                                                                                                                                                                                  NENEAKFITFSMLIFFIVMISFIPAVASTY-GKFVSAVEVIAILAASFGLLACIFFNKVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VILCRPELNNTEHFQASIQDYT
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                                                                                                                                                                                                                                                                                                                                                                                                    WLVMWTPRPTREYORFPHLVILECTEVN--SVGFLLAFTHNILLSISTFVCSYLGKELPE
                                                                                                                                                                                                                                                                                                                                                                                                                           WLYTAPPSSYRNHELEDEIIFITCHEGSLMALGSLIGYTC-LLAAICFFF-AFKSRKLPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                FGISFVLCISCILVKTNRVLLVEE--AKIPTSFHRKWWGLNLQELLVFLCTFMQILICII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LTAFVLGVFI-KFRNTPIVKATNRELSYLLLFSLLCCFSSSLF-FIGEPQDWTCRLRQPA
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  EX.
                                                                                                                                                                                                                                                          standard;
) BRIGHAM & WOM
) NPS PHARM INC
EM, Fuller FH,
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                               US-485588.

US-749451.

US-749451.

US-934161.

US-934161.

US-017127.

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WO-U12117.

WO-U12117.
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            WOMENS
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 Garrett JE,
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Best Loc
Matches
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The present sequence is rat kidney cell calcium receptor 3A (RakCaR 3A).

The specification includes details of molecules that can modulate one or more inorganic ion receptor activities, and antibodies and antibody fragments targetted to inorganic ion receptor proteins. In proteins, nucleic acids and antibodies may be used to treat disorders by modulating one or more inorganic ion receptor activities, preferably disorders of calcium homeostasis, e.g. hyperparathyroidism and osteoporosis.
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NFNEAKFITFSMLIFFIVWISFIPAYASTY-GKFVSAVEVIAILAASFGLLACIFFNKVY
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ISLIGSYGDYGQLGVQALEELAVPRGICVAFKDIVPFSARVGDPRMQSMXQHLAQARTTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HAVTTAALLGPELMPLVSYEASSVVLSAKRKFPSFLRTVPSDRHQVEVMVQLLQSFGWVW
                                           WLYTAPPSSYRNHELEDEIIFITCHEGSLMALGSLIGYTC-LLAAICFFF
                                                                                    FSLGFAIFLSCLTIRSFQLVIIFKFSTKVPT-FYRTWAQNHGAGLFVIVSSTVHLLICLT
                                                                                                               FGISFVLCISCILVKTNRVLLVFE--AKIPTSFHRKWWGLNLQFLLVFLCTFMQILICII
                                                                                                                                                LLVGTAGLFAWHFH-TPVVRSAGGRLCFLMLGSLVAG
                                                                                                                                                                                                                                                                                       KEVGYYNVYAKKGERLFINEEKILWSGFSREVPFSNCSRDCQAGTRKGIIEGEPTCCFEC
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                            WLVMWTPRPTREYQRFPHLVILECTEVN - - SVGFLLAFTHNILLSISTFVCSYLGKELPE
                                                                                                                                                                            LTAFVLGVFI-KFRNTPIVKATNRELSYLLLFSLLCCFSSSLF-FIGEPQDWTCRLRQPA
                                                                                                                                                                                                                                                                                                                                SEICS-RGPVYPWQLLQQIYKVNFLLH-ENTVAFDDNGDTLGYYDIIAWDWNGPE-WT-F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PNMTLGYRIFDTCNTVSKALEATLSFVAQNKIDSLNLDEFCNCSEHIPSTIAVVGATGSG
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272; Conse
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larity 31.6%;
Conservative
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Pred.
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Mismatches 285;
                                                                                                                                              -SCSFYSFFGEPTVPACLLRQPL
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Best Local S
Matches 26
                                                                                                                                                                                                                                                                                                                                                                         from cells found in the collecting duct or late distal tubule in the kidney, intestine, gill, rectal gland, gonad or brain; an antibody that specifically binds to a PVCR; and a method of screening for aquatic PVCR agonists and antagonists. Modulation of the expression of the aquatic PVCR activates or inhibits aquatic PVCR mediated ion transport and endocrine changes that permit fish to adapt to fresh or salt water. The method facilitates the aquaculture of marine fish and can provide for the development of marine fish that are easily adaptable to fresh water aquaculture. Sequence 1026 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This protein comprises dogfish shark kidney calcium receptor related protein (SKCaR-RP), an aquatic polyvalent cation-sensing receptor (PVCR). Its amino acid sequence was deduced from a kidney cDNA clone (see T89290). It shows 74% homology to rat kidney CPVR and bowine parathyroid PVCR and possesses general features that are homologous to PVCR proteins, including a large extracellular domain, 7 transmembrane domains and a cytoplasmic C-terminal domain. Also claimed are: an isolated PVCR present in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated Aquatic polyvalent cation-sensing receptor - u develop products for increasing or decreasing the salinity of fish for use in aquaculture Claim 9; Fig 5A-B; 57pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dogfish shark kidney calcium receptor related protein (SKCaR-RP). Calcium receptor related protein; CaR-RP; dogfish shark; SKCaR-RP polycation-sensing receptor; aquaculture; fish farming;
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W32059;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                erminal domain. Also claimed are: an isolated PVCR present in plasma membranes of aquatic species, especially on the apical brane of epithelial cells of elasmobranch fish, particularly
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Human parathyroid cell calcium receptor 5.2 (HuPCaR
Human parathyroid cell calcium receptor 5.2; HuPCaR
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The present sequence is human parathyroid cell calcium receptor 5.2 (HupCaR 5.2).

The specification includes details of molecules that can modulate one or more inorganic ion receptor activities, and antibodies and antibody fragments targetted to inorganic ion receptor proteins. I proteins, nucleic acids and antibodies may be used to treat disorders by modulating one or more inorganic ion receptor activities, preferably disorders of calcium homeostasis, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hyperparathyroidism and osteoporosis.
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                                                                                                                                               DWTCRLRQPAFGISFVLCISCILVKTNRVLLVFE--AKIPTSFHRKWWGLNLQFLLVFLC
                                                                                                                                                                                       EIIG--SA-SLSPVHLDINKTKIQWHG--KN----N--QVPVSVCTTDCLAGHHRVVV
                                                                                                                                                                                                                                                                                                                                                                                KEVGYYNVYAKKGERLFINEEKILWSGFSREPLTFVLSVLQVPFSNCSRDCLAGTRKGII
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-AFKSRKLPENFNEAKFITFSMLIFFIVWISFIPAYASTY-GKFVSAVEVIAILAASFGL
                                   STVHLLICLTWLVMWTPRPTREYQRFPHLVILECTEVN--SVGFLLAFTHNILLSISTFV
                                                                         TEMQIVICVIWLYTAPPSSYRNQELEDEIIFITCHEGSLMALGFLIGYTC-LLAAICFFF
                                                                                                             VPACLLRQPLFSLGFAIFLSCLTIRSFQLVIIFKFSTKVPT-FYRTWAQNHGAGLFVIVS
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larity 31.8%;
Conservative
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Best Local :
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Claim 6; Fig 48; 174pp; English.

The tissue from which the human parathyroid calcium receptor and receptors from bovine parathyroid and rat kidney are derived, respond to changes, and control changes, in calcium ion concentration, e.g. parathyroid hormone regulates Ca2+ homeostasis in blood and extracellular fluid, and kidney function alters through changes in Ca2+ levels in juxtaglomerular and proximal tubule cells in the kidney. The purified receptors (produced recombinantly) can be used to screen for compounds that modulate calcium receptor activity, especially those that thissues. They can also be used to raise antibodies for use in detection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     W54845;
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VVVFSN-RHLARVFFRSVVLANLIGKVWVASEDWA----IS-T-YITSVTG-IQ-GI--G
                                           IVVFSSGPDLEPLI-KEIVRRNITGKIWLASEAWASSSLIAMPQYFHVVGGTIGFALKAG
                                                                                                    ISLIGSYGDYGQLGVQALEELAVPRGICVAFKDIVPFSARVGDPRMQSMMQHLAQARTTV
                                                                                                                             VGTIAADDDYGRPGIEKFRESASERDICIDESSII--SQYSDSEEIQHVVEVIQNSTAKV
                                                                                                                                                                                                      HAVTTAALLGPFLMPLVSYEASSVVLSAKRKFPSFLRTVPSDRHQVEVMVQLLQSFGWVW
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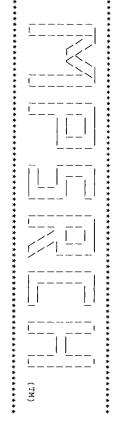
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07-JUN-1995; US-480751.
23-AUG-1991; US-749451.
11-FEB-1992; US-834044.
21-AUG-1992; US-934161.
12-FEB-1993; US-017127.
23-FEB-1993; US-017127.
23-FEB-1993; US-141248.
19-AUG-1994; US-292827.
21-OCT-1994; WS-273784.
                                                                                                                                                                                                                                                                                                                                              Parathyroid calcium receptor; inorganic ion receptor; osteoporosis; calcium homeostasis; hyperparathyroidism; selaure; stroke; epilepsy; spinal cord injury; hypoxia-induced nerve cell damage; cardiac arrest; neonatal distress; neurodegenerative disease; Alzheimer's disease;
                                                                                                                                                                                                                                                                                                                  Huntington's disease;
depression; anxiety.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      л 15
w89564 standard;
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                              Balandrin MF, Brown EN
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PHARM INC.
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CC contacting a recombinant cell with a test compound, where the
CC recombinant cell comprises a recombinant nucleic acid expressing the CR,
CC provided that the cell does not have functional CR expression from
CC endogenous nucleic acid; (B) determining the ability of the test
CC compound to affect one or more activities of the calcium receptor; and
CC (C) comparing the ability with the ability of the test compound to
CC affect the one or more CR activities in a cell not comprising the
CC recombinant nucleic acid. The present sequence represents human
CC parathyroid CR, designated a pHuPCaR 5.2. The nucleic acid sequence of
CC pHuPCaR 5.2 can be used as part of the recombinant nucleic acid in the
CC method described above. The compounds identified can be used to treat
CC disorders of disorders characterised by abnormal calcium homeostasis, e.g.
CC hyperparathyroidism, osteoporosis and other bone and mineral-related
CC disorders associated with disrupted CC2+ responses, e.g. seizures,
CC stroke, spinal cord injury, hypoxia-induced nerve cell damage such as in
CC cardiac arrest or neonatal distress, epilepsy, neurodegenerative
CC diseases such as Alzhelmer's disease, Huntington, depression, and anxiety
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A method has been developed of screening for a compound of sc
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LTLFAVLGIFLTAFVLGVFI-KFRNTPIVKATNRELSYLLLESLLCCFSSSLF-FIGEPQ | ::| |:| |:| |:| |:| |:| |:| |:| ||
                                                                                                                                                                                                                                                                                                                                                                                                       NGSCADIKKVEAWQVLKHLRHLINFTINIMGEQVTFDECGDLVGNYSIINWHLSPEDGSIVF: |: |: || || || || || : : ||
                                                                                                                                                                                                                                    EIIG--SA-SLSPVHLDINKTKIQWHG--KN----N--QVPVSVCTTDCLAGHHRVVV
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231; Mismatches 274;
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Search completed. Eri War 17 13.01.78 2000	803 FSGYFLPKCYVILCRPELNNTE 824	859 LACIFENKIYIILEKPSRNTIE 880	744 CSYLGKELPENYNEAKCVTFSLLLNEVSWIAFFTM-ASIYQGSYLPAVNVLAGLTTLSGG 802	801 -AFKSRKLPENFNEAKFITFSMLIFFIVWISFIPAYASTY-GKFVSAVEVIAILAASFGL 858	686 STVHLLICLTWLVMWIPRPTREYORFPHLVILECTEVNSVGFLLAFTHNILLSISTFV 743	742 TFMQIVICVIWLYTAPPSSYRNQELEDEIIFITCHEGSLMALGFLIGYTC-LLAAICFFF 800	627 VPACLLROPLESLGEAIFLSCLTIRSEQLVIIFKESTKVPT-FYRTWAQNHGAGLEVIVS 685	684 DWTCRLROPAFGISEVLCISCILVKINRVLLVFEAKIPTSFHRKWWGLNLQFLLVFLC 741	569 LIAANTLLLLLLVGTAGLFAWHFH-TPVVRSAGGRLCFLMLGSLVAG-SCSFYSFFGEPT 626

Search completed: Fri Mar 17 13:01:48 2000 Job time : 100 secs.



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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tabular output not generated Fri Mar 17 13:18:18 2000; MasPar time 113.49 Seconds 514.400 Million cell updates/sec

Description: Perfect Score: Sequence: >US-09-361-652-2 (1-842) from US09361652.pep 6366 MLFWAAHLLLSLQLAVAYCW.....NNTEHFQASIQDYTRRCGTT 842

Scoring table: PAM 150 Gap 11

Searched: 225878 seqs, 69334122 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

sptrembl12
1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human
1:sp_archea 2:sp_bacteria 7:sp_mhc 8:sp_organelle
5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle
9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified
13:sp_vertebrate 14:sp_virus

Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Mean 52.594; Variance 100.413; scale 0.524

SUMMARIES

Result	Score	% Query Match	Length DB	BID	Description	Pred. No.
1	5839	91.7	840 1	1 Q9Z0R8	PUTATIVE TASTE RECEPTO	0.00e+00
2	2026		4ω	1 Q9Z0R7	PUTATIVE TASTE RECEPTO	0.00e+00
ω	1421	22.3	68 1	3 073636	PHEROMONE RECEPTOR.	
4	1388	٠.	848 13	-	\circ	
ري ن	1358		4		PHEROMONE RECEPTOR.	6.14e-256
0	1334	۲.	40	07353	CALCIUM2+ SENSING RECE	
7	1279	20.1	4_	07363	PHEROMONE RECEPTOR.	
00	1258	9.	_	09355	PUTATIVE ODORANT RECEP	.52e-2
9	1251	9			PHEROMONE RECEPTOR.	1.52e-232
10	1236	9		07364		
11	1160	ω.	912 1:	41	PUTATIVE PHEROMONE REC	.0
12	1009		\vdash	1 070409	PUTATIVE PHEROMONE REC	. 7
13	974	15.3	779 1:	. 03526	PUTATIVE PHEROMONE REC	
14	881	w	۳,	3 093555	ODORANT RE	
15	832	ω	50 1	1 035189	PHEROMON	.33e-14
16	815	2	-ر	(J)	PUTATIVE ODORANT RECEP	.7C
17	798	2	03 1	1 035191	PUTATIVE PHEROMONE REC	.14e-
18	787		983 1	1 062916	METABOTROPIC GLUTAMATE	2.50e-132
19	785	2	66	526	PUTATIVE PHEROMONE REC	.67e-13
20	727	11.4		1 070413	PHEROMONE	.36€

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ALIGNMENTS

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181 RKFPSFLRTIPSDKYQVEVIVRLLQSFGWVWISLVGSYGDYGQLGVQALEELATPRGICV 240	179 RKFPSFLRTVPSDRHQVEVMVQLLQSFGMVMISLIGSYGDYGQLGVQALEELAVPRGICV 238	121 AQQGTGHLEMQRDLRNHSSKVVALIGPDNTDHAVTTAALLSPFLMPLVSYEASSVILSGK 180	119 ALQGPRHIEIQKDLRNHSSKYVAFIGPDNTDHAVTTAALLGPFLMPLVSYEASSVVLSAK 178	61 TSCDRSDSFNGHGYHLFQAMRFTVESINNSTALLPNITLGYELYDVCSESSNVYATLRVP 120	59 TSCDREDSENGHGYHLEQAMRETVEEINNSSALLPNITLGYELYDVCSESANVYATLRVL 118	1 MLFWAAHLLLSLQLAVAYCWAFSCQRTESSPGFSLFGDFLLAGLFSLHADCLQVRHRPLV 60	1 MLFWAAHLLLSLQL-V-YCWAFSCQRTESSPGFSLPGDFLLAGLFSLHGDCLQVRHRPLV 58	Query Match 91.7%; Score 5839; DE 11; Length 840; Best Local Similarity 90.0%; Pred. No. 0.00e+00; Matches 758; Conservative 55; Mismatches 27; Indels 2; Gaps 2;	EQUENCE 840 AA;	840 8	Receptor.	EMBL; AF127389; AAD18069.1;	Cell 96:541-551(1999).	selectivity.";	receptors: a	HOON M.A., ADDEK E., DINDEMELEK J., BATTEK J.F., KKBA N.J.F.,	9159821.	ISTAR;	SEQUENCE FROM N.A.	thi; Muridae; Murinae;	ota; Metazoa;	•	UTATIVE TASTE RECEPTOR TRI (FRAGMENT)	1-MAY-1999 (TremsI,re) 10.	-1999 (TERMBLEGE, 10, Creat		Q9Z0R8 PRELIMINARY; PRT; 840 AA.	

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                                                                                                                         O73636 PRELIMINARY; PKI; OVA....
O73636; OT-MIG-1998 (TREMBLrel. 07, Created)
O1-AUG-1998 (TREMBLrel. 07, Last sequence update)
O1-AUG-1998 (TREMBLrel. 12, Last annotation update)
O1-NOV-1999 (TREMBLrel. 12, Last annotation update)
PHEROMONE RECEPTOR.
CAO2.1.
Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
           SEQUENCE I
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LPAVNVLAGLATLSGGFSGYFLPKCYVILCRPELNNTEHF
                             TVAVEIFAILASSFGLILCIFAPKCFIILFKPEKNSKKHL 864
                                                          FLVAFAHNILLSISTFVCSYLGKELPENYNEAKCVTFSLLLHFVSWIAFFTMSSIYQGSY
                                                                           FWAVLGYIGLLAAVCLVLAVLARKLPDNFNEAKMITFSMLIFCAVWITFIPAYVSSPGKF
                                                                                                                 FYH-TWAQNHGAGIFVIVSSTVHLFLCLTWLAMWTPRPTREYQRFPHLVILECTEVNSVG
                                                                                                                                             SNVMKWFGPPQQRMTVVTFTSIQVLICIVWLVVNPPFPVRNLTTYKERIILECALGSSVG
                                                                                                                                                                                                       FSLTLCFLCSL-TFIGAPSHLSCMLRHTAFGITFVLCISCVLGKT--VVVLMAFRATLPG
                                                                                                                                                                                                                                                                                               VPVSVCTRDCLEGHHR-LVMGSHHCCFECMPCEAGTFLNTSELHTCQPCGTEEWAPEGSS
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Similarity 31.3%;
257; Conservative
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Pred. No. 9.53e-270;
208; Mismatches 320;
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Matches 25
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01-NOV-1999
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Proc. Natl. Acad. Sci. U.S.A. 95:11987-11992(1998).
EMBL: AF083081; AAC64076.1;
-FFAM: PF00003; 7tm_3; 1.
PFAM: PF010194; ANE receptor; 1.
PFRINTS; PR00248; GPCRMGR.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Neopteryqii; Teleostei; Euteleostei; Ostariophysi; (
Cyprinoidea; Cyprinidae; Cyprininae; Carassius.
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                              SLMICFICSI-TFIGRPTEWSCMIRHTAFGITFVLCISCVLGKTIVVLMAFE-ATLPGSN
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SLVAGS-CSLYSFFGKPTVPACLLRQPLFSLGFAIFLSCLTIRSFQLVIIFKFSTKVPTF
                                                                                                          CFSRTVEFLGWHEPISLVLLAANTLL-
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Pred. No. 1.64e-262;
216; Mismatches 310;
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01-AUG-1998
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EMBL; AB008859; BAA26124.1; -
PFAM; PF00003; 7tm_3; 1.
PFAM; PF01094; ANF_receptor; 1.
PRINTS; PR00248; GPCRMGR.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorpha;
Tetraodontiformes; Tetraodontoidei; Tetraodontidae; Fugu.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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                                                                                                                                                                                               SLVGSYGDYGQLGVQALE-ELATPRGICVAFKDVVPLSAQAGDPRNQRMMLRLARARTT-
                                                                                                                                                                                                                                                                                                       GLLVSDDDYGLHVARSFQSDLVQSGQGCLAYLEVLPWDNYLSENR--RIV-HVIKESTAR 277
                                                                                                                                                                                                                                                                                                                                                                                   TIASASVLGLYKIPMVSYFATCSCLINRQRFPSFFRTIPSDDFQVRAMIQILKHFGWTWV 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LPNLTLGYRLYDNCGALVVGFSGALALASGQEEA-FALQGG-CAGSPPVLGIVGDSLSTF 160
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VNFTTTFGDQVSFDENGDVLPIYDILNWQWLPDGRTQVQNVGEVKRSPSRGEELQIHEDK
                                       E-LGAFSMSAAYNVYEAVYAVAHGLHQLLGC----T-SG-TCARGP-VYPWQLLQQIYK
                                                                   EFLDVSNLRPEYNIYKAVYALAYALDDMLQCEPGRGPFSGGSCADIHKLEPWQFVHYLQH
                                                                                                                     QRQVPGLKEFEESY -- VQAVMGAP-RTCPE--G-SW-C--GTNQLCRECHAF-TTWNM-P
                                                                                                                                                            RGEITGLRDFLLRIRPGQSSNNTSYDMVQQFWEYSFQCKFGASGSAEACTGDENIQQVDA
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(TIEMBLIel. 07, Last sequence update)
(TIEMBLIel. 12, Last annotation updat
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Pred. No. 6.14e-256;
226; Mismatches 298;
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RESULT

O 073635

PRELIMINARY;

PRT; 940 AA.

AC 073635;

OT 01-AUG-1998 (TrEMBLrel. 07, Created)

DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)

DT 01-AUG-1999 (TrEMBLrel. 12, Last annotation update)

DE CALCIUM2+ SENSING RECEPTOR.

OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).

C Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;

OC Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorpha;

OC Tetraodontiformes; Tetraodontoidei; Tetraodontidae; Fugu.

RP SEQUENCE FROM N.A.

RA NALTO T., SAITO Y., YAMAMOTO J., NOZAKI Y., TOMURA K., HAZAMA M.,

RA NAKANISHI S., BRENNER S.;

RT FUGU."

PUCATIVE pheromone receptors related to the Ca2+-sensing receptor in Fugu."

RT FUGU. Natl. Acad. Sci. U.S.A. 95:5178-5181(1998).

DR EMBL; AB008857; BAA26122.1; -.

DR PFAM; PF00003; 7tm_3; 1.

DR PRINTS; PR00592; CASENSINGR.

SQ SEQUENCE 940 AA; 105814 MW; 034CB09E CRC32;
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                                                                                                          SAVSTAVANLLSLFYIPQISYASSSRLLSNKNQYKSFMRTIPTDEHQATAMADVIEYFQW
                                                                                                                                                                                       LLPNITLGYRIFDTCNTVSKALEATLSFYAQNKIDSLNLDEFCNCTDHIPATIAVVGAAG
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VWISLVGSYGDYGQLGVQALEELATPRGICVAFKDVVPLSAQAGDPRMQRMMLRLARART
                                                                                   TDHAVTTAALLSPFLMPLVSYEASSVILSGKRKFPSFLRTIPSDKYQVEVIVRLLQSFGW
                                                                                                                                                                  LLPNITLGYELYDVCSESSNVY-ATLRVPAQQGTGHLEMQR--DLRNHSSKVVALIGPDN 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YINSPGKYADAVEVFAILTSSFGLLVALFGPKCYIILFRPE 854
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                                                                                                                                                                                                                                                                                                                                    255;
                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                  238; Mismatches 283;
                                                                                                                                                                                                                                                                                                                                                      Score 1334;
Pred. No. 1
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l.10e-250;
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073639;
01-AUG-1998
01-AUG-1998
01-NOV-1999
                                                                                                                                                                                                                                              PHEROMONE CA13.
                                                                                       EMBL;
PFAM;
                                                                                                                                                                                                  Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
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                                                               PFAM; PF01094; ANF_receptor; PRINTS; PR00248; GPCRMGR.
                                                                                                                                            NAKANISHI
                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE; 98226788.
                                             SEQUENCE
                                                       Pheromone.
                                                                                                                       Fugu."
                                                                                                                                  *Putative
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                                                                                              Cyprinoidea;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Neopterygii, Teleostei; Diteleostei; Ostariophysi; '
Cyprinoidea; Cyprinidae; Cyprininae; Carassius.
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"Cloning and localization of two multigene receptor goldfish olfactory epithelium.";
Proc. Natl. Acad. Sci. U.S.A. 95:11987-11992(1998).
EMBL; AF083080; AAC64075.1; -.
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216; Mismatches 334;
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01-AUG-1998 (TrEMBLrel. (
01-AUG-1998 (TREMBLrel. (
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PHEROMONE RECEPTOR.
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PFAM; PF00003; 7tm_3; 1.
PFAM; PF01094; ANF_receptor; 1
PRINTS; PR00248; GPCRMGR.
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MEDLINE; 98226788.

NAITO T., SAITO Y., YAMAMOTO J., NOZAN

NAKANISHI S., BRENNER S.;

Putative pheromone receptors related

Fugu. ";

Proc. Natl. Acad. Sci. U.S.A. 95:5178-
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Eukaryota; Metazoa; Chordata; Cranitat; Vertebrata; Actinopterygil;
Neopterygil; Teleostel; Euteleostel; Acanthopterygil; Percomorpha;
Tetraodontiformes; Tetraodontoidel; Tetraodontidae; Fugu.
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Pred. No. 1.52e-232;
234; Mismatches 302;
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PFAM; PF00003; 7tm_3; 1.
PFAM; PF01094; ANF_receptor; PRINTS; PR00248; GPCRMGR.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorpha;
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SPSGTSHCTSPKGIKTTELLQHLSKVNFTTPQGKHLYFRGADIP-AMYDLINWQ-SGTDG
                                               CGTN-QL--C-RECHAFTTWN-MPE-LGAFS-MSAAYNVYEAVYAVAHGLHQLLGC----
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                                                                                                                                            TNVPGIQGIGT-VLGVAIQQRQVPG----LKEFE-----ESYVQAVMGAPRTC-PEGSW
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Pred. No. 2.86e-229;
222; Mismatches 315;
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                                                                                                                                                                                                                                                                     Query Match
Best Local
                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                     TISSUE-VOMERONASAL NEURONS;
RYBA N.J.P., TIRINDELLI R.;
Submitted (MAR-1998) to the EMBL;
EMBL; AF053986; AAC08413.1; -.
EMBL; AF053986; AAC08413.1; -.
EMBL; AF053986; AMF_receptor; 1.
PFAM; PF01094; AMF_receptor; 1.
PRINTS; PR00248; GPCRMGR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RYBA N.J., TIRINDELLI R.; "A new multigene family of putative Neuron 19:371-379(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=VOMERONASAL NEURONS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse)
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                                                                             LGYQIFDSCYTISKAMESSL-V-FL--TGQEEFKPNFRNSTGSTLAALVGSGGSSLSVAA 155
                                                                                                                                                 FLLAGLESLHADCLQVRHRPLVTSCDRSDSFNGHGYHLFQAMRFTVEEINNSTALLPNIT
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SRILGLYYMPQVGYTSSCSILSDKFQFPSYLRVLPSDNLQSEAIVNLIKHFGWVWVGAIA
                                                 LGYELYDVC-SESSNVYATLRVPAQQGTGHLEMQRDLRNHS-SKVVALIGPDNTDHAVTT
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                                                                                                                                                                                                                                                                        h 18.2%;
Similarity 29.4%;
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                                                                                                                                                                                                                                                   Conservative
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cches 296;
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                                          TISSUE-VOMERONASAL NEURONS;
MEDLINE; 97436753.
RYBA N.J., TIRINDELLI R.;
"A new multigene family of
Neuron 19:371-379(1997).
                                                                                                                                                                                                  O70409;
                                                                                                            PUTATIVE FRANCES (Mouse).

Mus musculus (Mouse).

Eukaryota; Metazoa; Chordata; Craniata;

Eukaryota; Mouse).

Andentia; Sciurognathi; Muridi
                                                                                                                                                      01-AUG-1998 (TIEMBLIEL. 07, Created)
01-AUG-1998 (TIEMBLIEL. 07, Last sequence update)
01-AUX-1999 (TIEMBLIEL. 10, Last annotation update)
PUTATIVE PHEROMONE RECEPTOR V2R1.
 TISSUE-VOMERONASAL RYBA N.J.P., TIRINI
                        SEQUENCE FROM N.A.
                                                                                                  SEQUENCE FROM N.A.
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 TIRINDELLI
DELLI R.;
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                                                      of putative
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                                                                                                                       Muridae;
                                                      pheromone
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                                                                                                                                 Vertebrata;
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                                                                                                                       Murinae;
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JLT 13 035269 035269; 01-JAN-1998 01-JAN-1998 01-MAY-1999

PRELIMINARY;

PRT;

779 AA

GTREMBLIEL.
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GTREMBLIEL.

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Best Local S
Matches 23
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ASSGYYQDADFVIGGLFPLRVTDGDTFISRSGVEDTSHIAEVVFCGSIKYYQHILAMVFA
                                                                                                                                                               GIGTVLGVAIQQRQVPGLKEF--E-ES--YVQAV-MGAPRTCPEG-SWCGTNQL-C-REC
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| VRLLQSFGWVWISLVGSYGDYGQLGVQALEELATPRGICVAFKD-VVPLSAQAGDPRMQR
                                                                                             ILAKTFIVVVAFK-AIKPGSILKMGMVTRLSNAIVCCGSIIQVCICAVWLGTYPPFPDVD
                                                                                                                        WRLHTPVVRSAGGRLCFLMLGSL-VAGSCSLYSFFGKPTVPACLLRQPLFSLGFAIFLSC
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                                                    LTIRSFQLVIIFKFSTKVPTFYHTWAQNHGAGIFVIVSSTVHLFLCLTWLAMWTPRPTRE
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                                                                                                                                           YR-ETPIVRANNRNLSYLLLISLKLCFFCSLI-FIGQPRTVTCVLRQIIFGIVFSIVISA
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28.6%;
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No. 5.72e-180;
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Best Loc
Matches
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EMBL; AF016182; AAC53329.1; --
FFAM; PF00003; 7tm_3; 1.
PFAM; PF01094; ANF_receptor; 1
SEQUENCE 779 AA; 88096 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-SPRAGUE-DAWLEY;
MEDLINE; 97433085.
HERRADA G., DULAC C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PUTATIVE PHEROMONE GO-VN5.
Rattus norvegicus (
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                      MLV-FCSVWVTFLPVYHSTKGKNMVAMEVFSILASSTSLLGIIFAPKCYLILLRPERNS
                                             REYOR-FPHLVILECTEVNSVGFLVAFAHNILLSISTFVCSYLGKELPENYNEAKCVTFS
                                                          KDAHSEHGHIIII-CNKGSAVAFHCNLGYLGALALVSYFMAFLSRNLPDTFNEAKFLAFS
                                                                                           CLTIRSFQLVIIFKFSTKVPTFYHTWAQNHGAGIFVI-VSSTVHLFLCLTWLAMWTPRPT
                                                                                                                TVLAKTITVVIAFKITS -- PGRIRRWLLISRAPNFIIPLCTLLQVFLSGIWLTTSPPFID
                                                                                                                                                                                      TSELHTCOPCGTEEWAPEGSSACFSRTVEFLGWHEPISLVLLAANTLLLLLIGTA-GLF
                                                                                                                                                                                                   ETDVDQCVKCPETHYANIEKIHCLQKTVTFLYYDDPLGKTL-CFMSLGFSSLTAAVLVVF
                                                                                                                                                                                                                                   P-VH-LDINKTKIQWHGKNNQVPVSVCTRDCLEGHHRLVMGSH-HCCFECMPCEAGTFLN
                                                                                                                                                                                                                                                 PWQLLQQIYKVNFLLHKKTVAFD-D-KGDPLGYYDIIAWDWNGPE-WTFEV-IGS-ASLS
                                                                                                                                                                                                                                                                                             PWQL-HPFLRERQLINONGANEDLDCTRKSHVEYDILNF-WNFPKGLGLNVKVGTFSPSA 410
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a; Chordata; Craniata; Vertebrata;
a; Sciurognathi; Muridae; Murinae;
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218; Mismatcl
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No. 2.05e-172;
Mismatches 307;
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Rattus.
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RESULT 14

ID 093555;

AC 093555;

DT 01-NOV-1998 (TYEMBLYEL 08, Created)
DT 01-NOV-1998 (TYEMBLYEL 10, Last sequenc
DT 01-MAY-1999 (TYEMBLYEL 110, Last annotat
DE PUTATIVE ODORANT RECEPTOR (FRAGMENT).

GN GFB7.

OC Carassius auratus (Goldfish).

OC Eukaryota; Metazoa; Chordata; Craniata;

OC Neopterygii; Teleostei; Euteleostei; Ost
Cyprinoidea; Cyprinidae; Cyprininae; Car
RN [1]

RP SEQUENCE FROM N.A.
TISSUE=OLFACTORY EPITHELIUM;
RX MEDLINE; 98426265.

RX MEDLINE; 98426265.

RT GOLORing and localization of two multige
RT goldfish olfactory epithelium.";
PTOC. Natl. Acad. Sci. U.S.A. 95:11987-1
DR EMBL; AF083084; AAC64079.1; -.
DR PFAM: PF00003; 7tm.3; 1.

SQ SEQUENCE 458 AA; 51119 MW; 8CB6FB43
RESULT 15

ID 035189

AC 035189;

DT 01-JAN-1998 (TIEMBLE DT 01-JAN-1998 (TIEMBLE DT 01-JAN-1999 (TIEMBLE DT 01-NOV-1999 (TIEMBLE DE PUTATIVE PHEROMONE R GN VZR1 OR VR1.

OS Mus musculus (Mouse)
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CAO Y., OH B.C., STRYER L.;

CAO I.C., STRYER L.;

CAO II.C., STRYER L.;

CAO
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Copterygii; Teleostei; Euteleostei; Ostariophysi; C
Cyprinoidea; Cyprinidae; Cyprininae; Carassius.
                                                                                                                                                                                                                                                                                                                                           798
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NYYKAVYAVAHSLHSLLNCKEQTGCEKSLTIQPKHVVEALKKVNFTVKFGDHVWFDSTGG
                                                                                                                                                                                                                                                                                                                                        LATISGGESGYFLPKCYVILCRPELNNTEH
                                                                                                                                                                                                                                                                                                                                                                                                     LASSFGLLFCIFAPKCYIILLKSDQNTKQH
                                                                                                                                                                                                                                                                                                                                                                                                                                                              LUSISTEVCSYLGKELPENYNEAKCVIFSLLLHEVSXIAFFIMSSIYQGSYLPAVNVLAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LLAVLCFILAFLARTLPDNFNEAKFITFSMLIFCAVWITFIPAYVSSPGKFTVAVEIFAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       L-TFIGRPTEWSCMLRHTAFGITFVLCISCILGKT--MVVLMAFKATLPGSNYMKWF-GP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CPPGTRKAAQKGREVCCYDCIPCAEGEISNETDSINCKQCPGEYWPNAEKNKCVLKAVEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PLGYYDIIAMDWNG-PEWTFEVIG--SASLSPVH-LDINKTKIQWHGKNNQVPVSVCTRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AVAHYEVVNWQQDSNRSLQFKPVGYFDTSLPPDQSFKLKTENVIWAGGQLEKPRSVCSES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAGIFVIVSST-VHLFLCLTWLAMWTPRPTREYQRFPHLVILECTEVNSVGFLVAFAHNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AQQRESVLAFTLIQVLICLLWLTISPPYPHKNMKYYKEKIIIECSLRSTLGFWAVLGYVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LYSFFGKPTVPACLLRQPLFSLGFAIFLSCLTIRSFQLVIIFKFSTKVPTFYH-TWAQNH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LGWHEPISLVLLAANTLLLLLIGTAGLFAWRLHTPVVRSAGGRLCFLMLGSL-VAGSCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LSFTEIMGIVLVFFSLFGVGLTVLVAILFYSKKNTPIVKANNSELSFLLLFSLSLCFLCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLEGHHRLV-MGSHHCCFECMPCEAGTFLNTSELHTCQPCGTEEWAPEGSSACFSRTVEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               h 13.8%;
Similarity 30.9%;
139; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 2.06e-
125; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence up
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 881;
Fred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8CB6FB43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 13; I
1.05e-152;
ches 171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CRC32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     families
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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PFAM; PF01094; ANF_receptor; 1.
SEQUENCE 850 AA; 97415 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MATSUNAMI H., BUCK L.B.;

A multigene family encoding a diverse array of putative pheromone receptors in mammals.";

Cell 90:775-784(1997),

EMBL; AF011411; AAC53401.1; -.

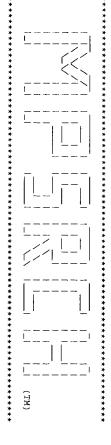
MGD; MGI:1316688; VZr1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. STRAIN-C57BL6/J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE; 97433087
                                                                                                                                                                                                                                             642
                                                                                                                   701 MWTPRPTREYQR-FPHLVILECTEVNSVGFLVAFAHNILLSISTFVCSYLGKELPENYNE
                                                                                                                                                                                                                                                                                659 LETVSVSTVLAKTITVVMAFKLTTPGRRM-RG-MMMTGAPKLVIPICTLIQLVLCGIWLV 716
                                                                                                                                                                                                                                                                                                                                                                       583
                                                                                                                                                                                                                                                                                                                                                                                                                         602 ILVT-FVKYK-DTPTVKANNRILSYILLISLVFCFLCSLL-FIGPPDQVTCIFQQTTFGV 658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                542 ENEISNETDMEQCVRCPDDKYANIEQTHCLSRAVSFLAYEDSLGMALGCMALSFSAITIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              483 LPCFPQRQKLHISDD-LEWAKGGTSPQVPSSVCSVACTAGFRKIYQKETADCCFDCVQCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               417 VY-PW-QLLQQIYKVN-FLLHK-KTVAFDDKGDPLGYYDIIAWDWNGPE-WTFEV-IGS- 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         365 IRMHHITFNNTLEWTSLHNYDV-AMSDEGYNLYNAVYAVAHTYHEYIFQQVESQKKAKPK 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       311 TNVPGIQGIGTVLGVAIQQR-QVPGLKEFEESYVQA--VMGAPRTCPE-GSW-CGTNQLC 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 253
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              133 FCYLDDSCAIGLTGPSWKT-SLKLA-MHSS--MPLVFFGPFNPNLRDHDRLPHVHQVAPK 188
   760
                                                                                                                                                                            717 TSPPFIDRDIQSEHGKIVIL-CNKGSVIAFHVVLGYLGSLALGSFTLAFLARNLPDTFNE 775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     525 AGTFLNTSELHTCQPCGTEEWAPEGSSACFSRTVEFLGWHEPISLVL--LAANTLLLLLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         249 YMTRATIYDKHIMTSSAKVVIIYGEMNSTLEASFRRWEELGA-R-RIWITTSQWDVITNK 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            74 YHLFQAMRFTVEEINNSTALLPNITLGYELYDVCSESSNVYATLRVPAQQGTGHLEMQRD 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    75 YEFLLVMFFAIDEINRNPYLLPNITLMFS-F-IGGNCQDLLRVMDQAYTQINGHMNFVNY 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 Match 13.1%; Score 832; DB 11; I
Local Similarity 26.8%; Pred. No. 6.33e-142;
les 210; Conservative 195; Mismatches 323;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RYFTACQQVSSLMKTRVFTNPVGELVNMKHRENQCTEYDIFI-IWNFPQGLGLKVKIGSY 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DTHLSHGMVSLMFHFRWTWIGLVISDDDQGIQFLSDLREESQRHGICLAFVNMIPENMQI 248
                                              AKFLTESMLV-FCSVWITFLPVYHSTRGRVMVVVEVFSILASSAGLLMCIFVPKCYVILI
                                                                                                                                                                                                                                          GFAIFLSCLTIRSFQLVIIFKFSTKVPTFYHTWAQNHGAGIFVI-VSSTVHLFLCLTWLA
                                                                                                                                                                                                                                                                                                                                                                 IGTAGLFAWRLHTPVVRSAGGRLCFLMLGSLVAGS-CSLYSFFGKPTVPACLLRQPLFSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -ASLSPVH-LDINKTKIQW-HG-KNNQVPVSVCTRDCLEGHHRLV-MGSHHCCFECMPCE 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -RECH-AFT-T--W-NMPELGAFSMSA-AYNVYEAVYAVAHGLHQ-LLG-CTSGTCARGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KDFT-LNLFHGIITFE-HHRFEIPKLNKFMQTMNTAKYPVDISHTILEWNYFNCSISKNS 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GDPRMQRMMLRLARARTTVVVVVFSNRH--LAGVFFRSVVLANLTGKVWIASEDWAISTYI 310
AKCVTFSLLLHFVS-WIAFFTMSSIYQGSYLPAVNVLAGLATLSGGFSGYFLPKCYVILC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3CA08744 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                601
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Search completed: Fri Mar 17 13:22:28 Job time: 250 secs.



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MPsrch_pp protein protein database search, using Smith-Waterman algorithm

Tabular output Run on: not generated Fri Mar 17 13:16:18 2000; MasPar time 44.86 Seconds 560.581 Million cell updates/sec

Description: Perfect Score: 6366 >US-09-361-652-2 (1-842) from US09361652.pep

Sequence: MLFWAAHLLLSLQLAVAYCW......NNTEHFQASIQDYTRRCGTT 842

Scoring table: PAM 150 Gap 11

82229 seqs, 29864866 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database swiss-prot38 1:swissprot

Statistics: Mean 53.985; Variance 93.429; scale 0.578

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
بر	1316	20.7	1085	_	CASR_BOVIN	EXTRACELLULAR CALCIUM-	9.34e-272
2	1293	20.3	1078	ш	CASR_HUMAN	CALC	.24e-26
ω	1282	20.1	1079	<u>, </u>	CASR_RAT		.44e-26
4	819	12.9	1212	-	MGR5_HUMAN	G	(J)
S	814	12.8	1203	_	MGR5_RAT	METABOTROPIC GLUTAMATE	.52e-1
σ	810	12.7	1199	ш	MGR1_RAT	METABOTROPIC GLUTAMATE	.93e-1
7	804	12.6	912	ш	MGR4_HUMAN	METABOTROPIC GLUTAMATE	.01e-1
8	799	12.6	912	۲.,	MGR4_RAT	METABOTROPIC GLUTAMATE	1.50e-148
o	800	12.6	1194	ш	MGR1_HUMAN	METABOTROPIC GLUTAMATE	.74e-1
10	769	12.1	872	ب	MGR2_RAT	METABOTROPIC GLUTAMATE	.60e-
11	764	12.0	877	μ.	MGR3_HUMAN	METABOTROPIC GLUTAMATE	.36e-
12	757		872	μ.	MGR2_HUMAN	METABOTROPIC GLUTAMATE	.02e-1
13	759	11.9	879	ш	MGR3_RAT	METABOTROPIC GLUTAMATE	.48e-13
14	741	11.6	877	ب	MGR6_HUMAN	METABOTROPIC GLUTAMATE	5.56e-135
15	740	11.6	908	۲	MGR8_MOUSE	METABOTROPIC GLUTAMATE	.51e-13
16	734	11.5	915	Н	MGR7_HUMAN	METABOTROPIC GLUTAMATE	
17	730	11.5	915	\vdash	MGR7_RAT	METABOTROPIC GLUTAMATE	.04e-13
18	727	11.4	871	ديم	MGR6_RAT	METABOTROPIC GLUTAMATE	.02e-13
19	728	11.4	806	ш	MGR8_RAT	METABOTROPIC GLUTAMATE	5.96e-132
20	718	11.3	908	-	MGR8_HUMAN	GLUTAMAT	.27e-12
21	533	8.4	976	دــو	MGR_DROME	METABOTROPIC GLUTAMATE	4.30e-87
22	356	5.6	999	ب	MGR1_CAEEL	PROBABLE METABOTROPIC	6.05e-48
23	160		1233	,_	NME3_HUMAN	GLUTAMATE [NMDA] RECEP	3.80e-09

45	44	43	42	41	40	39	38	37	36	35	34	ω ω	32	31	30	29	28	27	26	25	24
110	110	107	107	111	109	113	112	116	124	121	121	121	121	124	123	125	125	127	132	155	155 5
1.7	1.7	1.7	1.7	1.7	1.7		∵													2.4	
1482	1482	487	334	311	298	2749	532	420	2731	1464	1464	1125	986	938	415	1323	938	938	370	1239	1237
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NME2_RAT	NME2_MOUSE	CPS1_MOUSE	Y472_RICPR	HPRK_MYCGE	YC34_HELPY	IP3R_MOUSE	YHB7_YEAST	Y181_MYCGE	RRPB_CVMJH	NME1_MOUSE	NME1_RAT	CYGS_STRPU	CYGR_ARBPU	NMZ1_HUMAN	TNRC_MOUSE	NME4_MOUSE	NMZ1_MOUSE	NMZ1_RAT	Y454_AQUAE	NME3_MOUSE	NME3_RAT
[NMDA]	GLUTAMATE [NMDA] RECEP	CYTOCHROME P450 XXIAI	HYPOTHETICAL PROTEIN R	PROBABLE HPR(SER) KINA	HYPOTHETICAL PROTEIN H	INOSITOL 1,4,5-TRISPHO		PROT	TED RNA	GLUTAMATE [NMDA] RECEP		SPERACT RECEPTOR PRECU	RESACT RECEPTOR PRECUR	GLUTAMATE [NMDA] RECEP	LYMPHOTOXIN-BETA RECEP	GLUTAMATE [NMDA] RECEP	GLUTAMATE [NMDA] RECEP	GLUTAMATE [NMDA] RECEP	HYPOTHETICAL PROTEIN A	GLUTAMATE [NMDA] RECEP	GLUTAMATE [NMDA] RECEP
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PROSITE; PSUV; 1, 3; 1.

PFAM; PF00003; 7tm 3; 1.

PFAM; PF01094; ANF_receptor; 1

PFAM; Protein coupled receptor; Tr

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
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ROWN E.M., GAMBA G., RICCARDI D., LOMBARDI M., BUTTERS R., KIFOR (STROWN E.M., GAMBA G., LYTTON J., HEBERT S.C.;
SUN A., HEBIGER M.A., LYTTON J., HEBERT S.C.;
"Cloning and characterization of an extracellular Ca(2+)-sensing receptor from bovine parathyroid.";
Nature 366:575-580(1993).

-!- FUNCTION: SENSE CHANGES IN THE EXTRACELLULAR CONCENTRATION OF CALCIUM IONS. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY A G-PROTERIN THAT ACTIVATES A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM.
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CASR OR PCAR1.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae;
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TISSUE=PARATHYROID;
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Matches 27
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                                 VECPDGEYSDETDASACDKCPDDFWSNENHTSCIAKBIEFLSWTEPFGIALTLFAVLGIF
                                                          EVIG--SA-SLSPVHLDINKTKIQWHGKNNQVPVSVCTRDCLEGHHR-LVMGSHHCCFEC
                                                                    KEVGYYNVYAKKGERLFINDEKILWSGFSREVPFSNCSRDCLAGTRKGIIEGEPTCCFEC
                                                                                                                                                                              TVLGV-A-IQ--Q-RQ-VP-GL-KEF-EESY---VQ-AVMGA-P-----RTCPEG-SW-C
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LTAFVLGVFIKFR-NTPIVKATNRELSYLLLFSLLCCFSSSLF-FIGEPQDWTCRLRQPA
                   MPCEAGTFLNTSELHTCQPCGTEEWAPEGSSACFSRTVEFLGWHEPISLVLLAANTLLLL
                                                                                                 SGTCA-RGPVYPWQLLQQIYKVNFLLHK-KTVAFDDKGDPLGYYDIIAWDWNGPE-WT-F
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Similarity 31.9%;
272; Conservative
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Pred. No. 9.34e-272;
234; Mismatches 273;
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                                                                                                                                                                                                                                                                                                                      TISSUE-PARATHYROID;
MEDLINE; 95279439.
GARRETT J.E., CAPUA
                                                                                                                    thyroid carcinoma secretion.";
                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE; 96343808.
                                                                                                                                                                                                  Biochem.
                                                                            MEDLINE;
                                                                                                         Endocrinology 137:3842-3848(1996)
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POLLAK M.R. BROWN E.M., CHOU Y.H., HEBERT S.C., STEINMANN B., LEVI T., SEIDMAN C.E., SEIDMAN J.G "Mutations in the human Ca(2+)-sensing receptor hypocalciuric hypercalcemia and neonatal severe hyperparathyroidism."; Cell 75:1297-1303(1993).
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P41180; Q13912; Q16379; Q16108; Q16109; Q16110;

01-FEB-1995 (Rel. 31, Created)

01-NVP-1995 (Rel. 32, Last sequence update)

15-JUL-1999 (Rel. 38, Last annotation update)

EXTRACELLULAR CALCIUM-SENSING RECEPTOR PRECURSOR (CASR) (PARATHYROID CELL CALCIUM-SENSING RECEPTOR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GARRETT J.E., CAPPANO I.V., HAMMERLAND L.G., HEBERT S.C., NEMETH E.F., FULLER F.;
"Molecular cloning and functional expression calcium receptor cDNAs.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eukaryota; Metazoa; Catarrhini; Hominidae; Homo.
                                                                                                                                                                              VARIANTS FHH GLU-185; LYS-297 AND TRP-795
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of a putative Ca(2+)-sensing receptor cDNA from
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-I- FUNCTION: SENSE CHANGES IN THE EXTRACELLULAR CONCENTRATION OF CALCIUM LONS. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY A G-PROTEIN THAT ACTIVATES A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM.

-I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-I- ALTERNATIVE SPLICING.
-I- ALTERNATIVE SPLICING.
-I- TISSUE SPECIFICITY: FOUND IN KIDNEY, BUT NOT IN BRAIN, LUNG, LIVER, HEART, SKELETAL MUSCLE, OR PLACENTA.
-I- DISEASE: DEFECTS IN CASR ARE A CAUSE OF FAMILIAL HYPOCALCIURIC HYPERCALCEMIA (FHH) AND NEONATAL SEVERE HYPERPARATHYROIDISM (NSHPT), TWO INMERITED CONDITIONS CHARACTERIZED BY ALTERED CALCIUM HOMEOSTASIS. THE MUTATIONS REDUCE THE ACTIVITY OF THE RECEPTOR. FHH AFFECTED INDIVIDUALS EXHIBIT MILD OR MODEST HYPERCALCEMIA, RELATIVE HYPOCALCIURIA, AND INAPPROPRIATELY NORMAL PTH LEVELS. IN CONTRAST, NSHPT IS A RARE AUTOSOMAL RECESSIVE LIFE-THREATENING DISOMBER CHARACTERIZED BY VERY HIGH SERUM CALCIUM CONCENTRATIONS, SKELETAL DEMINERALIZATION, AND PARATHYROID HYPERPLASIA. IN SOME INSTANCES NSHPT HAS BEEN DEMONSTRATED TO BE THE HOMOZYGOUS FORM OF FRH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE; 96292293.
PEARCE S.H.S., TRUM
GRANT D.B., HEATH E
THAKKER R.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            associated with familial hy Hum. Mutat. 10:233-235(1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VARIANTS ADHP THR-116; HIS-681 AND SER-806, AND MEDLINE; 96311554.

BARON J., WINER K.K., YANOVSKI J.A., CUNNINGHAM ZIMMERMAN D., CUTLER G.B. JR.;

"Mutations in the Ca(2+) sensing receptor gene dominant and sporadic hypoparathyroidism.";

Hum. Mol. Genet. 5:601-606(1996).
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CHOU Y.-H.W., POLLAK M.R.,
ATKINSON A.B., PAPAPOULOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE; 95179179.

POLLAK M.R., BROWN E.M., ESTEP H.L., MCLAINE P.N., KIFOR O., HEBERT S.C., SEIDMAN C.E., SEIDMAN J.G.;

"Autosomal dominant hypocalcaemia caused by a Ca(2+)-sensing gene mutation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE; 97442275.
WARD B.K., STUCKEY B.G.A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RATAJCZAK T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VARIANT FHH ARG-174.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VARIANTS FHH MET-62; CYS-66; MET-138; GLU-143 AND GLN-227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "A novel mutation (L174R)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Calcium-sensing
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neonatal hyperparathyroidism.";
Clin. Invest. 96:2683-2692(1995).
                               CA(2+) LEVELS.
DISEASE: DEFECTS IN
HYPOPARATHYROIDISM
                                                                                                                                                HYPOCALCEMIA
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HYPERPHOSPHATEMIA DUE
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HEATH D.A.,
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                                                                                                                                        ECTS IN CASR ARE
(ADH) IN WHICH
                           IN PCAR1 ARE ALSO THE CAUSE OF AUTOSOMAL DOMINA SM (ADHP). ADHP IS CHARACTERIZED BY HYPOCALCEMIA
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                                                                                                                                        ARE ALSO THE CAUSE ICH THE RECEPTOR IS
TO INADEQUATE
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PATERSON C.R.,
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BROWN E.
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SECRETION OF PARATHYROID
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GCRDB; GCR_1874; -. GCRDB; GCR_2012; -. GCRDB; GCR_2013; -. GCRDB; GCR_2596; -. GCRDB; GCR_2697; -.
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AAA86503.1;
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BAA09453.1;
AAB46873.1;
AAB35262.1;
AAB3529414.1;
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                        66
                                        62
                                                                                                                                                                                                                                                                                                                  79; G_PROTEIN_RECEP_F3_1;
80; G_PROTEIN_RECEP_F3_2;
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7tm_3; 1.
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/FIId=VAR_003585.

R -> M (IN MILD FH
/FIId=VAR_003586.

R -> C (IN FHH).
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                                                                                                                         NYNEAKCYTFSLLLHFYSWIAFFTM-SSIYQGSYLPAVNVLAGLATLSGGFSGYFLPKCY
                                                                                                                                                 NFNEAKFITFSMLIFFIVWISFIPAYASTY-GKFVSAVEVIAILAASFGLLACIFFNKIY
                                                                                                                                                                                                    WLYTAPPSSYRNQELEDEIIFITCHEGSLMALGFLIGYTC-LLAAICFFF-AFKSRKLPE
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                                                                                                                                                                                                                                         FGISFVLCISCILVKTNRVLLVFE--AKIPTSFHRKWWGLNLQFLLVFLCTFMQIVICVI 741
                                                                                                                                                                                                                                                                             LLIGTAGLFA-WRLHTPVVRSAGGRLCFLMLGSLVAG-SCSLYSFFGKPTVPACLLRQPL
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Pred. No. 3.
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3.24e-266;
ches 274;
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CARBOHYD
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SIGNAL
                                                                                                             DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                          the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
EXTRACELLULAR CALCIUM-SENSING RECEPTOR PRECURSOR (CASR) (PARATHYROID CELL CALCIUM-SENSING RECEPTOR).
CASR OR PCAR1.
                                                                        CARBOHYD
                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00979; G_PROTEIN_RECEP_F3_1; PROSITE; PS00980; G_PROTEIN_RECEP_F3_2; PROSITE; PS00981; G_PROTEIN_RECEP_F3_3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Calcium sensing receptor: molecular cloning in rat to nerve terminals.";

Proc. Na+1 "---"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RICCARDI D., PARK J., LEE W., GAMBA G., BROWN E.M., "Cloning and functional expression of a rat kidney calcium/polyvalent cation-sensing receptor."; Proc. Natl. Acad. Sci. U.S.A. 92:131-135(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                                                           CARBOHYD
                                                                                    CARBOHYD
                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                            PFAM; PF00003; 7tm_3; 1.
PFAM; PF01094; ANF_receptor; 1
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STRAIN-SPRAGUE-DAWLEY;
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                                                                                                                                                              FRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C. NALL. ACAD. SCI. U.S.A. 92:3161-3165(1995).
FUNCTION: SENSE CHANGES IN THE EXTRACELLULAR CONCENTRATION OF CALCIUM IONS. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY A G-PROTEIN THAT ACTIVATES A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM.
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                                                                                                    NFNEAKFITESMLIFFIVWISFIPAYASTY-GKFVSAVEVIAILAASFGLLACIFFNKVY
                                                                                                                                                           FSLGFAIFLSCLTIRSFQLVIIFKFSTKVPT-FYHTWAQNHGAGIFVIVSSTVHLFLCLT
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                                                                IILFKPSRNTIEEVRSSTAAHA
                                                                                   NYNEAKCYTFSLLLHFYSWIAFFTM-SSIYQGSYLPAVNVLAGLATLSGGFSGYFLPKCY
                                                                                                                      WLAMWTPRPTREYORFPHLVILECTEVN--SVGFLVAFAHNILLSISTFVCSYLGKELPE
                                                                                                                                        WLYTAPPSSYRNHELEDEIIFITCHEGSLMALGSLIGYTC-LLAAICFFF-AFKSRKLPE
                                                                                                                                                                            FGISFVLCISCILVKTNRVLLVFE--AKIPTSFHRKWWGLNLQFLLVFLCTFMQILICII
                                                                                                                                                                                              LLIGTAGLFA-WRLHTPVVRSAGGRLCFLMLGSLVAG-SCSLYSFFGKPTVPACLLRQPL
                                                                                                                                                                                                                LTAFVLGVFIKER-NTPIVKATNRELSYLLLESLLCCESSSLE-FIGEPQDWTCRLRQPA
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                                                                                                                                                                                                                                                                                                                                               -CGTN-Q-LCRECHAFTTWNMPELGAFSMSAAYNVYEAVYAVAHGLHQL---L-GC---T
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Mismatches 280;
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GCRDB; GCR_13
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EMBL;
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SUBCELLULAR LOCA
ALTERNATIVE PROD
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GCR_1002;
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Ol-OCT-1995 (Rel. 32, Created)
Ol-OCT-1995 (Rel. 34, Last sequence update)
15-DEC-1999 (Rel. 39, Last annotation update)
METABOTROPIC GLUTAMATE RECEPTOR 5 PRECURSOR.
GRM5 OR MGLUR5.
Homo Sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sorsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MINAKAMI R., KATSUKI F., SUGIYAMA H.;

"A variant of metabotropic glutamate receptor subtype 5: an

"A variant of metabotropic glutamate receptor subtype 5: an

evolutionally conserved insertion with no termination codon.";

Biochem. Blophys. Res. Commun. 194:622-627(1993).

-!- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR IS

-!- FUNCTION: RECEPTOR FOR GLUTAMATES. A PHOSPHATIDYLINOSITOL-

MEDIATED BY A G-PROTEIN THAT ACTIVATES A PHOSPHATIDYLINOSITOL-

CALCIUM SECOND MESSENGER SYSTEM AND GENERATES A CALCIUM-ACTIVATED
                                                                                                                                                                                                                                                                                             PROSITE: PS00979; G_PROTEIN_RECEP_F3_1; PROSITE; PS00980; G_PROTEIN_RECEP_F3_2; PROSITE; PS00981; G_PROTEIN_RECEP_F3_3;
                                                                                                                                                                                                             PFAM, PF00003, 7tm_3, 1.

PFAM; PF01094; ANF_Teceptor; 1

G-protein coupled receptor; Ti

Multigene family; Alternative
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D28539; BAA05892.1;
S64316; AAD13954.1;
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etazoa; Chordata; Craniata; Vertebrata;
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III (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
IV (POTENTIAL).
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                                                     QLGIIVALFIMEPPDIMHDYPSIRE-VYLICNTIN-LGVVTPLGYNGLLILSCIF-YAFK
                                                                                      CLLRQPLFSLGFAIFLSCLTIRSFQLVIIFKFSTK-VPTFYHTWAQNHGAGIFVIVSSTV
                                                                                                                CYLQRIGIGLSPAMSYSALVTKTNRIARILAGSKKKICTKKPRFMSACAQLVIAFILICI
                                                                                                                                                                          ACLGLLATLEY-TVVFIIYR-DTPVVKSSSRELCYIILAGICLGYLCT-FCLIAKPKQIY
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                            HLFLCLTWLAMWTPRPTREYQRFPHLVILECTEVNSVGFLVAFAHNILLSIS-TFVCSYL
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METABOTROPIC GLUTAMATE RECEPTOR

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MGR5_RAT

P31424;

P31424;

01-JUL-1993 (Rel. 26, Created)

01-NOV-1995 (Rel. 32, Last sequence update)

15-DEC-1999 (Rel. 39, Last annotation update)

15-DEC-TOP99 (Rel. 39, Last annotation update)

Tenorropic GLUTAMATE RECEPTOR 5 PRECURSOR.
Multigene
SIGNAL
CHAIN
                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sor.send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MINAKAMI R., KATSUKI F., SUGIYAMA H.;

"A variant of metabotropic glutamate receptor subtype 5: an
evolutionally conserved insertion with no termination codon.";
Biochem. Biophys. Res. Commun. 194:622-627(1993).

-i- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR
MEDIATED BY A G-PROTEIN THAT ACTIVATES A PHOSPHATIDYLINOSITOL-
CALCIUM SECOND MESSENGER SYSTEM AND GENERATES A CALCIUM-ACTIVATE
CHLORIDE CURRENT.
                    PFAM; PF01094; ANT_receptor; 1.
6-protein coupled receptor; Transmembrane;
Multigene family; Alternative splicing.
SIGNAL 1 20 POTENTIAL.
                                                                                                                     PROSITE; PS00979; G_PROTEIN_RECEP_F3_1; PROSITE; PS00980; G_PROTEIN_RECEP_F3_2; PROSITE; PS00981; G_PROTEIN_RECEP_F3_3; PFAM; PF00003; 7tm_3; 1.
                                                                                                                                                                                                                         GCRDB; GCR_0740;
GCRDB; GCR_0760;
                                                                                                                                                                                                                                                                     EMBL; D10891; -; NOT_ANNOTATED_CDS.
EMBL; S64315; AAB27666.1; -.
PIR; A42916; A42916.
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"Molecular characterization
receptor mGluR5 coupled to i
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STRONGEST, TO MGLUR1.
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METABOTROPIC GLUTAM
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PIN J.-P.,
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                                                                                                                                                                                                                                                                                                                                                                                                             HOUAMED K.M., KUIJPER J.L., GILBERT T.L., MULVIHILL E.R., ALMERS W., HAGEN F.S.; "Cloning, expression, and gene structure (glutamate receptor from rat brain."; Science 252:1318-1321(1991).
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                                                                                                                                                                                        PIN J.-P., WAEBER C., PREZEAU L., BOCKAERT J., HEINEMANN S.F.; "Alternative splicing generates metabotropic glutamate receptors inducing different patterns of calicium release in Xenopus oocytes.", Proc. Natl. Acad. Sci. U.S.A. 89:10331-10335(1992).
-:- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR
                                                                                                                                                                                                                                                                            TISSUE=BRAIN,
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                      MEDIATED BY A G-PROTEIN THAT ACTIVATES À PHOSPHATIDYLINOSITOL-
CALCIUM SECOND MESSENOER SYSTEM. MAY PARTICIPATE IN THE CENTRAL
ACTION OF GLUTAMATE IN THE CNS, SUCH AS LONG-TERM POTENTIATION I
THE HIPPOCAMEUS AND LONG-TERM DEFRESSION IN THE CEREBELLUM.
SUSCELLULAR LOCATION: INTERRAL MEMBRANE PROTEIN.
ALTERNATIVE PRODUCTS: THREE ISOFORMS; IA (SHOWN HERE), 1B AND 1C
ARE PRODUCED BY ALTERNATIVE SPLICING. 1B AND 1C ARE C-TERMINALLY
TRUNCATED FORMS OF 1A.
TISSUE SPECIFICITY: IS PREDOMINANTLY EXPRESSED IN CEREBELLAR
PURKINUE CELLS, CA2-CA3 PYRAMIDAL CELLS OF THE HIPPOCAMPUS, AND
MITRAL AND TUFTED CELLS OF THE OLFACTORY BULB.
MISCELLANEOUS: ACTIVATED BY QUISQUALATE > GRUTAMATE > IBOTENATE
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ARE C-TERMINALLY
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: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS TO MGLUR5.

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    DIVKRYNWTYVSAVHTEGNYGESGMDAFKELAAQEGLCIAHSDKI-YSN-AGEKSFDRLL
                      A-LIGPDNTDHAVTTAALLSPFLMPLVSYEASSVILSGKRKFPSFLRTIPSDKYQVEVIV
                                         AGVIGPGSSSVAIQVQNLLQLFDIPQIAYSATSIDLSDKTLYKYFLRVVPSDTLQARAML
                                                           PHITLGYELYDVCSESS-----NV-Y--ATL-RVPAQ-QGTGH-LEMQRDLR-NHSSKVV
                                                                           PNITLGSEIRDSCWHSSVALEQSIEFIRDSLISIRDEKDGLNRCLPDGQTLPPGRTKKPI 156
                                                                                             LPGDFLLAGLFSLHADCLQVRHRPLVTSCDRSDSFNGHGYHLFQAMRFTVEEINNSTALL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   X57569; CAA40799.1;
M61099; AAA19497.1;
S48085; AAB24138.1;
                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PS00979; G_PROTEIN_RECEP_F3_1; PS00980; G_PROTEIN_RECEP_F3_2; PS00981; G_PROTEIN_RECEP_F3_3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          family;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        email to license@isb-sib.ch).
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ANF_receptor;
                                                                                                                                                                       ΑA;
                                                                                                                                                                                                                                                       Alternative splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    receptor;
                                                                                                                                           12.7%;
27.6%;
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                                                                                                                                           Score 810;
Pred. No. 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transmembrane; Glycoprotein;
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                                                                                                                                                                                                                                                                                         VII (POTENTIAL)
CYTOPLASMIC (POT
GLN/PRO-RICH.
                                                                                                                                                                                                                            POTENTIAL.
                                                                                                                                                                                                                                              POTENTIAL.
                                                                                                                                                                              MISSING (IN ISOFORM 1B).
SNGKSVSWSE -> FALDRONTVY
MISSING (IN ISOFORM 1C).
                                                                                                                                                                                                                                                                                                                                                                 CYTOPLASMIC IV (POTENTIA
                                                                                                                                                                                                          AQL
                                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC
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                                                                                                                                                                                                                   NSNGKSVSWSEPGGRQAPKG
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                                                                                                                                   Mismatches
                                                                                                                                                                       EB211AF2
                                                                                                                                                                                                         (IN ISOFORM 1B)
                                                                                                                                                                                                                                                                                                                                                                                    (POTENTIAL)
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1.93e-151
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                                                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL).
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                                                                                                                                                                                        ISOFORM
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RESULT
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01-NOV-1997 (Rel.
01-NOV-1997 (Rel.
15-DEC-1999 (Rel.
                                                                                                                                                                                                                                                                                                                                                                     MARDLINE; PULL MAKOFF A., LELCHUK R., OXER; MAKOFF A., LELCHUK R., OXER; MAKOFF A., ELLCHUK R., OXER; MAKOFF A., ELLCHUK R., OXER; MAKOFF A., 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GRM4
WUS., WRIGHT R.A., ROCKEY P.K., BURGETT S.G., ARNOLD J.S ROSIECK P.K. JR., JCHNSON B.G., SCHOEPP D.D. BLAGAJE R. "Group III human metabotropic glutamate receptors 4, 7 ar molecular cloning, functional expression, and comparison pharmacological properties in RGT cells."; Brain Res. Mol. Brain Res. 53:88-97(1998).
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Matches 20
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"Molecular cloning, fi"
"molecular cloning of t
                                                                                                                   CARBOHYD
SEQUENCE
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Multigene
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TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                             MIM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               . or
                                                                                                                                      CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00979; G_PROTEIN_RECEP_F3_1; PROSITE; PS00980; G_PROTEIN_RECEP_F3_2; PROSITE; PS00981; G_PROTEIN_RECEP_F3_3;
                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X80818; CAA56784.1; -. EMBL; U92457; AAB51762.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Neuropharmacology 34:149-155(1995).
-!- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF 1
IS MEDIATED BY A G-PROTEIN THAT INHIBITS ADENYLATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM
TISSUE=BRAIN;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

TISSUE SPECIFICITY: STRONGLY EXPRESSED IN THE CEREBELLUM.

EXPRESSED AT LOW LEVELS IN HIPPOCAMPUS, HYPOTHALAMUS AND
THALAMUS. NO EXPRESSION DETECTED IN LIVER.

SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRONGEST,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IS MEDIATED ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SWISS-PROT entry is copyright.
 H-LEMQRDLRNHSSKVVALIGPDNTDHAVTTAALLSPFLMPLVSYEASSVILSGKRKFPS
                                     GYHLFQAMRFTVEEINNSTALLPNITLGYELYDVCS-ESSNVYATLR-VPA--Q-QGTG-
                                                        GIHRLEAMLFALDRINNDPDLLPNITLGARILDTCSRDTHALEQSLTFVQALIEKDGTEV
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                  RCGSGGPPIITKPERVVGVIGASGSSVSIMVANILRLFKIPQISYASTAPDLSDNSRYDF
                                                                                                                                                                                                                                                                                                                                                                                                                      GCR_2069; -
                                                                          th 12.6%; Similarity 26.3%; 209; Conservative
                                                                                                                                                                                                                                                                                                                                                   0003: 7tm_3; 1.
1094; ANF_receptor;
coupled receptor;
                                                                                                                                                                                                                                                                                                                                           tamily.
                                                                                                                  TO MGLUR6
                                                                                                                          the human
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                                                                                                                   101867
                                                                          Score 804;
Pred. No. 1.
224; Mismatc
                                                                                                                   MW.
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CYTOPLASMIC
POTENTIAL.
                                                                                                                                             POTENTIAL. POTENTIAL.
                                                                                                                                                                                                      CYTOPLASMIC
VI (POTENTIA
                                                                                                                                                                                                                                  EXTRACELLULAR (POTENTIAL)
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METABOTROPIC GLUTAMATE RECEPTOR
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                                                                                                                                                                                             EXTRACELLULAR (POTENTIAL)
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                                                                                                                                                                                                                                                                                  (POTENTIAL)
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Mismatches 300;
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RESULT 8

RESULT 8

RR4 RAT

AC 931423;

DT 01-JUL-1993;

DT 15-JUL-1993;

DT 15-JUL-1993;

DE METABOTROPIC
GN GRM4 OR MGLUG
OS RATUS NOTVEC
CC EUKATYOTA; MC
OC EUKATYOTA; MC
OC EUKATYOTA; MC
RN [1]

RR MEDLINE; 9211

RA TANABE Y, MA
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MEDLINE; 9211
TANABE Y., MA:
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Ol-JUL-1993 (Rel. 26, Last segmence up
15-JUL-1999 (Rel. 38, Last annotation
METABOTROPIC GLUTAMATE REFERENCE
GRAM OF THE COLUMN CREAT OF THE C
TISSUE=BRAIN;
MEDLINE; 93332699
O'HARA P.J., SHEP
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Rattus norvegicus (Rat)
                                                                                                                    SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                           DLINE; 92110002.

NABE Y., MASU M., ISHII family of metabotropic uron 8:169-179(1992).
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       P.O.,
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glutamate
       THOGERSEN H.,
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ae; Murinae;
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       VENEZIA D.,
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Multigene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long as its content modified and this statement is not removed. Usage by ar entitles requires a license agreement (See http://www.isbor send an email to license@isb-sib.ch).
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Neuron 11:41-52(1993).
-!- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY A G-PROTEIN THAT INHIBITS ADENYLATE CYCLASE
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PFAM; PF01094;
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EMBL; M90518;
                                                                                                                                                                                                                                                                                                            SEQUENCE
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GCRDB; GCR_0363
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SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

TISSUE SPECIFICITY: IS WIDELY DISTRIBUTED IN THE CNS. PREDOMINANT EXPRESSION IS SEEN IN THE GRANULE CELLS OF THE CEREBELLUM.

EXPRESSION IS SELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - Buropean Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                             GIHRLEAMLFALDRINNDPDLLPNITLGARILDTCSRDTHALEQSLTFVQALIEKDGTEV 134
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                                          FSRVVPSDTYQAQAMVDIVRALKWNYVSTLASEGSYGESGVEAFIQKSRENGGVCIA-QS
                                                                                                                                                      GYHLFQAMRFTVEEINNSTALLPNITLGYELYDVCS-ESSNYYATLR-VPA--Q-QGTG- 126
       FLRTIPSDKYQVEVIVRLLQSFGWVWISLVGSYGDYGQLGVQALEELATPRG-ICVAFKD
                                                                                H-LEMORDLRNHSSKVVALIGPDNTDHAVTTAALLSPFLMPLVSYEASSVILSGKRKFPS
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M90518; AAA93190.1; -.
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                                                                                                                                                                                                                                   Conservative
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25.9%;
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Pred. No. 1
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EXTRACELLULAR (POTENTIAL)
VII (POTENTIAL).
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CYTOPLASMIC (E
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V (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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METABOTROPIC GLUTAMATE RECEPTOR
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                SEQUENCE FROM N.A.
MEDLINE; 97231349.
STEPHAN D., BON C., HOLZWARTH J.A., GALVAN M.,
"Human metabotropic glutamate receptor 1: mRNA
chromosome localization and functional expressi
variants.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MGR1_HUMAN STANDARD; PRT; 1194 AA. Q13255; Q13256; Q14757; Q14758; Q1-NOV-1997 (Rel. 35, Careated) Q1-NOV-1997 (Rel. 35, Last sequence update) 15-DEC-1999 (Rel. 39, Last annotation update) METABOTROPIC GLUTAMATE RECEPTOR 1 PRECURSOR.
                                                                                                                                                                                                                                       alpha: enhanced coupling on
transporter.";
                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE; 96029774.
DESAI M.A., BURNETT J.P.,
"Cloning and expression of
                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota;
Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GRM1 OR MGLUR1
Homo sapiens (
Neuropharmacology 35:1649-1660(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YKVIGSWT-DHLHLRIER--MQWPGSGQQLPRSICSLPCQPGERKKTVKGMACCWHCEPC
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                                                                                                                                                                                                                                                                                                                                                                                                                          ; Metazoa;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                               (Human).
etazoa; Chordata; Craniata; Ver
imates; Catarrhini; Hominidae;
                                                                                                                                                                                                              48:648-657(1995)
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Best Local S
Matches 22
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EMBL; U31216; AAA87844.1; -.
EMBL; U76627; AAB05337.1; -.
EMBL; L76627; AAB05337.1; -.
GCRDB; GCR.1825; -.
GCRDB; GCR.1825; -.
GCRDB; GCR.1982; -.
GCRDB; GCR.1983; -.
GCRDB; GCR.1983; -.
PROSITE; PS000979; G_PROTEIN_RECEP_F3_1; 1.
PROSITE; PS00980; G_PROTEIN_RECEP_F3_2; 1.
PROSITE; PS00981; G_PROTEIN_RECEP_F3_3; 1.
PFAMM; PF00003; 7tm_3; 1.
                                                                                                    CONFLICT
SEQUENCE
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Multigene
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                                                                                                                                                                                                                                                                                                                                                                                                                      TRANSMEM
FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR.

MEDIATED BY A G-PROTEIN THAT ACTIVATES A PHOSPHATIDYLINOSITOL-
CALCIUM SECOND MESSENGER SYSTEM. MAY PARTICIPATE IN THE CENTRAL
ACTION OF GLUTAMATE IN THE CNS, SUCH AS LONG-TERM POTENTIATION 1
THE HIPPOCAMPUS AND LONG-TERM DEPRESSION IN THE CEREBELLUM.
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
ALTERNATIVE PRODUCTS: TWO ISOFORMS; ALPHA (SHOWN HERE) AND BETA,
ARE PRODUCED BY ALTERNATIVE SPLICING.
SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SWISS-PROT entry is copyright. It is produced through the Swiss Institute of Bioinformatics and the EN
                                            l Similarity 27.3% 229; Conservative
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1194
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809
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841
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1067
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773
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217;
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CYTOPLASMIC (POGLN/PRO-RICH.
GLN/PRO-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                      III (POTENTIAL)
CYTOPLASMIC (PO
IV (POTENTIAL).
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SER-RICH.
POTENTIAL.
                                                                                                                AQL (IN ISOFORM BETA).
MISSING (IN ISOFORM BETA)
NSNGKSVSWESPGGGVPKG -> K
VQL (IN ISOFORM BETA, REF
P -> S (IN REF. 2).
                                                                                                                                                                                                                 POTENTIAL.
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SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

TISSUE SPECIFICITY: IS WIDELY DISTRIBUTED IN THE CNS AND PROMINENT
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SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS
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                                                                                             GVIGGSYSDVSIQVANLLRLFQIPQISYASTSAKLSDKSRYDYFARTVPPDFFQAKAMAE
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                             ILRFFNWTYVSTVASEGDYGETGIEAFELEARARNICVATSEKVGRAMSRAAFEGVVRAL
                                                                -LIGPDNTDHAVTTAALLSPFLMPLVSYEASSVILSGKRKFPSFLRTIPSDKYQVEVIVR
                                                                                                                                LLPNITLGYELYDVCSESSNVYA-TL---RVPAQQGT-G--HL--EMQRDLRNHSSKVVA 143
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PS00980; G_PROTEIN_RECEP_F3_2;
PS00981; G_PROTEIN_RECEP_F3_3;
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Brain Res. Mol. Brain Res. 40.55-63(1996).
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METABOTROPIC GLUTAMATE
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                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human)
Eukaryota; Metazoa; (
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                                                                                                                                                                                                                                                                                                                             TISSUE-BRAIN;
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                                                                                                             SUBCELLULAR LOCATION: :
SIMILARITY: BELONGS TO
STRONGEST, TO MGLUR2.
                                                                                                                                                                                        FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF T IS MEDIATED BY A G-PROTEIN THAT INHIBITS ADENYLATE
                                                                                                                                                                                                                                                                                                                                                                                                                                         OR MGLUR3
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VCCWICIPCEPYEYL-ADEF-TCMDCGSGQWPTADLTGCYDLPEDYIRWEDAWAIGPVTI
                   WDWNGPEWTFEVIGSASLSPVHLDINKTKIQWHGKNNQVPVSVCTRDCLEGHHRLVMGSH
                             RDFWEQKFQCSLQNK-RNHRRVCDKHLAIDSSNYEQESKIMFVVNAVYAMAHALHKMQRT
                                                                                                                                      LTGKVWIASEDWAISTYITNVPGIQGIGTV-LGVAIQQ-RQVPGLKEFEESYVQAVMGAP
                                                                                                                                                        -ASFTWVASDGWGAQESIIKGSEHVAYGAITLELASQPVRQFDRYFQSLNPYNNHRNPWF
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                                                                           LCPNTTKLCDAMKILDGKKLYKDYLLKINFTAPFNPNKDADSIVKFDTFGDGMGRYNVFN
                                                                                               RTCPEGSW-CGTNQLCRECHAFTTWNMP-ELGAFSMSAAYN-VYEAVYAVAHGLHQLL-G
                                                          -CTSGT - - C - A - R - -
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PF01094; ANF_receptor;
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IV (POTENTIAL)
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. No. 2.36e-140;
Mismatches 338;
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KUHN R.;
                            G-protein coupled receptor; Multigene family.
                                                                                                                                           PROSITE; PS00979; G_PROTEIN_RECEP_F3_1; PROSITE; PS00980; G_PROTEIN_RECEP_F3_2; PROSITE; PS00981; G_PROTEIN_RECEP_F3_3;
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      SIGNAL
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                                                                                                                     PFAM; PF00003;
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SUBGELULIAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

TISSUE SPECIFICITY: WIDELY EXPRESSED IN DIFFERENT ADULT BRAIN AS WELL AS IN FETAL BRAIN.

SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LLSLQLAVAYCWAFSCORTESSPGFSLPGDFLLAGLFSLHADCLQVRHRPLVTSCDRSDS
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Pred. No. 1.02e-138;
234; Mismatches 336;
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IV (POTENTIAL).
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PIR; JH0562; JH05
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MGR3_RAT

MGR3_RAT

P31422;

01-JUL-1993 (Rel. 26, Created)

01-JUL-1993 (Rel. 26, Last sequence update)

15-JUL-1999 (Rel. 38, Last annotation update)

The portropic GLUTAMATE RECEPTOR 3 PRECURSOR.
                                                    This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restructed by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Rat).
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "AANABE Y., MASU M., ISHII T., SHIGEMOTO R., NAKANISHI S.;
"A family of metabotropic glutamate receptors.";
Neuron 8:169-179(1992).
-i-FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS REC!
-IS_MEDIATED BY A G-PROTEIN THAT INHIBITS ADENYLATE CYCLASE
                                                                                                                                                                                                                                                                                                                             ACTIVITY.

SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

TISSUE SPECIFICITY: IS WIDELY DISTRIBUTED IN THE CNS. PREDOMINAN EXPRESSION IS SEEN IN THE NEURONAL CELLS OF THE CEREBRAL CORTEX, DENTATE GYROS, AND GLIAL CELLS THROUGHOUT BRAIN REGIONS.
                                                                                                                                                                                                                                                                                    SIMILARITY: BELONGS T
STRONGEST, TO MGLUR2.
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NOT_ANNOTATED_CDS.
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Rattus.
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JH0562. .ch/announce/

PROSITE; PS00979; G_PROTEIN_RECEP_F3_1; PROSITE; PS00980; G_PROTEIN_RECEP_F3_2; PROSITE; PS00981; G_PROTEIN_RECEP_F3_3;

7 tm_3;

ANF_receptor; led receptor; Transmembrane; Glycoprotein;

Signal;

22 879 576 599 613 634 664 709 734 EXTRACELLULAR (POTENTIAL) V (POTENTIAL). CYTOPLASMIC (F EXTRACELLULAR (
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 LPKCYVILCRPELNNTEH
                        APKVHIVLFQPQKNVVTH
                                                                       KCPENFNEAKFIGFTMYTTCIIWLAFLPIFYVTSSDYRVQTTTMCISVSLSGFVVLGCLF
                                                                                              LCLTWLAMWTPRPTREYQ-REPH-LVILECTEVNSVGFLVAFAHNILLSISTFVCSYLGK
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                                                 ELPENYNEAKCVTFSLLLHFVSWIAFFTMSSIYQGSYLPAVNVLAGLATLSGGFS-GY-F
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202; Mismatches 340;
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15-7UL-1998 (Rel. 36, Last sequence update)
15-DEC-1999 (Rel. 39, Last annotation update)
15-DEC-1999 (Rel. 39, Last annotation update)
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NAKANISHI S.;
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DOMAIN
                                                                                                                                                                                                                                                                                         PFAM; PF00003; 7tm_3; 1.
PFAM; PF01094; ANE_receptor; G-protein coupled receptor; Multigene family; Vision.
                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and foentities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced between the Swiss Institute of Bioinformatics and the European Bioinformatics Institute. There are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene
                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00979; PROSITE; PS00980;
                                                                                                                                                                                                                                                                                                                                                                      GCRDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE; 97358610.
HASHIMOTO T., INAZAWA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GRM6 OR MGLUR6.
Homo sapiens (Human)
Eukaryota; Metazoa;
                                                                                                                                     TRANSMEM
                                                                                                                                                                          TRANSMEM
                                                                                                                                                                                             TRANSMEM
                                                                                                                                                                                                               TRANSMEM
                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                 TRANSMEM
                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                  SIGNAL
                                                                                                                                                                                                                                                                                                                                 PROSITE;
                                                                                                                                                                                                                                                                                                                                                             MIM; 604096
                                                                                                                                                                                                                                                                                                                                                                               EMBL; U82083;
                                                                                                                                                                 DOMAIN
                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                         CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MGR6_HUMAN
                  64
 72
                                                        Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  e whole nucleotide sequence and chromosomal localization of the for human metabotropic glutamate receptor subtype 6.";
J. Neurosci. 9:1226-1235(1997).
FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY A G-PROTEIN THAT INHIBITS ADENYLATE CYCLASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: 1 SIMILARITY: BELONGS TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRONGEST, TO MGLUR4.
           QGVHRLEAMLYALDRVNADPELLPGVRLGARLLDTCSRDTYALEQALSFVQALIRGRGDG
 HGYHLFQAMRFTVEEINNSTALLPNITLGYELYDVCS-ESSNVYATLR-VPAQ-QGTGHL 128
                                              Similarity
                                                                                                                                                                                                                                                                                                                               PS00979; G_PROTEIN_RECEP_F3_1;
PS00980; G_PROTEIN_RECEP_F3_2;
PS00981; G_PROTEIN_RECEP_F3_3;
                                                                          11.6%;
larity 25.3%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                AAB82058.1;
                                                                           Ã,
                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chordata;
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                                                                           W.
                                    Score
Pred.
233; M
                                                                                           CYTOPLASMIC (POTENTIAL).
VI (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
VII (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                    Transmembrane;
                                                                           POTENTIAL.
D5A5C038
                                                                                                                                                                                                                      II (POTENTIAL)
EXTRACELLULAR
                                                                                                                                                                                                                                          I (POTENTIAL)
CYTOPLASMIC (
                                                                                                                                                                          EXTRACELLULAR (POTENTIAL)
V (POTENTIAL).
                                                                                                                                                                                           CYTOPLASMIC IV (POTENTIA
                                                                                                                                                                                                                                                              EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                               III (POTENTIAL)
                                                                                                                                                                                                                                                                         METABOTROPIC
                                                                                                                                                                                                                                                                                  POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata;
                                                                                                                                                                         (POTENTIAL)
                                    re 741; DP 1; Le
1. No. 5.56e-135;
Mismatches 297;
                                                                                                                                                                                            (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hominidae;
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3 OF G-PROTEIN COL
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                                                                                                                                                                                                    (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8
                                                                                                                                                                                                                                           (POTENTIAL).
                                                                                                                                                                                                                                                                       GLUTAMATE RECEPTOR
                                                                                                                                                                                                                                                                                                   Glycoprotein;
                                                                                                                                                                                                                        (POTENTIAL)
                                                       Length
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                                     Indels
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                                                        877:
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tent is in no
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                                                                                                                                                                                                                                                                                                   Signal;
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L outstation -
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                                                                                                                                                                                                                                                                                                                                                                MGR8_MOUSE
P47743;
01-FEB-1996
01-FEB-1996
15-JUL-1998
                                                                                                                                                                                                                                                                                                           01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation updat-
METABOTROPIC GLUTAMATE RECEPTOR 8 PRECURSOR
GRM8 OR MGLUR8.
                                           MEDIJINE: 95239344.

MEDIJINE: 95239344.

DUVOISIN R.M., ZHANG C., RAMONEI
"A novel metabotropic glutamate
"A novel metabotropic glutamate
"ifactory bulb.";
                          olfactory bulb.
J. Neurosci. 15
                                                                                                                                                                                                                                                  GRM8 OR FULL MOUSE).
Mus musculus (Mouse).
Chordata;
                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-C57BL/6; TI
                                                                                                                                                                                                                                     Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HLFLCLTWLAMWTPRPTREY -- QR-F-P-HL-VILECTEVNSVGFLVAFAHNILLSISTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     - VGM-IAWLGARPPHSVIDYEEQRTVDPEQARGVLKC-DMSDLSLIGCLGYSLLLMVTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -NGPEWT--FEVIGSASLSPVHLDINKTKIQWHGKNNQVPVSVCTRDCLEGHHR-LVMGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MHQALCPGHTGLCPAMEPTDGRMLLQYIRAVRENGSAGTPVMFNENGDAPGRYDIFQYQA 477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRYDFFSRVVPPDSYQAQAMVDIVRALGWNYVSTLASEGNYGESGVEAFVQISREAGGV
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                                                                                                                                                                                                                                  Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -G-YFLPKCYVILCRPELN
                        15:3075-3083(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                         TISSUE-RETINA;
                                                                                                                                                                                                                                  Chordata; Craniata;
Sciurognathi; Murida
                                                                                                      RAMONELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             823
                                                                                                                                                                                                                                                                                                                                        tation update)
8 PRECURSOR.
                                                                           receptor expressed in
                                                                                                         ×.;
                                                                                                                                                                                                                                  Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          908
                                                                                                                                                                                                                                                               Vertebrata;
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                                                                                                                                                                                                                                     Mus.
                                                                                                                                                                                                                                                               Mammalia;
                                                                           the
                                                                              retina
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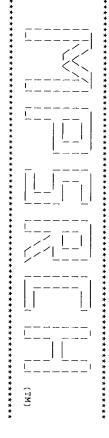
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CARBOHYD
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PROSITE; PS00979; G_PROTEIN_RECEP_F3_1;
PROSITE; PS00980; G_PROTEIN_RECEP_F3_3;
PROSITE; PS00981; G_PROTEIN_RECEP_F3_3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                SEQUENCE
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PFAM; PF01094; ANF_receptor;
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SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
TISSUE SPECIFICITY: STRONGLY EXPRESSED IN OLFACTORY BULB,
ACCESSORY OLFACTORY BULB, AND MAMMILLARY BODY: WEAKER EXPRESSION
ACCESSORY OLFACTORY BULB, AND MAMMILLARY BODY: WEAKER EXPRESSION
IN THE RETINA, AND IN SCATTERED CELLS IN THE CORTEX AND HINDBRAIN.
SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY A G-PROTEIN THAT INHIBITS ADENYLATE CYCLASE
KEKGIHRLEAMLYAIDQTNKDPDLLSNITLGVRILDTCSRDTYALEQSLTFVQALIEKDA 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                 LAVAYCWAFSC-QRTES---SPGFSLPGDFLLAGLFSLHADCLQVRHRPLVTSCDRSDSF 69
                                                                                                                                                                                                                                            LTAKFYWILTMMQRTHSQEYAHSIRLDGDIILGGLFPVHA---KG-ERG-V-PC--GDLK
                                         FPSFLRTIPSDKYQVEVIVRLLQSFGWVWISLVGSYGDYGQLGVQALEELATPRG-ICVA
                                                                   YDFFSRVVPPDSYQAQAMVDIVTALGWNYVSTLASEGNYGESGVEAFTQISREIGGVCIA 248
                                                                                                  GHLE-MQRD--LRNHSSKVVALIGPDNTDHAVTTAALLSPFLMPLVSYEASSVILSGKRK
                                                                                                                             SDVKCANGDPPIFTKPDKISGVIGAAASSVSIMVANILRLFKIPQISYASTAPELSDNTR 188
                                                                                                                                                         NGHGYHLFQAMRFTVEEINNSTALLPNITLGYELYDVCS-ESSNVYATLR-VPA--QQGT
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                                                                                                                       643 FAIFLSCLTIRSFOLVIIFKESTK-VPTFYHTWAQNHGAGIFVIVSSTVHLFLCLTWLAM
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                                                                                                                                                                                                                                                                                                                                                                                                                                         407 CTS--GTCAR-GPVYPWQLLQQIYKVNFLLHKKT-VAFDDKGDPLGYYDIIAWDWNGPEW 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                             424 CPGYIGLCPRMVTIDGKELLGYIRAVNENGSAGTPVTFNENGDAPGRYDIFQYQINNKST 483
 810 LPKCYVILCRPELN 823
                                                            756 NYNEAKCVTFSLLLHFVSWIAFFTMS-SIYQGS---YLPAVNVLAGLATLSGGFS-G-YF
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                          MPKVYIIIFHPEQN 848
                                                                                 TFNEAKPIGFTMYTTCIIWLAFIPIFFGTAQSAEKMYIQTTTLTVSMS-LSASVSLGMLY
                                                                                                                                                                                                                                                                                                                CEAGTFLNTSELHTCQPCGTEEWAPEGSSACFSRTVEFLGWHEPISLVLLAANTLLLLLL 582
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EGNFGCKSGSHGKRNSHIKKCTGLERIARDSSYEQEGKVQFVIDAVYSMAYALHNMHKEL 423
                                                                                                                                                                                                                   MCFSYAALLTKTNRIHRIFEQGKKSVTAPKFISPASQLVITFSLIS--VQLLGVFVWFVV 716
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Search completed: Fri Mar 17 13:17:59 2000 Job time : 101 secs.

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Run on: MPsrch_pp protein - protein database search, using Smith-Waterman algorithm Fri Mar 17 13:15:12 2000: MasPar time 35.30 Seconds 955.673 Million cell updates/sec

Tabular output not generated.

>US-09-361-652-2 (1-842) from US09361652.pep 6366

Description: Perfect Score: Sequence: 1 MLFWAAHLLLSLQLAVAYCW.....NNTEHFQASIQDYTRRCGTT 842

Scoring table: PAM 150 Gap 11

Searched: 122810 seqs, 40068593 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: pir62 1:pir1 2:pir2 3:pir3 4:pir4

Statistics: Mean 52.559; Variance 107.285; scale 0.490

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

Db 327 QIPGFREFLQKVHPXXSVHNGFAKBFWEETFNCHLQEGAKGPLPVDTFLRGHEEGGARLS 386 : : : : : : : : : : : : :	Db 268 IVVFSSGPDLEPLI-KEIVRRNITGRIWLASEAWASSSLIAMPEYFHVVGGTTGFGLKAG 326	Db 210 VGTIAADDDYGRPGIEKFREEAESRDICIDFSELISOYSDE-E-KIQQVVEVIQNSTAKV 257 ::::: ::::::::::::::::::::::::::::	Db 150 ISTAVANLLGLEYIPQVSYASSSRLLSNKNQEKSELRTIPNDEHQATAMADIIEYERWNW 209 :: : : : : : : :	Db 90 PNMTLGYRIFDTCNTVSKALEATLSFVAQNKIDSLNLDEFCNCSEHIPSTIAVVGATGSG 149 : :: : :	Db 31 GDIILGGLFPIHFG-VAVKDQDLKSRPESVECIRYNFRGFRWLQAMIFAIEEINSSPALL 89 :: : :: : :: : 37 GDFLLAGLFSLHADCLQVRHRPLVTSCDRSDSFNGHGYHLFQAMRFTVEEINNSTALL 94	Query Match 20.7%; Score 1316; DB 2; Length 1085; Best Local Similarity 31.9%; Pred. No. 6.36e-231; Matches 272; Conservative 234; Mismatches 273; Indels 73; Gaps 51;	#title Cloning and characterization of an extracellular Ca (2+)-sensing receptor from bovine parathyroid. #cross-references MUID:94077182 #accession \$40476 ##status preliminary ##nolecule_type mRNA ##residues 1-1085 ##label BRO \$UMMARY #length 1085 #molecular-weight 121170 #checksum 5738	RENCE authors		,
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                                                                                                                                                                                                                               #authors Pollak, M.R.; Brown, E.M.; Chou, Y.H.; Hebert, S.C.; Marx, S.J.; Steinmann, B.; Levi, T.; Seidman, C.E.; Seidman, Cell (1993) 75:1297-1303
#title Mutations in the human Ca(2+)-sensing receptor gene cause familial hypocalciuric hypercalcemia and neonatal severe hyperparathyroldism.
#cross-references MUID:94094324
#accession A49419
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##cross-references EMBL:X81086
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pearce, S.H.S.; Thakker, R.V. submitted to the EMBL Data Library, $49341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 $49341 #type complete
calcium-sensing receptor - human
formal_name Homo sapiens #common_name man
16_Feb-1995 #sequence_revision 12-May-1995
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S49341
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                                           sequence inconsistent with nucleotide translation sequence modified after extraction from NCBI backbone 186-Arg mutation is associated with familial hypocalciuric hypercalcemia and neonatal severe
  sequence
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hyperparathyroidism
equence extracted from NCBI backbone (NCBIN:142453)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FGISFVLCISCILVKTNRVLLVFE--AKIPTSFHRKWWGLNLQFLLVFLCTFMQIVICVI 741
                                                                                                                                                                        VECPDGEYSDETDASACNKCPDDFWSNENHTSCIAKEIEFLSWTEPFGIALTLFAVLGIF
                                                                                                                                                                                                                                                                                                                                      NGSCADIKKVEAWQVLKHLRHLNFTNNMGEQVTFDECGDLVGNYSIINWHLSPEDGSIVF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   TVLG----VA-IQQRQ-VP-GL-KEF-EESY---VQ-AVMGA-P-----RTCPE-GSW--
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 FSLGFAIFLSCLTIRSFQLVIIFKFSTKVPT-FYHTWAQNHGAGIFVIVSSTVHLFLCLT
                                                                       LLIGTAGLFA-WRLHTPVVRSAGGRLCFLMLGSLVAG-SCSLYSFFGKPTVPACLLRQPL 638
                                                                                                                                                  MPCEAGTFLNTSELHTCQPCGTEEWAPEGSSACFSRTVEFLGWHEPISLVLLAANTLLLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PNLTLGYRIFDTCNTVSKALEATLSFVAQNKIDSLNLDEFCNCSEHIPSTIAVVGATGSG 148
                                                                                                            LTAFVLGVFIKFR-NTPIVKATNRELSYLLLFSLLCCFSSSLF-FIGEPQDWTCRLRQPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence modified after extraction from NCBI backbone 298-Lys mutation is associated with familial hypocalciuric hypercalcemia and neonatal severe hyperparathyroidism sequence extracted from NCBI backbone (NCBIN:142455) C49419
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th 1078 #molecular-weight 120672 #checksum 8159
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Pred. No. 7.84e-227;
234; Mismatches 274;
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Brown, E.M.; Hebert, S.C.; Nemeth, E.F.; F
#journal J. Biol. Chem. (1995) 270:12919-12925
#title Molecular cloning and functional expression
parathyroid calcium receptor cDNAs.
#cross-references MUID:95279439
#accession A56715
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NDS glycoprotein; receptor; transmembrane protein
**Y #length 1078 #molecular-weight 120573 #chec
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                                                          SGTCA-RGPVYPWQLLQQIYKVNFLLHK-KTVAFDDKGDPLGYYDIIAWDWNGPE-WT-F
                                                                                                                         NGSCADIKKVEAWQVLKHLRHLNFTNNMGEQVTFDECGDLVGNYSIINWHLSPEDGSIVF
                                                                                                                                                                                              -CGTN-Q-LCRECHAFTTWNMPELGAFSMSAAYNVYEAVYAVAHGLHQL---L-GC---T
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##EXPORTIMENTAL

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725-744
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Cloning and functional expression of a rat kidney
extracellular calcium/polyvalent cation-sensing
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                                              VILCRPELNNTEHFQASIQDYT
                                                                    IILFKPSRNTIEEVRSSTAAHA 880
                                                                                                           NENEAKFITESMLIFFIVWISFIPAYASTY-GKFVSAVEVIAILAASFGLLACIFFNKVY
                                                                                                                                                        WLYTAPPSSYRNHELEDEIIFITCHEGSLMALGSLIGYTC-LLAAICFFF-AFKSRKLPE
                                                                                                                                                                                                       FGISFVLCISCILVKTNRVLLVFE--AKIPTSFHRKWWGLNLQFLLVFLCTFWQILICII
                                                                                                                                                                                                                                      LLIGTAGLFA-WRLHTPVVRSAGGRLCFLMLGSLVAG-SCSLYSFFGKPTVPACLLRQPL
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                                                                                                                                                                                                                                                                                                                                                         KEVGYYNVYAKKGERLFINEEKILWSGFSREVPFSNCSRDCQAGTRKGIIEGEPTCCFEC
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                                                                                             NYNEAKCYTFSLLLHFYSWIAFFTM-SSIYQGSYLPAVNYLAGLATLSGGFSGYFLPKCY
                                                                                                                                           WLAMWTPRPTREYQRFPHLVILECTEVN--SVGFLVAFAHNILLSISTFVCSYLGKELPE
                                                                                                                                                                                       FSLGFAIFLSCLTIRSFQLVIIFKFSTKVPT-FYHTWAQNHGAGIFVIVSSTVHLFLCLT
                                                                                                                                                                                                                                                            LTAFVLGVFIKFR-NTPIVKATNRELSYLLLFSLLCCFSSSLF-FIGEPQDWTCRLRQPA 683
                                                                                                                                                                                                                                                                                    MPCEAGTFLNTSELHTCQPCGTEEWAPEGSSACFSRTVEFLGWHEPISLVLLAANTLLLL
                                                                                                                                                                                                                                                                                                            VECPDGEYSGETDASACDKCPDDFWSNENHTSCIAKEIEFLAWTEPFGIALTLFAVLGIF
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Similarity 31.2%; Pred. No. 5.70e-224;
269; Conservative 240; Mismatches 280;
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kinase C) #status predicted\
#binding_site phosphate (Ser) (covalent) (by
kinase A) #status predicted

pth 1079 #molecular-weight 120867 #checksum
#type complete
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#title Molecular cloning and functional expression of parathyroid calcium receptor cDNAs.
#cross-references MUID:95279439
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##cross-references GB:U20760; NID:g683746; PID:g683747
RDS glycoprotein; receptor; transmembrane protein
#length 1088 #molecular-weight 121799 #check
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ##molecule_type mRNA
##rosid....
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                                                                                 DWTCRLRQPAFGISEVLCISCILVKTNRVLLVFE--AKIPTSFHRKWWGLNLQFLLVFLC 741
                                                                                                                                                             LAANTLLLLLIGTAGLFA-WRLHTPVVRSAGGRLCFLMLGSLVAG-SCSLYSEFGKPT
                                                                                                                                                                                                                                                                                                      EGEPTCCFECVECPDGEYSDETDASACNKCPDDFWSNENHTSCIAKEIEFLSWTEPFGIA 625
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                                                  VPACLLRQPLFSLGFAIFLSCLTIRSFQLVIIFKFSTKVPT-FYHTWAQNHGAGIFVIVS
                                                                                                                                                                                                                                                                    MGSHHCCFECMPCEAGTFLNTSELHTCQPCGTEEWAPEGSSACFSRTVEFLGWHEPISLV
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TFMQIVICVIWLYTAPPSSYRNOELEDEIIFITCHEGSLMALGFLIGYTC-LLAAICFFF
                                                                                                                                                                                                                  LTLFAVLGIFLTAFVLGVFIKFR-NTPIVKATNRELSYLLLFSLLCCFSSSLF-FIGEPQ 683
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l Similarity 31.6%;
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#formal_name Homo sapiens #common_name man
19-Oct-1995 #sequence_revision 19-Oct-1995
17-Mar-1999
B56715
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                               J. Biol. Chem. (1992) 267:13361-13368 Molecular characterization of a novel receptor mGluR5 coupled to inositol
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Best Local
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##residues 1-1171 ""
                 817
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                                                  751
                                                                                 761
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Local Similarity 27.1%;
nes 234; Conservative
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                                                                                                                                    LGIIVALFIMEPPDIMHDYPSIRE-VYLICNTTN-LGVVTPLGYNGLLILSCTF-YAFKT
                                                                                                                                                                                                                                                                                                                                       CCWTCTPCKENEYVF-DE-YTCKACQLGSWPTDDLTGCDLIPVQYLRWGDPEPIAAVVFA
                                                                                                                                                                                                                                                                                                                                                                                                           EMGKDY-FDYINVGSWDNGELKMDDDEV-WSKKNNIIR-SVCSEPCEKGQIKVIRKGEVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                  WFQEFWQHRFQ-CRLEGFAQENSKYNKTCNSSLTLRTHHVQDSKMGFVINAIYSMAYGLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DKTLFKYFMRVVPSDAQQARAMVDIVKRYNWTYVSAVHTEGNYGESGMEAFKDMSAKEGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEEEEGLVRCVDGSSSFRSKKPIVGVIGPGSSSVAIQVQNLLQLFNIPQIAYSATSMDLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SFNGHGYHLFQAMRFTVEEINNSTALLPNITLGYELYDVCSESSNVYA-TLR-VPAQQ-G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R-EQYGIQRVEAMLHTLERINSDPTLLPNITLGCEIRDSCWHSAVALEQSIEFIRDSLIS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LLLSLQLAVAYCWAFSCQRTESSPGFSLPGDFLLAGLFSLHADCLQVRHRPLVTSCDRSD
|:|| |:|| | | | | |
                                                                               RNVPANFNEAKYIAFTMYTTCIIWLAF--VP-IYFGSNYKIITMCFSVS-LSATVALGCM 816
                                                                                                                                                                                   LLRQPLFSLGFAIFLSCLTIRSFQLVIIFKFSTK-VPTFYHTWAQNHGAGIFVIVSSTVH
                                                                                                                                                                                                                    YLQRIGIGLSPAMSYSALVTKTNRIARILAGSKKKICTKKPRFMSACAQLVIAFILICIQ
                                                                                                                                                                                                                                                    ANTILLLLIGTAGLEAWRLHTPYVRSAGGRLCELMLGSLVAGS-CSLYSEFGKPTVPAC
                                                                                                                                                                                                                                                                                    CLGLLATLFY-TVIFIIYR-DTPVVKSSSRELCYILLAGICLGYLCT-FCLIAKPKQIYC
                                                                                                                                                                                                                                                                                                                    CCFECMPCEAGTFLNTSELHTCQPCGTEEWAPEGSSACFSRTVEFLGW-H-EPISLVLLA
                                                                                                                                                                                                                                                                                                                                                                                    WNGPEWTFEVIGSASLSPVHLDINKTKIQWHGKNNQVPVSVCTRDCLEGHHRLV-MGSHH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NMQMSLCPGYAGLCDAMKPIDGRKLLDSLMKTNFTGVSGDMILFDENGDSPGRYEIMNFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    - PEGSWCGTNQLCR-E--CHAFTTWNMPELGAFSMSAAY--N--V-Y--EAVYAVAHGLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    K-VWIASEDWAISTYITNVPGIQGIGTVLGVAIQQRQVPGLKEFEESYVQAVMGAP-RTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EFLLLGSDGWA-DRYDVT-DGYQ-REAVGGITIKL-QSPDVKWFDDYYLKLRPETNLRNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CVAFKDVVPLSAQAGDPRMQRMMLRL-AR-ARTTVVVVFSN-RHLAGVFFRSVVLANLTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CIAHSYKI-YSN-AGEQSFDKLLKKLRSHLPKARVVACFCEGMTVRGLLMAMRRLG-LAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GKRKFPSFLRTIPSDKYQVEVIVRLLQSFGWVWISLVGSYGDYGQLGVQALEELATPRGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGHLE-MQR--D-LRN-HSSK-VVALIGPDNTDHAVTTAALLSPFLMPLVSYEASSVILS
                                                  KELPENYNEAKCVTFSLLLHFVSWIAFFTMSSIYQGSYLPAVNVLAGLATLSGGFS-GY-
                                                                                                                   LFLCLTWLAMWTPRPTREYQRFPHLVILECTEVNSVGFLVAFAHNILLSIS-TFVCSYLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      G protein-coupled receptor; transmembrane protein #length 1171 #molecular-weight 128289 #checksum 8594
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Pred. No. 2.86e-129;
222; Mismatches 340;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1171;
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FLPKCYVILCRPELNNTEHFQAS

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ACCESSIONS
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SUMMARY
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Best Local Similarity
Matches 231; Conser
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#title Sequence and expression of
#cross-references MUID:91156047
#accession S15362
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##cross-references EMBL:X57569; NID:g56646; PID:g56647
##cross-references EMBL:X57569; NID:g56647
##cross-references EMBL:X57569; NID:g56646; PID:g56647
##cross-references EMBL:X57569; NID:g56646; PID:g56647
##cross-references EMBL:X57569; NID:g56646; PID:g56646; PID:g56646; PID:g56646; PID:g56646; PID:g56646; PID:g56646; PID:g56646; PID:g56646; PID:g56646; PID:g5
   421
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##residnes
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##experimental_source cerebellum
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##molecule_type nucleic acid
##residues 1-1199 ##label HOU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PNITLGYELYDVCSESS-----NV-Y--ATL-RVPAQ-QGTGH-LEMQRDLR-NHSSKVV 142
   QLLQQIYKVNFL-LHKKTVAFDDKGDPLGYYDIIAWDWNGPEWTFEVIGSASLSPVHLDI
                                                                   KLLDFLIKSSFVGVSGEEVWFDEKGDAPGRYDIMNLQYTEANR-YDYVHVGTWHEGVLNI
                                                                                                                                                                                                   NFKKVCTGNESLEENYVQDSKMGFVINAIYAMAHGLQNMHHALCPGHVGLCDAMKPIDGR
                                                                                                                                                                                                                                                                                                                                           VEANGGITIKL-OSPEVRSFDDYFLKLRLDTNTRNPWFPE-FWQHRFQ-CRLPGHLLENP
                                                                                                                                                                                                                                                                                                                                                                                                                  LRL-AR-ARTTVVVVFSN-RHLAGVFFRSVVLANLTGKVWIASEDWAISTYITNVPGIQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RKLRERLPKARVVVCFCEGMTVRGLLSAMRRLGVVGEFSLIGSDGWADRDEV--IEGYE- 331
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGVIGPGSSSVAIQVQNLLQLFDIPQIAYSATSIDLSDKTLYKYFLRVVPSDTLQARAML 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PNITLGSEIRDSCWHSSVALEQSIEFIRDSLISIRDEKDGLNRCLPDGQTLPPGRTKKPI 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LPGDFLLAGLFSLHADCLQVRHRPLVTSCDRSDSFNGHGYHLFQAMRFTVEEINNSTALL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MDGDVIIGALFSVHHQPPAEKV-P-ERKC--GEIREQYGIQRVEAMFHTLDKINADPVLL
                                                                                                                                       NMPEL--GAFSMSAAY--N--V-Y--EAVYAVAHGLHQLL-G-CTS--GTC-ARGPVYPW
                                                                                                                                                                                                                                                                              IGTVLGVAIQQRQVPGLKEFEESYVQAVMGA-PRTC--PEGSWCGTNQLCR-ECHAFTTW
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G protein-coupled glutamate receptor - rat
#formal_name Rattus norvegicus #common_name Norway rat
#formar-1993_*sequence_revision 18-Nov-1994 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S15362 Tanabe,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12.7%; Score 810; DB 2; Le larity 27.6%; Pred. No. 1.80e-128; Conservative 216; Mismatches 325;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S
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                                                                                                                                                                                                              448
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                                                                         Matches
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625-645
657-675
700-720
751-772
786-807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #authors Tanabe, Y.; Masu, M.; Ish
#journal Neuron (1992) 8:169-179
#title A family of metabotropic
#cross-references MUID:92110002
#accession JH0563
                                                                                                                                                                                                                                             98,301,
569
                                                                                                                                                                                     621,689,695,859,
870
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ##experimental_source brain
This protein is coupled to a G protein and evokes a variety
This protein is coupled to a G protein and evokes a variety
functions by mediating intracellular signal transduction.
IFICATION #superfamily metabotropic glutamate receptor 4
RDS G protein-coupled receptor; glycoprotein; phosphoprote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ##residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ##molecule_type mRNA
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GYHLFQAMRETVEEINNSTALLPNITLGYELYDVCS-ESSNVYATLR-VPA--Q-QGTG- 126
                                    GIHRLEAMLFALDRINNDPDLLPNITLGARILDTCSRDTHALEQSLTFVQALIEKDGTEV 134
                                                                                                                                                                                                                                                              ,454,484,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LAF--VP-IYFGSNYKIITTCFAVSLSVTVALGCMFT?XXYIIIAKPERNVRSAFTTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LVILECTEVNSVGFLVAFAHNILLSIS-TFVCSYLGKELPENYNEAKCVTFSLLLHFVSW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VRSAGGRICFLMLGSLVAG-SCSLYSFFGKPTVPACLLRQPLFSLGFAIFLSCLTIRSFQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NKIKIQWHGKNNQVPVSVCTRDCLEGHHRLV-MGSHECCFECMPCEAGTFLNISELHTCQ 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DDYKIQ-MNKSGMVR-SYCSEPCLKGQIKVIRKGEVSCCWICTACKENEFVQ-DEF-TCR 563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IAFFTMSSIYQGS-YLPAVNVLAGLATLSGGFSGYFLPKCYVILCRPELNNTEHFQAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -VYLIC-NTSNLGVVAPVGYNGLLIMSCTY-YAFKTRNVPANENEAKYIAFTMYTTCIIW 798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LVIIFKFSTK-VPTFYHTWAQNHGAGIFVIVSSTVHLFLCLTWLAMWTPRPTREYQRFPH 715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IARILAGSKKKICTRKPRFMSAWAQVIIASILISVQLTLVVTLIIMEPPMPILSYPSIKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PCGTEEWAPEGSSACFSRTVEFLGWHEPISLVLLAANTLLLLLIGTAGLFA-WRLHTPV
                                                                                        12.6%;
Similarity 25.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    metabotropic glutamate receptor 4 precursor - rat #formal_name Rattus norvegicus #common_name Norway rat 30-Jun-1992 #seguence_revision 30-Jun-1992 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JH0563
                                                                                                                                                #length
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#domain transmembrane #status predicted
                                                                                                                                                                                   #binding_site phosphate (Ser) (covalent) #status
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#product metabotropic glutamate
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1912 #molecular-weight 101818 #checksum
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                                                                         222; Mismatches
                                                                       Score 799; DB 2; Le
Pred. No. 2.81e-126;
222: Mismatches 307;
                                                                                                                                                                                                                                           carbohydrate
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                                                                                                            Length
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Indels 59;

Gaps

50;

244

301

818

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#authors O'Hara, P.J.; Sheppard, P.O.; Thogersen, H.; Venezia, D.;
Haldeman, B.A.; McGrane, V.; Houamed, K.M.; Thomsen, C.;
Gilbert, T.L.; Mulvihill, E.R.

#journal Neuron (1993) 11:41-52
#title The ligand-binding domain in metabotropic glutamate receptors
is related to bacterial periplasmic binding proteins.
#cross-references MUID:93332699
#accession 158149
      ##residues
                          ##molecule_type mRNA
                                             ##status
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VDPSHSVVDFQDQRTLDPRFARGVLKC-DISDLSLICLLGYSMLLMVTCTVYAIKTRGVP 778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GFAIFLSCLTIRSFQLVIIFKFSTK-VPTFYHTWAQNHGAGIFVIVSSTVHLFLCLTWLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GMSISYAALLTKTNRIYRIFEQGKRSVSAPRFISPASQLAITFILISLQL-LGICV-WFV 719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LIGTAGLFAWRLHTPVVRSAGGRLCFLMLGSLVAGSCSLYSFFGKPTVPACLLRQPLFSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EAGTFLNTSELHTCQPCGTEEWAPEGSSACFSRTVEFLGWHEP-ISLVL-LAANTLLLLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  V-VPLSAQAGD-PRMQRMMLRLARARTTVVVVFSNRHLAGVFFRSVVLANLTGKV-WIAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       LPKCYVILCRPELN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ETFNEAKPIGFTMYTTCIVWLAFIPIFFGTSQSADKLYIQTTTLTVSVSLSASVSLGMLY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -TG-YQYQVDRYTCKTCPYDMRPTENRTSCQPIPIVKLEWDSPWAVLPLFLAVVGIAATL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEVIGSASLSPVHLDINKTKIQWHGKNNQVPVSVCTRDCLEGHHRLVMGSHHCCFECMPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S--GTCAR-GPVYPWQLLQQIYKVNFL-LHKKTVAFDDKGDPLGYYDIIAWD-WNGPEWT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EDW-AISTYITNVPGIQGIGTVLGVAIQQRQVPGL-KEFEESYVQAVMGAPRTCP--EGS
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                                                                                                                                                                                                                                                                                                  metabotropic glutamate receptor - rat
#formal_name Rattus norvegicus #common_name Norway rat
26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change
                                                                                                                                                                                                                                                             I58149
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Local Similarity 25.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S--GTCAR-GPVYPWQLLQQIYKVNFL-LHKKTVAFDDKGDPLGYYDIIAWD-WNGPEWT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GRVGLCPRWDPVDGTQLLKYIRNVNFSGIAGNPVTFNENGDAPGRYDIYQYQLRNGSA-E 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EDW-AISTYITNVPGIQGIGTVLGVAIQQRQVPGL-KEFEESYVQAVMGAPRTCP--EGS 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FLRTIPSDKYQVEVIVRLLQSFGWVWISLVGSYGDYGQLGVQALEELATPRG-ICVAFKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GIHRLEAMLFALDRINNDPDLLPNITLGARILDTCSRDTHALEQSLTFVRALIEKDGTEV 134
                                                                                                                                                                                            MPKVYIILFHPEQN
                                                                                                                                                                                                                                                                                                                          MWTPRPTREYO--R-F-PHLV--ILECTEVNSVGFLVAFAHNILLSISTFVCSYLGKELP
                                                                                                                                                                                                                                                                                                                                                           VDPSHSVVDFQDQRTLDPRFARGVLKC-DISDLSLICLLGYSMLLMVTCTVYAIKTRGVP 778
                                                                                                                                                                                                                                                                                                                                                                                                             GFAIFLSCLTIRSFQLVIIFKFSTK-VPTFYHTWAQNHGAGIFVIVSSTVHLFLCLTWLA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FHCKLSRHALKKGSHIKKCTNRERIGQDSAYEQEGKVQFVIDAVYAMGHALHAMHRDLCP 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DSWGSKSAPVLRLEEVAE-GAV-TILPKRMSVRGFDRYFSSRTLDNNRRNIWFAEFWEDN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VKIPREPKTGEFDKIIKRLLETSNARG--IIIFANEDDIRRVLEAARRANQTGHFFWMGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FSRVVPSDTYQAQAMVDIVRALKWNYVSTLASEGSYGESGVEAFIQKSRENGGVCIA-QS 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        H-LEMQRDLRNHSSKVVALIGPDNTDHAVTTAALLSPFLMPLVSYEASSVILSGKRKFPS
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                                                                                                                                                      LPKCYVILCRPELN
                                                                                                                                                                                                                                       ENYNEAKCVTFSLLLHFVSWIAFFTMS-SIYQGSY-L-PAVNVLAGLATLSGGFS-G-YF
                                                                                                                                                                                                                                                                               ETFNEAKPIGETMYTTCIVWLAFIPIFFGTSQSADKLYIQTTTLTVSVSLSASVSLGMLY 838
                                                                                                                                                                                                                                                                                                                                                                                                                                                GMSISYAALLTKTNRIYRIFEQGKRSVSAPRFISPASQLAITFILISLQL-LGICV-WFV 719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FVVVT--FVRYNDTPIVKASGRELSYVLLAGIFLCYATTFLMIAEPDLGTCSLRRIFLGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -TG-YQYQVDRYTCKTCPYDMRPTENRTSCQPIPIVKLEWDSPWAVLPLFLAVVGIAATL
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$71376  #type complete
glutamate receptor homolog - cherry salmon
#formal_name Oncorhynchus masou #common_name cherry
11-Mar-1998 #sequence_revision 17-Apr-1998 #text_cha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #length 912 #molecular-weight 101846 #checksum
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Pred. No. 4.45e-1
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##residues 1-1218 ##label KUB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MLRL-AR-ARTTVVVVVFSN-RHLAGVFFRSVVLANLTGK-VWIASEDWAISTYITNVPGI 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VRLLQSFGWVWISLVGSYGDYGQLGVQALEELATPRGICVAFKDVVPLSAQAGDPRMQRM 260
  VRSAGGRLCFLMLGSLVAG-SCSLYSFFGKPTVPACLLRQPLFSLGFAIFLSCLTIRSFQ
                                    VKSSSRELCYIILAGIFLGYICP-FTLIAQPTVASCYLQRLLVGLSATMCYSALVTKTNR
                                                                                                                                                      NKTKIQWHGKNNQVPVSVCTRDCLEGHHRLV-MGSHHCCFECMPCEAGTFLNTSELHTCQ
                                                                                                                                                                                         DDYMMO-INRSDMV-LSVCSEPCSKGEIKVIRKGEVSCCWICTACKDNEIVO-DEF-TCT 573
                                                                                                                                                                                                                                                                     QLLEFLMRTSFTGVSGEDVWFDENGDTPGRYEIMNLQYVEPG-AFDYINVGSWHEGQLSI 517
                                                                                                                                                                                                                                                                                                         NMPEL-GAF-SMSAAY--N--V-Y--EAVYAVAHGLHQLLG--CTS--GTC-ARGPVYPW 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LRKLRERLPKARVVVCFCEGMTVRGLLMAMRRLG-VAGEFLLIGSDGWADRDEVVEGYEQ 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IAGVIGPGSSSVAIQVQNLLQLFNIPQIAYSATSIDLSDKTLFKYFLRVVPSDTLQARAI 225
                                                                                                                ACDLGWWPDPELEGCEPITLRYLEWGNPESIVQVVFACLGILVTSFVTFIFVLYR-DTPV 632
                                                                                                                                                                                                                                 QLLQQIYKVNFL-LHKKTVAFDDKGDPLGYYDIIAWDWNGPEWTFEVIGSASLSPVHLDI 479
                                                                                                                                                                                                                                                                                                                                                NYRKNCSGYESLEDNYVQDSKMGFVINAIYAMAQGLHDMHSHLCPGHVGLCKAMDPIDGS 458
                                                                                                                                                                                                                                                                                                                                                                                        QGIGTVLGVAIQQRQVPGLKE-FEESYVQAVMGAPRTCPEGSWCGTNQLCREC-HAFTTW 374
                                                                                                                                                                                                                                                                                                                                                                                                                          EAVGGI-TVKLHSEEVTSFDDYFLKLRLNTNTRNPWF-PE-FWQHRFQ-CRIPGHPLENM 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LDIVKRYNWTYVSAVHTEGNYGESGMEAFKELASQEGLCIAHSDKI-YSN-AGEKHFDRL 283
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l Similarity 27.8%;
201; Conservation
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Kubokawa, K.; Miyashita, T.; Nagasawa, H.; Kubo, Y.

FEBS Lett. (1996) 392:71-76

Cloning and characterization of a bifunctional metabotropic

Cloning and characterization of a bifunctional metabotropic

receptor activated by both extracellular calcium and
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kinase C) # status predicted\
#binding_site phosphate (Ser) (covalent) ()
cAMP-dependent kinase) # status predicted
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#binding_site phosphate (Ser)
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#journal Meuron (1992) 8:169-179
#title A family of metabotropic
#cross-references_MUID:92110002
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Pred. No. 2.64e-120;
218; Mismatches 343;
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#journal Neuron (1992) 8:189-179
#title A family of metabotropic glutamate
#cross-references_MUID:92110002
    577-599
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                                                                ##experimental_source brain

NT This protein is coupled to a G protein and evokes a variety functions by mediating intracellular signal transduction. 
IFICATION #superfamily metabotropic glutamate receptor 4

RDS G protein-coupled receptor; glycoprotein; phosphoprote transmembrane protein
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##residues 1-87
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metabotropic glutamate receptor 3 precursor - rat
#formal_name Rattus norvegicus #common_name Norway rat
30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change
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 #domain signal sequence #status
#product metabotropic glutamate
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735-756
770-791
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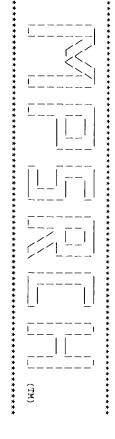
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Query Match 11.9%;
Best Local Similarity 25.8%;
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                                                                                                                                                                                                                                                                    MVSVWLILETP-GTRRYTLPEKRETVILKC-NVKDSSMLISLTYDVVLVILCTVYAFKTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ITGKVWIASEDWAISTYITNVPGIQGIGTV-LGVAIQQ-RQVPGLKEFEESYVQAVMGAP
LPKCYVILCRPELNNTEH
                                                    APKVHIVLFQPQKNVVTH
                                                                                                              ELPENYNEAKCYTFSLLLHFYSWIAFFTMSSIYQGSYLPAVNYLAGLATLSGGFS-GY-F
                                                                                                                                                                                                                                  LCLTWLAMWTPRPTREYQ-RFPH-LVILECTEVNSVGFLVAFAHNILLSISTFVCSYLGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACLGFLCTCIVITVFIKHNNTPLVKASGRELCYILLFGVSLSYCMTFFFIAKPSPVICAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VCCWICIPCEPYEYL-VDEF-TCMDCGPGQWPTADLSGCYNLPEDYIKWEDAWAIGPVTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WDWNGPEWTFEVIGSASLSPVHLDINKTKIQWHGKNNQVPVSVCTRDCLEGHHRLVMGSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LCPNTTKLCDAMKILDGKKLYKEYLLKINFTAPFNPNKGADSIVKFDTFGDGMGRYNVFN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -ASFTWVASDGWGAQESIVKGSEHVAYGAITLELASHPVRQFDRYFQSLNPYNNHRNPWF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TPRGICVAFKDVVPLSA-QAGDPRMQRMMLRLARARTTVVVVFSNRHLAGVFFRSVVLAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDRSDSFNGHGYHLFQAMRFTVEEINNSTALLPNITLGYELYDVCS-ESSNVYATLR-VP 120
                                                                                                                                                                        KCPENFNEAKFIGFTMYTTCIIWLAFLPIFYVTSSDYRVQTTTMCISVSLSGFVVLGCLF
                                                                                                                                                                                                                                                                                                                                                    RQPLFSLGFAIFLSCLTIRSFQLVIIFKFSTKVPTFYHTWAQNHGAGIFVIVSST-VHLF
                                                                                                                                                                                                                                                                                                                                                                                                           RRLGLGTSFAICYSALLTKTNCIARIFD-GVKNGAQRPKFI-SPSSQVFICLGLILVQIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NTLLLLLIGTAGLFAWRLHTPVVRSAGGRLCFLMLGSLVAGSCSLYSFFGKPTVPACLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HCCFECMPCEAGTFLNTSELHTCQPCGTEEWAPEGSSACFSRTVEFLGWHEPISLVLLAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ASLTKVDEAEYMCPDGSYAIQENIPLLIAGVIGGSYSSVSIQVANLLRLFQIPQISYAST 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -CTSGT--C-A-R---GP-VYPWQLLQQIYKVNFLLHK--KTVA-FDDKGDPLGYYDIIA
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#binding_site carbohydrate (Asn) (covalent) #status
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Pred. No. 2.
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2.56e-11
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d #label III\
d #label TIV\
d #label TRV\
d #label TVI\
d #label TVI\
d #label VII\
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CLASSIFICATION
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#authors
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Best Local :
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#title
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MCFSYAALLTKTNRIHRIFEQGKKSVTAPKFISPASQLVITFSLIS--VQLLGVFVWFVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LTAKFYWILTMMQRTHSQEYAHSIRLDGDIILGGLFPVHA---KG-ERG-V-PC--GDLK 68
                                IGTAGLFAWRLHTPVVRSAGGRLCFLMLGSLVAGSCSLYSFFGKPTVPACLLRQPLFSLG
                                                                  TFVIVTFVRYNDTPIVRASGRELSYVLLTGIFLCYSITFLMIAAPDTIICSFRRIFLGLG
                                                                                                                                       CEGYNY-QVDEL-SCELCPLDQRPNINRTGCQRIPIIKLEWHSPWAVVPVLIAILGIIAT
                                                                                                                                                                         TFEVIGSASLSPVHLDINKTKIQWHGKNNQVPVSVCTRDCLEGHHRLVMGSHHCCFECMP
                                                                                                                                                                                                          EYKIIGHWT-NQLHLKVED--MQWANREHTHPASVCSLPCKPGERKKTVKGVPCCWHCGR
                                                                                                                                                                                                                                              CTS--GTCAR-GPVYPWQLLQQIYKVNFLLHKKT-VAFDDKGDPLGYYDIIAWDWNGPEW
                                                                                                                                                                                                                                                                             CPGYIGLCPRMYTIDGKELLGYIRAVNENGSAGTPVTENENGDAPGRYDIFQYQINNKST
                                                                                                                                                                                                                                                                                                               EGSW-C-GTNOLCRECHAFT-T-WN-MPELGAFSMSAAYN-VYEAVYAVAHGLHQLL-G-
                                                                                                                                                                                                                                                                                                                                                 EGNFGCKSGSHGKRNSHIKKCTGLERIARDSSYEQEGKVQFVIDAVYSMAYALHNMHKEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                      FKDVVPLSAQAGD-PRMQRMMLRLARARTTVVVVVFSNRH-LAGVFFRSVVLANLTGK-VW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QSQKIPREPRPGEFEKIIKRLLETPNARA--VIMFANEDDIRGILEAAKKL-NQSGHFLW 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FPSFLRTIPSDKYQVEVIVRLLQSFGWVWISLVGSYGDYGQLGVQALEELATPRG-ICVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YDFFSRVVPPDSYQAQAMVDIVTALGWNYVSTLASEGNYGESGVEAFTQISREIGGVCIA 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GHLE-MQRD--LRNHSSKVVALIGPDNTDHAVTTAALLSPFLMPLVSYEASSVILSGKRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KEKGIHRLEAMLYAIDQTNKDPDLLSNITLGVRILDTCSRDTYALEQSLTFVQALIEKDA 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LAVAYCWAFSC-QRTES----SPGFSLPGDFLLAGLFSLHADCLQVRHRPLVTSCDRSDSF
                                                                                                     CEAGTFINTSELHTCQPCGTEEWAPEGSSACFSRTVEFLGWHEPISLVLLAANTLLLLLL
                                                                                                                                                                                                                                                                                                                                                                                    IASEDWAISTYITNVPGIQGIGTVLGVAIQQRQ-VPGL-KEFEESYVQAVMGAPR-T-CP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SDVKCANGDPPIFTKPDKISGVIGAAASSVSIMVANILRLFKIPQISYASTAPELSDNTR 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NGHGYHLFQAMRFTVEEINNSTALLPNITLGYELYDVCS-ESSNVYATLR-VPA--QQGT 125
                                                                                                                                                                                                                                                                                                                                                                                                                    IGSDSWG-SK-IAPVYQQEEIAEGAVTILPKRASIDGFDRYFRSRTLANNRRNVWFAEFS
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Similarity 24.6%;
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J. Neurosci. (1995) 15:3075-3083
A novel metabotropic glutamate recep-
retina and olfactory bulb.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         #superfamily metabotropic glutamate receptor 4
neurotransmitter receptor
#length 908 #molecular-weight 101413 #checksum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        metabotropic glutamate receptor 8 - mouse
#formal_name Mus musculus #common_name house mouse
02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
13-Sep-1998
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                                                 NYNEAKCYTESILLHEVSWIAFFTMS-SIYQGS---YLPAVNVLAGLATLSGGFS-G-YF
                                                                                                                     DPPHTIIDYGEQRTLDPENARGVLKC-DISDLSLICSLGYSILLMVTCTVYAIKTRGVPE 775
                                                                                                                                                          EAIFLSCLTIRSFQLVIIFKFSTK-VPTFYHTWAQNEGAGIEVIVSSTVHLFLCLTWLAM
 LPKCYVILCRPELN
                                                                             TENEAKPIGETMYTTCIIWLAFIPIFFGTAQSAEKMYIQTTTLTVSMS-LSASVSLGMLY
823
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Search completed: Fri Mar 17 $13:16:00\ 2000$ Job time : 48 secs.

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tabular output not generated Fri Mar 17 13:22:47 2000: MasPar time 14.26 Seconds $785.421\ \mathrm{Million}\ \mathrm{cell}\ \mathrm{updates/sec}$

Description: Perfect Score: >US-09-361-652-2 (1-842) from US09361652.pep 6366

Sequence: 1 MLFWAAHLLLSLQLAVAYCW......NNTEHFQASIQDYTRRCGTT 842

Scoring table:

PAM 150 Gap 11

Searched: 134018 segs, 13297625 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: a-issued 1:5A_COMB 2:5B_COMB 3:6_COMB 4:PCT9_COMB 5:backfiles1

Mean 36.380;

Variance 177.107;

scale 0.205

Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

22221111111111111111111111111111111111	Result
1316 1316 1316 1316 1316 1293 1293 1293 1293 1293 1282 1282 1282 1282 1282 1282 1282 128	Score
20.7 20.7 20.7 20.7 20.7 20.7 20.3 20.3 20.3 20.3 20.3 20.3 20.3 20.3	% Query Match
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US-08-484-485-485-485-485-485-485-485-485-48	ID
Sequence 5, Sequence 5, Sequence 5, Sequence 7, Sequence 7, Sequence 7, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 6, Sequence 7, Sequence 8, Sequence 8, Sequence 8, Sequence 9, Sequen	Description
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1.69e 100 1.69e 100 1.69e 100 1.69e 100 1.69e 100 1.69e 100 1.70e 98 1.70e 98 1.70e 98 1.70e 98 1.70e 98 1.70e 98 1.70e 99 1.54e 97 1.54e 97 1.54e 97 1.54e 97 1.70e 90 1.70e 90	Pred. No.

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ALIGNMENTS

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PPLICATION NUMBER: U.S. CILING DATE: 22 October, 1	ATION NUMBER: U.S. DATE: 23 August,	FILING DATE: 21 October, 1994	TLING DATE: 9 December, 1994	APPLICATION NUMBER: 08/353,784	PRIOR APPLICATION DATA: INCIDENTLY application	RIOR APPLICATION DATA: including applicat	CLASSIFICATION: 435	FILING DATE: 7 June, 1995	CATION DATA:	FASTSEQ	OPERATING SYSTEM: PC-DOS/MS-DOS	TBY 5.0	ER READABLE FORM:	IP: 9	RY: USA	TATE: Califor	ITY: Los Angeles	STREET: 633 West Fifth Street	HARRIE FLESC	DDRESSEE: Lyon & Lyon	PONDENCE ADDRESS	R OF SEQUENCES: 20	OF INVENTION: MOLECULES	INVENTION: CALCIUM REC	CANT: James E. Garrett,	CANT: Steven C.	3	CENERAL INC. 5/65568	quence 5,		Sequence 5, Application US/08484565			XXXXXX	US-US-484-565-5 STANDARD; PRT; 1085 AA.	

755

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321 TVLGV-A-IQ--Q-RQ-VP-GL-KEF-EESY---VQ-AVMGA-P-----RTCPEG-SW-C
                                                                                                                                                                                                                                                                                                                                                                                                                                                      272 VVVFSN-RHLAGVFFRSVVLANLTGKVWIASEDWA----IS-T-YITNVPG-IQ-GI--G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: U.S. 08/009,389
FILING DATE: 23 February, 1993
APPLICATION NUMBER: U.S. 08/017,127
FILING DATE: 12 February, 1993
APPLICATION NUMBER: U.S. 07/934,161
FILING DATE: 21 AUGUST, 1992
APPLICATION NUMBER: U.S. 07/834,044
FILING DATE: 11 February, 1992
APPLICATION NUMBER: U.S. 07/749,451
FILING DATE: 23 AUGUST, 1991
APTLICATION NUMBER: U.S. 07/749,451
FILING DATE: 23 AUGUST, 1991
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFORMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
                                                                                                                                                                          KEVGYYNYYAKKGERLFINDEKILWSGFSREVPFSNCSRDCLAGTRKGIIEGEPTCCFEC 566
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PNMTLGYRIFDTCNTVSKALEATLSFVAQNKIDSLNLDEFCNCSEHIPSTIAVVGATGSG 149
                                                                                                            VECPDGEYSDETDASACDKCPDDFWSNENHTSCIAKEIEFLSWTEPFGIALTLFAVLGIF
                                                                                                                                                                                                                                                               NGSCADIKKVEAWQVLKHLRHLNFTSNMGEQVTFDECGDLAGNYSIINWHLSPEDGSIVF 506
                                                                                                                                                                                                                                                                                                      -G-TN-Q-LCRECHAFTTWNMPELGAFSMSAAYNVYEAVYAVAHGLHQLLGC----T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PNITLGYELYDVCSESSNYY-ATLRVPAQQGTGHLEMQR--DLRNHSSKVVALIGPDNTD 151
     LLIGTAGLFA-WRLHTPVVRSAGGRLCFLMLGSLVAG-SCSLYSFFGKPTVPACLLRQPL
                                    LTAFVLGVFIKFR-NTPIVKATNRELSYLLLFSLLCCFSSSLF-FIGEPODWTCRLROPA 684
                                                                           MPCEAGTFLNTSELHTCQPCGTEEWAPEGSSACFSRTVEFLGWHEPISLVLLAANTLLLL
                                                                                                                                                   EVIG--SA-SLSPVHLDINKTKIQWHGKNNQVPVSVCTRDCLEGHHR-LVMGSHHCCFEC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Heber, Sheldon O. REGISTRATION NUMBER: 38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION: APPLICANT: Edward
                                                                                                                                                              PRIOR APPLICATION DATA: described bell Application NUMBER: 08/353,784
FILING DATE: 9 December, 1994
APPLICATION NUMBER: PCT/US/94/12117
FILING DATE: 21 October, 1994
APPLICATION NUMBER: U.S. 08/292,827
FILING DATE: 23 August, 1994
FILING DATE: 23 August, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA: PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: FASTSEQ CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: James E. Garrett, Jr.
TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: MOLECULES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VILCRPELNNTE 826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NENEAKEITESMLIFEIVWISEIPAYASTY-GKEVSAVEVIAILAASEGLLACIEFNKVY 859
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NYNEAKCVTFSLLLHFVSWIAFFTM-SSIYQGSYLPAVNYLAGLATLSGGFSGYFLPKCY 814
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FILING DATE:

APPLICATION NUMBER: U.S. 1993
FILING DATE: 12 February, 1993
FILING DATE: U.S. 07/934,161
FILING DATE: 07/834,044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 633 West I
CITY: Los Angeles
STATE: California
                                              APPLICATION NUMBER: U.U. APPLICATION NUMBER: U.U. 1993
TWO DATE: 23 February, 1993
TWO DATE: U.S. 08/017,127
                                                                                       APPLICATION NUMBER: U.S. 1993
TING DATE: 22 OCTOBER, 1993
TING DATE: 1993
TING DATE: 1993
TING DATE: 1993
                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE: 7 June
                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     First Interstate World Center Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      633 West Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Steven C. Hebert
Forrest H. Fuller
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Edward M. Brown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lyon & Lyon
                                                                                                                                                                                                                                                                                                                                                         7 June, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20
                                                                                                                                                                                                                                                              : including application described below: 9 08/353,784
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               152 HAVTTAALLSPFLMPLVSYEASSVILSGKRKFPSFLRTIPSDKYQVEVIVRLLQSFGWVW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPAX: (213) 955-0440

TELEX: 67-3510

TELEX: 67-3510

TELEX: 67-3510
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APPLICATION NUMBER: U.S. 07/
FILING DATE: 23 August, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Heber, Sheldon O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: 1: MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 1085 amino acids
                                                                                                                                                            MPCEAGTFLNTSELHTCOPCGTEEWAPEGSSACFSRTVEFLGWHEPISLVLLAANTLLLL
                                                                                                                                                                                                                                                                                                                                                                                                  TVLGV-A-IQ--Q-RQ-VP-GL-KEF-EESY---VQ-AVMGA-P----RTCPEG-SW-C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GDFLLAGLFSLHADCLQVRHRPLVTSCDRSDS--FNGHGYHLFQAMRFTVEEINNSTALL
                                                                                                                                                                                                                                                                                                                                                                                                                              QIPGFREFLQKVHPRKSVHNGFAKEFWEETFNCHLQEGAKGPLPVDTFLRGHEEGGARLS 386
             WLNTAPPSSYRNHELEDEIIFITCHEGSLMALGFLIGYTC-LLAAICFFF-AFKSRKLPE
                                                                                                                                                                                         VECPDGEYSDETDASACDKCPDDFWSNENHTSCIAKEIEFLSWTEPFGIALTLFAVLGIF
                                                                                                                                                                                                                       EVIG--SA-SLSPVHLDINKTKIQWHGKNNQVPVSVCTRDCLEGHHR-LVMGSHHCCFEC
                                                                                                                                                                                                                                                                                 SGTCA-RGPVYPWQLLQQIYKVNFLLHK-KTVAFDDKGDPLGYYDIIAWDWNGPE-WT-F
                                                                                                                                                                                                                                                                                                             NGSCADIKKVEAWQVLKHLRHLNFTSNMGEQVTFDECGDLAGNYSIINWHLSPEDGSIVF 506
                                                                                                                                                                                                                                                                                                                                                                    NSPTAFRPLCTGEENISSVETPYMDYTHLRISYNVYLAVYSIAHALQDIYTCIPGRGLFT 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                           VVVFSN-RHLAGVFFRSVVLANLTGKVWIASEDWA----IS-T-YITNVPG-IQ-GI--G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IVVFSSGPDLEPLI-KEIVRRNITGRIWLASEAWASSSLIAMPEYFHVVGGTIGFGLKAG 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VGTIAADDDYGRPGIEKFREEAEERDICIDFSELISQYSDE-E-KIQQVVEVIQNSTAKV 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PNITLGYELYDVCSESSNVY-ATLRVPAQQGTGHLEMQR--DLRNHSSKVVALIGPDNTD 151
                                          FSLGFAIFLSCLTIRSFQLVIIFKFSTKVPT-FYHTWAQNHGAGIFVIVSSTVHLFLCLT
                                                                       FGISFVLCISCILVKTNRVLLVFE--AKIPTSFHRKWWGLNLQFLLVFLCTFMQIVICAI 742
                                                                                                    LLIGTAGLEA-WRLHTPVVRSAGGRLCFLMLGSLVAG-SCSLYSFFGKPTVPACLLRQPL
                                                                                                                                LTAFVLGVFIKFR-NTPIVKATNRELSYLLLFSLLCCFSSSLF-FIGEPQDWTCRLRQPA 684
                                                                                                                                                                                                                                                   KEVGYYNVYAKKGERLFINDEKILWSGFSREVPFSNCSRDCLAGTRKGIIEGEPTCCFEC
                                                                                                                                                                                                                                                                                                                                          -G-TN-Q-LCRECHAFTTWNMPELGAFSMSAAYNVYEAVYAVAHGLHQLLGC-----T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ISTAVANLLGLFYIPQVSYASSSRLLSNKNQFKSFLRTIPNDEHQATAMADIIEYFRWNW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PNMTLGYRIFDTCNTVSKALEATLSFVAQNKIDSLNLDEFCNCSEHIPSTIAVVGATGSG 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ch 20.7%;
l Similarity 31.9%;
272; Conservative
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1085 AA; 121170 MW; 6189757 CN;
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UMBER: U.S. 07/74
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 Length 1085;
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                                                                                                                                            Seguence
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Patent No. 5858684
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA: Incl
PRIOR APPLICATION DATA: incl
PRIOR APPLICATION DATA: desc
APPLICATION NUMBER: 08/353
FILING DATE: 9 December, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Edward M. Brown
APPLICANT: Edward M. Brown
APPLICANT: Steven C. Hebert
APPLICANT: Forrest H. Fuller
APPLICANT: James E. Garrett, Jr.
APPLICANT: James E. Garrett, Jr.
APPLICANT: James E. Garrett
                      APPLICATION NUMBER: U.S. 07/
FILING DATE: 11 February, 19
APPLICATION NUMBER: U.S. 07/
FILING DATE: 23 August, 1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: FASTSEQ
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NYNEAKCVTFSLLLHFVSWIAFFTM-SSIYQGSYLPAVNVLAGLATLSGGFSGYFLPKCY 814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE.
APPLICATION NUMBER: U.S. 07/93
FILING DATE: 12 February, 1993
APPLICATION NUMBER: U.S. 07/934,161
APPLICATION NUMBER: U.S. 07/834,044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET:
STREET:
CITY: L
STATE:
                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE: 7 June
                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
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I: First Interstate World Center
I: Suite 4700
I: 633 West Fifth Street
Los Angeles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       90071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Application US/0848075
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NUMBER:
                                                                                                                                     23 February, 1993

DMBER: U.S. 08/017,127
                                               MBER.
11 February, 1992
π S. 07/749,451
                                                                                                                                                                                                                                                                                                                                                                  7 June, 1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Diskette, 1.44 Mb
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A: described
08/353,784
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SEQUENCE CHARACTERISTICS: LENGTH: 1085 amino aci

1085 amino acids linear

TYPE: amino acid

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387 NSPTAFRPLCTGEENISSVETPYMDYTHLRISYNYYLAVYSIAHALQDIYTCIPGRGLFT 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEFAX: (273) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31 GDIILGGLFPIHFG-VAVKDQDLKSRPESVECIRYNFRGFRWLQAMIFAIEEINSSPALL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QIPGFREFLQKVHPRKSVHNGFAKEFWEETFNCHLQEGAKGPLPVDTFLRGHEEGGARLS
                                                                                                                                                                                                                                                                                                                                                                                                        KEVGYYNVYAKKGERLFINDEKILWSGFSREVPFSNCSRDCLAGTRKGIIEGEPTCCFEC 566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NGSCADIKKVEAWQVLKHLRHLNFTSNMGEQVTFDECGDLAGNYSIINWHLSPEDGSIVF 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VVVFSN-RHLAGVFFRSVVLANLTGKVWIASEDWA----IS-T-YITNVPG-IQ-GI--G
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                                                                                                                     WLNTAPPSSYRNHELEDEIIFITCHEGSLMALGFLIGYTC-LLAAICFFF-AFKSRKLPE 800
                                                                                                                                                                                                                                                                                                   MPCEAGTFLNTSELHTCQPCGTEEWAPEGSSACFSRTVEFLGWHEPISLVLLAANTLLLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TVLGV-A-IQ--Q-RQ-VP-GL-KEF-EESY---VQ-AVMGA-P-----RTCPEG-SW-C
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                                                      NFNEARFITFSMLIFFIVWISFIPAYASTY-GKFVSAVEVIAILAASFGLLACIFFNKVY 859
                                                                                                                                                                                   FGISFVLCISCILVKTNRVLLVFE--AKIPTSFHRKWWGLNLQFLLVFLCTFMQIVICAI 742
                                                                                                                                                                                                                              LLIGTAGLFA-WRLHTPVVRSAGGRLCFLMLGSLVAG-SCSLYSFFGKPTVPACLLRQPL 638
                                                                                                                                                                                                                                                    | TAFVLGVFIKFR-NTPIVKATNRELSYLLLFSLLCCFSSSLF-FIGEPQDWTCRLRQPA 684
                                                                                                                                                                                                                                                                                                                                                                                                                                         SGTCA-RGPVYPWQLLQQIYKVNFLLHK-KTVAFDDKGDPLGYYDIIAWDWNGPE-WT-F
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                     NYNEAKCVTFSLLLHFVSWIAFFTM-SSIYQGSYLPAVNVLAGLATLSGGFSGYFLPKCY
                                                                                        WLAMWTPRPTREYQRFPHLVILECTEVN--SVGFLVAFAHNILLSISTFVCSYLGKELPE
                                                                                                                                                         FSLGFAIFLSCLTIRSFQLVIIFKFSTKVPT-FYHTWAQNHGAGIFVIVSSTVHLFLCLT
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1085 AA; 121170 MW; 6189757 CN;
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 5,
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                                    INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FASTSEQ
CURRENT APPLICATION DATA:
                                                                                                                                FILING DATE: 11 February, 1992
APPLICATION NUMBER: U.S. 07/749,451
FILING DATE: 23 August, 1991
ATTORNEY/ACENT INFORMATION:
NAME: Heber, Sheldon O.
REGISTRATION NUMBER: 38,179
REGISTRATION NUMBER: 38,179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Edward M. Brown
APPLICANT: Steven C. Hebert
APPLICANT: James E. Garrett,
 SEQUENCE CHARACTERISTICS:
LENGTH: 1085 amino aci
                                                                                 REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 7-June-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE TITLE OF INVENTION: MOLECULES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
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APPLICATION NUMBER: U.S. 00/01.
FILING DATE: 12 February, 1993
APPLICATION NUMBER: U.S. 07/934,161
PTITING DATE: 21 August, 1992
TTITING DATE: 21 August, 1992
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STATE:
                                                                  TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 21 OC
APPLICATION NUMBER:
FILING DATE: 23 Au
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                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
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: California
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                                                    (213) 955-0440
67-3510
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1085 amino acids
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NUMBER: U.S. 08/292,827
23 August, 1994
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22 October, 1993
MBER: U.S. 08/009,389
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Matches

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Query Match SEQUENCE

Match 20.7%; Local Similarity 31.9%;

TOPOLOGY: 1
MOLECULE TYPE:

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Query Match Best Local Matches

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US-08-353-784-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31 GDIILGGLEPIHEG-VAVKDQDLKSRPESVECIRYNERGERWLQAMIFAIEEINSSPALL
                                                                                        VILCRPELNNTE
                                                                                                                                                                                                                                                                                                                                                                                                                                      MPCEAGTFLNTSELHTCQPCGTEEWAPEGSSACFSRTVEFLGWHEPISLVLLAANTLLLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VECPDGEYSDETDASACDKCPDDFWSNENHTSCIAKEIEFLSWTEPFGIALTLFAVLGIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KEVGYYNVYAKKGERLFINDEKILWSGFSREVPFSNCSRDCLAGTRKGIIEGEPTCCFEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TVLGV-A-IQ--Q-RQ-VP-GL-KEF-EESY---VQ-AVMGA-P-----RTCPEG-SW-C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QIPGFREFLQKVHPRKSVHNGFAKEFWEETFNCHLQEGAKGPLPVDTFLRGHEEGGARLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GDFLLAGLFSLHADCLQVRHRPLVTSCDRSDS--FNGHGYHLFQAMRFTVEEINNSTALL
                                                                                                                         IILFKPSRNTIE
                                                                                                                                                                                          NFNEAKFITESMLIFFIVWISFIPAYASTY-GKFVSAVEVIAILAASFGLLACIFFNKVY
                                                                                                                                                                                                                              WLAMWTPRPTREYQRFPHLVILECTEVN--SVGFLVAFAHNILLSISTFVCSYLGKELPE
                                                                                                                                                                                                                                                              WLNTAPPSSYRNHELEDEIIFITCHEGSLMALGFLIGYTC-LLAAICFFF-AFKSRKLPE
                                                                                                                                                                                                                                                                                                                                   FGISFVLCISCILVKTNRVLLVFE--AKIPTSFHRKWWGLNLQFLLVFLCTFMQIVICAI
                                                                                                                                                                                                                                                                                                                                                                     LLIGTAGLEA-WRLHTPVVRSAGGRLCFLMLGSLVAG-SCSLYSFFGKPTVPACLLRQPL
                                                                                                                                                                                                                                                                                                                                                                                                      LTAFVLGVFIKFR-NTPIVKATNRELSYLLLFSLLCCFSSSLF-FIGEPQDWTCRLRQPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EVIG--SA-SLSPVHLDINKTKIQWHGKNNQVPVSVCTRDCLEGHHR-LVMGSHHCCFEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SGTCA-RGPVYPWQLLQQIYKVNFLLHK-KTVAFDDKGDPLGYYDIIAWDWNGPE-WT-F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IVVFSSGPDLEPLI-KEIVRRNITGRIWLASEAWASSSLIAMPEYFHVVGGTIGFGLKAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VGTIAADDDYGRPGIEKFREEAEERDICIDFSELISQYSDE-E-KIQQVVEVIQNSTAKV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ISTAVANLLGLFYIPQVSYASSSRLLSNKNQFKSFLRTIPNDEHQATAMADIIEYFRWNW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PNMTLGYRIFDTCNTVSKALEATLSFVAQNKIDSLNLDEFCNCSEHIPSTIAVVGATGSG 149
                                                                                                                                                           NYNEAKCYTFSLLLHFYSWIAFFTM-SSIYQGSYLPAVNVLAGLATLSGGFSGYFLPKCY
                                                                                                                                                                                                                                                                                                  FSLGFAIFLSCLTIRSFQLVIIFKFSTKVPT-FYHTWAQNHGAGIFVIVSSTVHLFLCLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -G-TN-Q-LCRECHAFTTWNMPELGAFSMSAAYNVYEAVYAVAHGLHQLLGC-----T
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                     STANDARD;
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Pred. No. 1.69e-100;
234; Mismatches 273;
                     PRT;
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                                                                    Query Match
Best Local S
Matches 27
                                                                    SEQUENCE
                                                                                                                                   TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SED ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1085 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5, Application US/08353784
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PRIOR APPLICATION DATA: including applic PRIOR APPLICATION DATA: including applic PRIOR APPLICATION DATA: described below: APPLICATION NUMBER: PCT_US/94/12117

FILING DATE: 21 October, 1994

APPLICATION NUMBER: U.S. 08/292,827

FILING DATE: 23 August, 1994

APPLICATION NUMBER: U.S. 08/14,248

APPLICATION NUMBER: U.S. 08/14,248

FILING DATE: 22 October, 1993

APPLICATION NUMBER: U.S. 08/009,389
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: FASTSEO
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 9 December
                                                                                   TOPOLOGY: 1
MOLECULE TYPE:
                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Heber, Sheldon O.
REGISTRATION NUMBER: 38,;
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                             FILING DATE: 12 February, 1993
APPLICATION NUMBER: U.S. 07/34,161
FILING DATE: 21 August, 1992
APPLICATION NUMBER: U.S. 07/834,044
FILING DATE: 11 February, 1992
APPLICATION NUMBER: U.S. 07/749,451
FILING DATE: 23 August, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Edward F. Nemeth, Edward M. APPLICANT: Brown, Steven C. Hebert, APPLICANT: Bradford C. Van Wagenen, Manuel APPLICANT: F. Balandrin, Forrest H. Fuller, APPLICANT: Eric G. DelMar, and Scott T. Moe TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: CALCIUM RITITLE OF INVENTION: MOLECULES NUMBER OF SEQUENCES: 20
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 al Similarity
272; Conser
                                                                                                                       TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 23 February, 1993
APPLICATION NUMBER: U.S. 08/017,127
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STREET: 633 West Fifth
CITY: Los Angeles
STATE: California
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20.7%;
larity 31.9%;
Conservative
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                                                                  PE: protein
AA; 121170
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Score 1316; DB 3;
pred. No. 1.69e-100;
234; Mismatches 273;
                                                                    MW; 6189757 CN;
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                              Length 1035;
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Sequence 7, Application US/08943986
                                                                                                                                                               US-08-943-986-7
                                                                                                                                                                                                                                815 VILCRPELNNTE 826
     Sequence 7, Application US/08943986 Patent No. 5962314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       152 HAVTTAALLSPFLMPLVSYEASSVILSGKRKFPSFLRTIPSDKYQVEVIVRLLQSFGWVW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  268 IVVFSSGPDLEPLI-KEIVRRNITGRIWLASEAWASSSLIAMPEYFHVVGGTIGFGLKAG
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                                                                                                                                                                                                                                                               IILFKPSRNTIE 871
                                                                                                                                                                                                                                                                                                   WLAMWTPRPTREYQREPHLVILECTEVN--SVGFLVAFAHNILLSISTFVCSYLGKELPE
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                                                                                                                                                                                                                                                                                                                                  NFNEAKFITESMLIFFIVWISFIPAYASTY-GKFVSAVEVIAILAASFGLLACIFFNKVY 859
                                                                                                                                                                                                                                                                                                                                                                                                     WLNTAPPSSYRNHELEDEIIFITCHEGSLMALGFLIGYTC-LLAAICFFF-AFKSRKLPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FGISFVLCISCILVKTNRVLLVFE--AKIPTSFHRKWWGLNLQFLLVFLCTFMQIVICAI 742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LLIGTAGLEA-WRLHTPVVRSAGGRLCFLMLGSLVAG-SCSLYSFFGKPTVPACLLRQPL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MPCEAGTFLNTSELHTCQPCGTEEWAPEGSSACFSRTVEFLGWHEPISLVLLAANTLLLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QIPGFREFLQKVHPRKSVHNGFAKEFWEETFNCHLQEGAKGPLPVDTFLRGHEEGGARLS
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                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 11 February, 1992
APPLICATION NUMBER: U.S. 07/74
FILING DATE: 23 AUGUST, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Heber, Sheldon 0.
REGISTRATION NUMBER: 38,179
REFERENCE/DOCKET NUMBER: 213/0
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 9 December, 1994
APPLICATION NUMBER: PCT/US/94/12117
FILING DATE: 21 October, 1994
APPLICATION NUMBER: U.S. 08/292,827
FILING DATE: 23 AUGUST, 1994
APPLICATION NUMBER: U.S. 08/141,248
FILING DATE: 22 October, 1993
APPLICATION NUMBER: U.S. 08/009,389
                                                                                                                                                                                                            MOLECULE TYPE:
JENCE 1078 AA
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CLASSIFICATION: 530
PRIOR APPLICATION DATA:
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SOFTWARE: FASTSEQ
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
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                                PNLTLGYRIFDTCNTVSKALEATLSFVAQNKIDSLNLDEFCNCSEHIPSTIAVVGATGSG 148
                                                                                                     GDIILGGLFPIHFG-VAAKDQDLKSRPESVECIRYNFRGFRWLQAMIFAIEEINSSPALL 88
PNITLGYELYDVCSESSNVY-ATLRVPAQQGTGHLEMOR--DLRNHSSKVVALIGPDNTD
                                                                   GDFLLAGLFSLHADCLQVRHRPLVTSCDRSDS--FNGHGYHLFQAMRFTVEEINNSTALL 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 23 FELT. S. 08/UL., APPLICATION NUMBER: U.S. 08/UL., APPLICATION NUMBER: U.S. 07/934,161
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APPLICATION NUMBER: U.S. V.,
TYTING DATE: 11 February, 19
                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: U.S. 07/934,161 FILING DATE: 21 August, 1992 APPLICATION NUMBER: U.S. 07/834,044
                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                            TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Los Angeles
STATE: California
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STREET: First Interstate World Center
STREET: Suite 4700
STREET: 633 West Fifth Street
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                                                                                                                                                          Similarity
                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                1078 amino acids
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Steven C. Hebert
James E. Garrett, Jr.
VENTION: CALCIUM RECEPTOR-ACTIVE
NVENTION: MOLECULES
                                                                                                                                                                                                            PE: protein AA; 120573 MW; 6153012 CN;
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03-OCT-1997
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                                                                                                                                        Score 1293; DB 2;
Pred. No. 1.70e-98;
234; Mismatches 274;
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CANT: Edward F. Nemeth, Edward M.
CANT: Brown, Steven C. Hebert,
CANT: Bradford C. Van Wagenen, Manuel
CANT: F. Balandrin, Forrest H. Fuller,
CANT: Eric G. DelMar, and Scott T. Moe
OF INVENTION: CALCIUM RECEPTOR-ACTIVE
OF INVENTION: MOLECULES
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FILING DATE: 23 August, 1991
ATTORREY/AGENT INFORMATION:
NAME: Heber, Sheldon O.
REGISTRATION NUMBER: 38,179
REFERENCE/DOCKET NUMBER: 209/(
TELECOMMUNICATION INFORMATION:
TELEPAN: (213) 489-1600
TELEFAX: (213) 955-0440
TELEFAX: 67-3510
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1078 amino acids
""""" - amino acid
                                                                                                                                                                                                                                                                                                                                          SEQUENCE
   212
                                    209
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APPLICATION NUMBER: U.S. 07/934,161
APPLICATION NUMBER: U.S. 07/834,044
TYPE DATE: 21 August, 1992
TYPER: U.S. 07/834,044
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                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                   VGTIAADDDYGRPGIEKFREEAEERDICIDFSELISQYSDEEE--IQHVVEVIQNSTAKV 266
                                                                                       VSTAVANULGLFYIPQVSYASSSRLLSNKNQFKSFLRTIPNDEHQATAMADIIEYFRWNW 208
                                                                                                                                                                                                  GDIILGGLFPIHFG-VAAKDQDLKSRPESVECIRYNF?GFRWLQAMIFAIEEINSSPALL
   ISLVGSYGDYGQLGVQALEELATPRGICVAFKDVVPLSAQAGDPRMQRMMLRLARARTTV
                                                                    HAVTTAALLSPFLMPLVSYEASSVILSGKRKFPSFLRTIPSDKYQVEVIVRLLQSFGWVW
                                                                                                                                   PNITLGYELYDVCSESSNVY-ATLRVPAQQGTGHLEMQR--DLRNHSSKVVALIGPDNTD 151
                                                                                                                                                                     PNLTLGYRIFDTCNTVSKALEATLSFVAQNKIDSLNLDEFCNCSEHIPSTIAVVGATGSG 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 21 October, 1994
APPLICATION NUMBER: U.S. 08/292,827
FILING DATE: 23 AUGUST, 1994
APPLICATION NUMBER: U.S. 08/141,248
FILING DATE: 22 October, 1993
APPLICATION NUMBER: U.S. 08/009,389
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STREET: Suite 4700
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: U.S. 07/
FILING DATE: 11 February, 19
APPLICATION NUMBER: U.S. 07/
FILING DATE: 23 August, 1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
                                                                                                                                                                                                                                                                     l Similarity 31.8%;
271; Conservative
                                                                                                                                                                                                                                                                                                                                        LE TYPE: protein
1078 AA; 120573 MW; 6153012 CN;
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234; Mismatches
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Pred. No. 1.70e-98;
234; Mismatches 274;
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RESULT ID US

US-08-353-784-7

STANDARD;

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VILCRPELNNTE IILFKPSRNTIE 870

Sequence 7, Application US/08353784

Sequence 7, Application US/08353784 Patent No. 6011068

GENERAL INFORMATION:
APPLICANT: Edward
APPLICANT: Brown,

APPLICANT: APPLICANT:

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                                                                                                                                                                                                                                                                                                                                                  Sequence 7, Application US/08485588 Patent No. 5688938
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                                                                                                                                                                                                                                                                                                   GENERAL INFOR APPLICANT:
                                                                                                                                                                                          APPLICANT: Steven C. Hebert
APPLICANT: Forrest H. Fuller
APPLICANT: James E. Garrett, Jr.
TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
TITLE OF INVENTION: MOLECULES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VVVESN-RHLAGVEERSVVLANLIGKVWIASEDWA----IS-T-YIINVPG-IQ-GI--G
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                                                                                                                                              CORRESPONDENCE ADDRESS
                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NENEAKFITESMLIFFIVWISFIPAYASTY-GKFVSAVEVIAILAASFGLLACIFFNKIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ESLGPAIFLSCLTIRSFQLVIIFKESTKVPT-FYHTWAQNHGAGIFVIVSSTVHLFLCLT
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                                                              STREET:
                                                                         ADDRESSEE: Lyon & Lyon
STREET: First Interstate World Center
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                           INFORMATION:
                                            Los Angeles
                        California
                                                              633 West Fifth Street
                                                                                                                                                                                                                                                                                                     Edward M. Brown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FASTSEQ
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: (213) 489-1600 TELEFAX: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA: PRIOR APPLICATION DATA: APPLICATION NUMBER: 0
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MOLECULE TYPE:
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LENGTH: 1078 amino acids
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                                                                                                                                                                                                                                                                             VSTAVANLLGLFYIPQVSYASSSRLLSNKNQFKSFLRTIPNDEHQATAMADIIEYFRWNW 208
                      QIPGFREFLKKVHPRKSVHNGFAKEFWEETFNCHLQEGAKGPLPVDTFLRGHEESGDRFS
                                                                                                    IVVFSSGPDLEPLI-KEIVRRNITGKIWLASEAWASSSLIAMPQYFHVVGGTIGFALKAG
                                                                                                                                                                                                                                     HAVTTAALLSPFLMPLVSYEASSVILSGKRKFPSFLRTIPSDKYQVEVIVRLLQSFGWVW
                                                                                                                                                                                                                                                                                                                       PNITLGYELYDVCSESSNVY-ATLRVPAQQGTGHLEMQR--DLRNHSSKVVALIGPDNTD 151
                                                                                                                                                                                                                                                                                                                                                                   PNLTLGYRIFDTCNTVSKALEATLSFVAQNKIDSLNLDEFCNCSEHIPSTIAVVGATGSG 148
                                                                                                                                                                                                                                                                                                                                                                                                              GDFLLAGLFSLHADCLQVRHRPLVTSCDRSDS--FNGHGYHLFQAMRFTVEEINNSTALL
                                                                VVVFSN-RHLAGVFFRSVVLANLTGKVWIASEDWA----IS-T-YITNVPG-IQ-GI--G
                                                                                                                                                                                          VGTIAADDDYGRPGIEKFREEAEERDICIDFSELISQYSDEEE--IQHVVEVIQNSTAKV
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APPLICATION NUMBER: U.S. 08/292,827
APPLICATION NUMBER: U.S. 08/294,827
APPLICATION NUMBER: 1994
A
                                                                                                                                                  ISLVGSYGDYGQLGVQALEELATPRGICVAFKDVVPLSAQAGDPRMQRMMLRLARARTTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: U.S. ... 1993
TITING DATE: 12 February, 1993
U.S. 07/934,161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 11 February APPLICATION NUMBER: U.S. 07/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLIANG DATE: U.S. APPLICATION NUMBER: U.S. 1993
TTIMG DATE: 22 October, 1993
TTIMG DATE: 1993
TTIMG DATE: 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 1992
FILING DATE: 21 August, 1992
APPLICATION NUMBER: U.S. 07/834,044
FILING DATE: 11 February, 1992
FILING DATE: 11 February, 1992
FILING TOWNSHIP OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF T
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REFERENCE/DOCKET NUMBER: 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE: 7 June
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                271;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: protein
1078 AA; 120573 MW; 6153012 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20.3%;
llarity 31.8%;
Conservative :
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9 December, 1954
11MBER: PCT/US/94/12117
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; Score 1293;
; Pred. No. 1.
234; Mismatc
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1.70e-98;
Lches 274;
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Patent No. 5763569
GENERAL INFORMATION:
APPLICANT: Edward |
APPLICANT: Steven |
APPLICANT: James E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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Patent No. 5763569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 859
                                                                                                                                                                                                                                                                                                APPLICANT: Edward M. Brown
APPLICANT: Steven C. Hebert
APPLICANT: James E. Garrett, Jr.
TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
TITLE OF INVENTION: MOLECULES
                                 COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.4.
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FASTSEQ
                                                                                                                                      STREET: First Interstate World C
STREET: Suite 4700
STREET: Suive 4700
STREET: 533 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: USA
CURRENT APPLICATION DATA APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IILFKPSRNTIE 870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NYNEAKCVTFSLLLHFVSWIAFFTM-SSIYQGSYLPAVNVLAGLATLSGGFSGYFLPKCY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MPCEAGTFLNTSELHTCQPCGTEEWAPEGSSACFSRTVEFLGWHEPISLVLLAANTLLLL
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Best Local :
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TELEPHONE: (213) 489-1600
TELEPAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1078 amino acids
TYPE: amino acid
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                446 NGSCADIKKVEAWQVLKHLRHLNFTNNMGEQVTFDECGDLVGNYSIINWHLSPEDGSIVF
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Local Similarity 31.8%;
es 271; Conservati
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein JENCE 1078 AA; 120573 MW; 6153012 CN;
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                                                                                                                                                                                            VVVFSN-RHLAGVFFRSVVLANLTGKVWIASEDWA----IS-T-YITNVPG-IQ-GI--G
                                                                                                                                                                                                                                                                                                                                                           VSTAVANLLGLFYIPQVSYASSSRLLSNKNQFKSFLRTIPNDEHQATAMADIIEYFRWNW 208
                                                                                                                                                                                                                                                                                                   VGTIAADDDYGRPGIEKFREEAEERDICIDFSELISQYSDEEE---IQHVVEVIQNSTAKV 266
                                                   -CGTN-Q-LCRECHAFTTWNMPELGAFSMSAAYNVYEAVYAVAHGLHQL---L-GC---T
                                                                                                                                                       QIPGFREELKKVHPRKSVHNGFAKEFWEETFNCHLQEGAKGPLPVDTFLRGHEESGDRFS
                                                                                                                                                                                                             IVVFSSGPDLEPLI-KEIVRRNITGKIWLASEAWASSSLIAMPQYFHVVGGTIGFALKAG
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                                                                                                                      TVLG----VA-IQQRQ-VP-GL-KEF-EESY---VQ-AVMGA-P-----RTCPE-GSW--
                                                                                                                                                                                                                                                                  ISLVGSYGDYGQLGVQALEELATPRGICVAFKDVVPLSAQAGDPRMQRMMLRLARARTTV
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                                                                                                                                                                                                                                                                                                                                                                                                                                            PNLTLGYRIFDTCNTVSKALEATLSFVAQNKIDSLNLDEFCNCSEHIPSTIAVVGATGSG 148
                                                                                   NSSTAFRPLCTGDENISSVETPYIDYTHLRISYNVYLAVYSIAHALQDIYTCLPGRGLFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 11 February, 1992
APPLICATION NUMBER: U.S. 07/749,451
FILING DATE: 23 August, 1991
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TING DATE: 23 February, 1993
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TING DATE: 1993
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NUMBER: U.S. 08/292,827

23 August, 1994

NUMBER: U.S. 08/141,248

22 October, 1993

NUMBER: U.S. 08/009,389
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N: 435
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UMBER: U.S. 07/934,161
21 August, 1992
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;UMBER: PCT/US/94/12117
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Pred. No. 1.70e-98;
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APPLICANT:
                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10
                                                                                                                      CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: James E. Garrett, Jr.
TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
TITLE OF INVENTION: MOLECULES
NUMBER OF SEQUENCES: 20
                PRIOR APPLICATION DATA: PRIOR APPLICATION DATA: PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                            COUNTRY:
ZIP: 900
                                                                                                                                                                                                                                                            STREET: First Interstate Worl-
STREET: Suite 4700
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
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                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: FASTSEQ
                                                                    APPLICATION NUMBER: UFILING DATE: 7 June, CLASSIFICATION: 435
   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7, Application US/08480751
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5. 5858684
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First Interstate World
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Edward M. Brown
Steven C. Hebert
Forrest H. Fuller
                                                                                                                                                                                                                                          USA
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                                                                                      us/08/480,751
e, 1995
: including application
: described below: 9
  08/353,784
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TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARATTERISTICS:
LENGTH: 1078 amino acids
TYPE: amino acid
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                 465
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                                                  506 KEVGYYNVYAKKGERLFINEEKILWSGFSREVPFSNCSRDCLAGTRKGIIEGEPTCCFEC
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Local Similarity 31.8%;
les 271; Conservative
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FILING DATE: 23...
APPLICATION NUMBER: U.S. ...
APPLICATION NUMBER: U.S. 07/934,161
APPLICATION NUMBER: U.S. 07/934,161
APPLICATION NUMBER: U.S. 07/834,044
TTING DATE: 192
TTING DATE: NUMBER: U.S. 07/834,044
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FILING DATE: 11 February, 1992
APPLICATION NUMBER: U.S. 07/74
FILING DATE: 23 August, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Heber, Sheldon O.
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                            GDELLAGLESCHADCLQVRHRPLVTSCDRSDS--FNGHGYHLFQAMRFTVEEINNSTALL
                                                                                                                                                                                                                          TVLG----VA-IQQRQ-VP-GL-KEF-EESY---VQ-AVMGA-P----RTCPE-GSW--
                                                                                                                                                                                                                                                                                                                                                                                                 VGTIAADDDYGRPGIEKFREEAEERDICIDFSELISQYSDEEE--IQHVVEVIQNSTAKV
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                 EVIG--SA-SLSPVHLDINKTKIQWHGKNNQVPVSVCTRDCLEGHHR-LVMGSHHCCFEC
                                                                                                                  \tt NGSCADIKKVEAWQVLKHLRHLNFTNNMGEQVTFDECGDLVGNYSIINWHLSPEDGSIVF
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                                                                                    SGTCA-RGPVYPWQLLQQIYKVNFLLHK-KTVAFDDKGDPLGYYDIIAWDWNGPE-WT-F
                                                                                                                                                        -CGTN-Q-LCRECHAFTTWNMPELGAFSMSAAYNVYEAVYAVAHGLHQL---L-GC---T
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1078 AA; 120573 MW; 6153012 CN;
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22 October, 1993
UMBER: U.S. 08/009,389
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IUMBER: U.S. 08/2

23 August, 1994
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Pred. No. 1.70e-98;
Pred. Mismatches 274;
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GENERAL INFORM
APPLICANT:
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                                                            Sequence 8, Application US/08484565 Patent No. 5763569
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MEDIUM TYPE: 3.5" Diskette, 1.44
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                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
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CITY: LC
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                                 APPLICATION NUMBER: PCT/US/94/12117
FILING DATE: 21 October, 1994
APPLICATION NUMBER: U.S. 08/292,827
FILING DATE: 23 August, 1994
                                                                                                                                                                                                                      OPERATING SYSTEM:
                                                                                                                                                                                                                                   COMPUTER:
          APPLICATION NUMBER: U.S. FILING DATE: 22 October,
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Edward M. BLU..
Steven C. Hebert
James E. Garrett, Jr.
James E. Garrett, Jr.
CALCIUM RECEPTOR-ACTIVE
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Suite 4700
633 West Fifth Street
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          U.S. 08/141,248 ober, 1993
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 21 August, 1992
APPLICATION NUMBER: U.S. 07/834,044
FILING DATE: 11 February, 1992
APPLICATION NUMBER: U.S. 07/749,451
FILING DATE: 23 August, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Heber, Sheldon O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
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LENGTH: 1079 amino acids
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TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEFAX: 67-3510
                                                                                  VECPDGEYSGETDASACDKCPDDFWSNENHTSCIAKEIEFLAWTEPFGIALTLFAVLGIF
                                                                                                                            KEVGYYNVYAKKGERLFINEEKILWSGFSREVPFSNCSRDCQAGTRKGIIEGEPTCCFEC
                                                                                                                                                                             NGSCADIKKVEAWQVLKHLRHLNFTNNMGEQVTFDECGDLVGNYSIINWHLSPEDGSIVF
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         LLIGTAGLFA-WRLHTPVVRSAGGRLCFLMLGSLVAG-SCSLYSFFGKPTVPACLLRQPL
                                 LTAFVLGVFIKFR-NTPIVKATNRELSYLLLFSLLCCESSSLF-FIGEPQDWTCRLRQPA 683
                                                           MPCEAGTFUNTSELHTCOPCGTEEWAPEGSSACFSRTVEFLGWHEPISLVLLAANTLLLL
                                                                                                            EVIG--SA-SLSPVHLDINKTKIQWHGKNNQVPVSVCTRDCLEGHHR-LVMGSHHCCFEC
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                                                                                                                                                                                                                   -CGTN-Q-LCRECHAFTTWNMPELGAFSMSAAYNVYEAVYAVAHGLHQL---L-GC---T
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TYMC DATE: 12 February, 1993
TYMC DATE: 1992
TYMC DATE: 1992
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Fred. No. 1
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1. No. 1.54e-97;
Mismatches 280;
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                                                                                          APPLICATION NUMBER: PCT/US/94/1211/
FILING DATE: 21 October, 1994
APPLICATION NUMBER: U.S. 08/292,827
FILING DATE: 23 August, 1994
APPLICATION NUMBER: U.S. 08/141,248
FILING DATE: 22 October, 1993
APPLICATION NUMBER: U.S. 08/009,389
APPLICATION NUMBER: U.S. 08/009,389
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 7 June, 1
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TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
TITLE OF INVENTION: MOLECULES
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STREET: First Interstate World Center
STREET: Suite 4700
STREET: 633 West Fifth Street
          APPLICATION NUMBER: U.C. 1993
APPLICATION NUMBER: U.C. 1993
TIME DATE: 12 February, 1993
1992
                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 08/3 FILING DATE: 9 December,
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Steven C. Hebert
Forrest H. Fuller
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  NUMBER:
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7 June, 1995
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U.S.
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  07/834,044
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30 GDIILGGLFPIHFG-VAAKDQDLKSRPESVECIRYNFRGFRWLQAMIFAIEEINSSPSLL
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SEQUENCE CHARACTERISTICS:
LENGTH: 1079 amino acids
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REFERENCE/DOCKET NUMBER: 21:
TELECOMMUNICATION INFORMATION:
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WLYTAPPSSYRNHELEDEIIFITCHEGSLMALGSLIGYTC-LLAAICFFF-AFKSRKLPE
                                                                                                                                                                                                                                                KEVGYYNVYAKKGERLFINEEKILWSGFSREVPFSNCSRDCQAGTRKGIIEGEPTCCFEC
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                                                           FSLGFAIFLSCLTIRSFQLVIIFKFSTKVPT-FYHTWAQNHGAGIFVIVSSTVHLFLCLT
                                                                                                FGISFVLCISCILVKTNRVLLVFE -- AKIPTSFHRKWWGLNLQFLLVFLCTFMQILICII 741
                                                                                                                                                                                 LTAFVLGVFIKFR-NTPIVKATNRELSYLLLESLLCCFSSSLF-FIGEPQDWTCRLRQPA 683
                                                                                                                                                                                                                         MPCEAGTFLNTSELHTCQPCGTEEWAPEGSSACFSRTVEFLGWHEPISLVLLAANTLLLL
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                                                                                                                                           LLIGTAGLFA-WRLHTPVVRSAGGRLCFLMLGSLVAG-SCSLYSFFGKPTVPACLLRQPL
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RMATTON FOR TAXABLE CONTRACTOR TO TAXABLE CONTRACT
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APPLICATION NUMBER: U.S. 07/749
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Similarity 31.2%;
269; Conservative
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Pred. No. 1
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No. 1.54e-97;
Mismatches 280;
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                                           APPLICATION NUMBER: U.S. 08/00,389
FILING DATE: 23 February, 1993
APPLICATION NUMBER: U.S. 08/017,127
FILING DATE: 12 February, 1993
APPLICATION NUMBER: U.S. 07/934,161
FILING DATE: 12 February, 1992
APPLICATION NUMBER: U.S. 07/834,044
FILING DATE: 11 February, 1992
APPLICATION NUMBER: U.S. 07/834,044
FILING DATE: 11 February, 1992
APPLICATION NUMBER: U.S. 07/834,044
FILING DATE: 23 AUGUST, 1991
FILING DATE: 23 AUGUST, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Heber, Sheldon O.
                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA: including applic
PRIOR APPLICATION DATA: described below-
PRIOR APPLICATION UMBER: PCT/US/94/12117
FILING DATE: 21 October, 1994
APPLICATION NUMBER: U.S. 08/292,827
FILING DATE: 23 August, 1994
APPLICATION NUMBER: U.S. 08/141,248
APPLICATION NUMBER: U.S. 08/141,248
FILING DATE: 22 October, 1993
APPLICATION NUMBER: U.S. 08/09,389
APPLICATION NUMBER: U.S. 08/09,389
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MEDION TYPE: 3.5° Diskette, 1.44
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FASTSEQ
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APPLICATION NUMBER: US
FILING DATE: 9 Decembe
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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ZIP: 900
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STREET: First Interstate
STREET: Suite 4700
STREET: 633 West Fifth St
                   REGISTRATION NUMBER: 38,179
REFERENCE/DOCKET NUMBER: 20
                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8, Application US/08353784
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Brown, Steven C. Hebert,
Bradford C. Van Wagenen, Manuel
F. Balandrin, Forrest H. Fuller,
Eric G. DelMar, and Scott T. Moe
VENTION: CALCIUM RECEPTOR-ACTIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                     9 December,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: protein
MOLECULE 1079 AA; 120867 MW;
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LENGTH: 1079 amino aci
TYPE: amino acid
IILFKPSRNTIEEVRSSTAAHA
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                                                  NYNEAKCVTFSLLLHFVSWIAFFTM-SSIYQGSYLPAVNVLAGLATLSGGFSGYFLPKCY
                                                                                    NFNEAKFITFSMLIFFIVWISFIPAYASTY-GKFVSAVEVIAILAASFGLLACIFFNKVY
                                                                                                                     WLAMWTPRPTREYQRFPHLVILECTEVN--SVGFLVAFAHNILLSISTFVCSYLGKELPE
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(213) 955-0440
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Pred. No. 1
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RESULT
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                                                                   APPLICATION NUMBER: U.S. 07/834,044
FILING DATE: 11 February, 1992
APPLICATION NUMBER: U.S. 07/749,451
FILING DATE: 23 August, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Heber, Sheldon O.
REGISTRATION NUMBER: 38,179
REFERENCE/DOCKET NUMBER: 213/006
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
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FILING DATE: 03-OCT-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/484,565
FILING DATE: 7-June-1995
APPLICATION NUMBER: 08/353,784
FILING DATE: 9 December, 1994
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                                                 TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                  APPLICATION NUMBER: PCT/US/94/12117
FILING DATE: 21 October, 1994
APPLICATION NUMBER: U.S. 08/292,827
FILING DATE: 23 AUGUST, 1994
APPLICATION NUMBER: U.S. 08/141,248
FILING DATE: 22 October, 1993
APPLICATION NUMBER: U.S. 08/009,389
FILING DATE: 23 February, 1993
APPLICATION NUMBER: U.S. 08/0017,127
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APPLICANT: Steven C. Hebert
APPLICANT: James E. Garrett, Jr.
TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
TITLE OF INVENTION: MOLECULES
NUMBER OF SEQUENCES: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: PC-D
SOFTWARE: FASTSEQ
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: IBM PC compatible
                   SEQUENCE CHARACTERISTICS:
LENGTH: 1079 amino acids
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                                                   TELEFAX: (2-
TELEFAX: 67-3510
                                                                                                                                                                                           FILING DATE: U.S. U8/U1/,---
APPLICATION NUMBER: U.S. U8/U1/,---
FILING DATE: 12 February, 1993
APPLICATION NUMBER: U.S. 07/934,161
FILING DATE: 21 August, 1992
FILING DATE: 21 August, 1992
FILING DATE: U.S. 07/834,044
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TOPOLOGY:
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633 West Fifth Street
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VILCRPELNNTEHFQASIQDYT 836
                                                                                                                                                                  WLAMWTPRPTREYORFPHLVILECTEVN--SVGFLVAFAHNILLSISTFVCSYLGKELPE
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                                                                                  NYNEAKCVTFSLLLHFVSWIAFFTM-SSIYQGSYLPAVNVLAGLATLSGGFSGYFLPKCY
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RESULT ID US

US-08-485-588-8

STANDARD;

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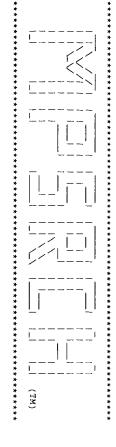
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Query Match
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                                                                                          MOLECULE TYPE: SEQUENCE 1079 AA;
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
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APPLICANT: Steven C. Hebert
APPLICANT: Forrest H. Fuller
APPLICANT: James E. Garrett, Jr.
TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
TITLE OF INVENTION: MOLECULES
NUMBER OF SEQUENCES: 20
CORRESPONDENCES: 20
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FILING DATE: 9 December, 1994
APPLICATION NUMBER: PCT/US/94/12117
FILING DATE: 21 October, 1994
APPLICATION NUMBER: U.S. 08/292,827
FILING DATE: 23 August, 1994
APPLICATION NUMBER: U.S. 08/141,248
FILING DATE: 22 October, 1993
APPLICATION NUMBER: U.S. 08/09,389
APPLICATION NUMBER: U.S. 08/009,389
                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: U.S. 07/8
FILLING DATE: 11 February, 199
APPLICATION NUMBER: U.S. 07/8
APPLI
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MEDIUM TYPE: 3.5" Di
COMPUTER: IBM PC com
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STREET: 533 West F:
CITY: LOS Angeles
STATE: California
COUNTRY: USA
ZIP: 90071
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APPLICATION NUMBER: U.S. 08/017,127
TMR DATE: 23 February, 1993
TMR DATE: 1993
TMR DATE: 1993
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SOFTWARE: FASTSE
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Suite 4700
633 West Fifth Street
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Score 1282; DB 1; 1
Pred. No. 1.54e-97;
240; Mismatches 280;
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VILCRPELNNTEHFOASIODYT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QIPGFREFLQKVHPRKSVHNGFAKEFWEETFNCHLQEGAKGPLPVDTFVRSHEEGGNRLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VSTAVANLLGLEYIPQVSYASSSRLLSNKNQYKSFLRTIPNDEHQATAMADIIEYFRWNW : : | | | : | : | | | | : ::: | | | |
                                                                                       WLYTAPPSSYRNHELEDEIIFITCHEGSLMALGSLIGYTC-LLAAICFFF-AFKSRKLPE
                                                                                                                                                                                                                                                                                                                                              MPCEAGTFLNTSELHTCQPCGTEEWAPEGSSACFSRTVEFLGWHEPISLVLLAANTLLLL
                                                                                                                                                                                                                                                                                                                                                                                VECPDGEYSGETDASACDKCPDDFWSNENHTSCIAKELEFLAWTEPFGIALTLFAVLGIF
                                                                                                                                                                                                                                                                                                                                                                                                                 EVIG--SA-SLSPVHLDINKTKIQWHGKNNQVPVSVCTRDCLEGHHR-LVMGSHHCCFEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                KEVGYYNVYAKKGERLFINEEKILWSGFSREVPFSNCSRDCQAGTRKGIIEGEPTCCFEC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NSSTAFRPLCTGDENINSVETPYMDYEHLRISYNVYLAVYSIAHALQDIYTCLPGRGLFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VVVFSN-RHLAGVFFRSVVLANLIGKVWIASEDWA----IS-T-YITNVPG-IQ-GI--G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IVVFSSGPDLEPLI-KEIVRRNITGRIWLASEAWASSSLIAMPEYFHVVGGTIGFGLKAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VGTIAADDDYGRPGIEKFREEAEERDICIDFSELISQYSDEEE---IQQVVEVIQNSTAKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HAVTTAALLSPELMPLVSYEASSVILSGKRKFPSELRTIPSDKYQVEVIVRLLQSFGWVW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GDIILGGLFPIHFG-VAAKDQDLKSRPESVECIRYNFRGFRWLQAMIFAIEEINSSPSLL
                                 IILFKPSRNTIEEVRSSTAAHA
                                                                     NYNEAKCVTFSLLLHFVSWIAFFTM-SSIYQGSYLPAVNVLAGLATLSGGFSGYFLPKCY
                                                                                                                                       WLAMWTPRPTREYQRFPHLVILECTEVN--SVGFLVAFAHNILLSISTFVCSYLGKELPE
                                                                                                                                                                                                          FSLGFAIFLSCLTIRSFQLVIIFKFSTKVPT-FYHTWAQNHGAGIFVIVSSTVHLFLCLT
                                                                                                                                                                                                                                        FGISFVLCISCILVKTNRVLLVFE--AKIPTSFHRKWWGLNLQFLLVFLCTFMQILICII 741
                                                                                                                                                                                                                                                                          LIGTAGLEA-WRLHTPYVRSAGGRLCELMLGSLVAG-SCSLYSEEGKPTVPACLLRQPL
                                                                                                                                                                                                                                                                                                          LTAFVLGVFIKER-NTPIVKAINRELSYLLLFSLLCCESSSLF-FIGEPQDWTCRLRQPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SGTCA-RGPVYPWQLLQQIYKVNFLLHK-KTVAFDDKGDPLGYYDIIAWDWNGPE-WT-F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -CGTN-Q-LCRECHAFTTWNMPELGAFSMSAAYNVYEAVYAVAHGLHQL---L-GC---T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ISLVGSYGDYGQLGVQALEELATPRGICVAFKDVVPLSAQAGDPRMQRMMLRLARARTTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PNITLGYELYDVCSESSNVY-ATLRVPAQQGTGHLEMQR--DLRNHSSKVVALIGPDNTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PNMTLGYRIFDTCNTVSKALEATLSFVAQNKIDSLNLDEFCNCSEHIPSTIAVVGATGSG 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GDFLLAGLFSLHADCLQVRHRPLVTSCDRSDS--FNGHGYHLFQAMRFTVEEINNSTALL
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Search completed: Fri Mar 17 13:23:19 2000 Job time : 32 secs.



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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Mar 17 13:13:13 2000; MasPar time 39.37 Seconds 506.520 Million cell updates/sec Tabular output not generated.

Title: >US-09-361-652-2

Description: (1-842) from US09361652.pep

Perfect Score: 6366

Sequence: 1 MLFWAAHLLLSLQLAVAYCW.....NNTEHFQASIQDYTRRCGTT 842

Scoring table:

PAM 150 Gap 11

earched: 188963 seqs, 23686106 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: a-geneseq36 1:geneseqp

Statistics: Mean 38.664; Variance 175.009; scale 0.221

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

1 3 3 3 4 4 4 4 7 6 6 7 7 8 8 8 7 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Result No.
1316 1316 1316 1316 1293 1293 1293 1293 1298 1282 1282 1282 1282 1282 1200 1200 120	Score
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Human metabotropic glu	ropic	Rat pheromone receptor		Rat metabotropic gluta	Human mGluR7a.		Metabotropic glutamate	Human mGluR3.	Metabotropic glutamate	Human mGluR3.	Human metabotropic glu	Rat pheromone receptor	Mouse pheromone recept	HSmGluR1.	Amino acid sequence of	Human mGluR4.	Human mGluR4.	Human mGluR1B.	Human mGluR5c.	Human mGluR5b.	GLU-G-R SUDTYPE La.
. 10e	6.56e-52	9.87e-53	2.26e-53		3.44e-53	2.26e-53	.16e	.39e	.77e-5	4.03e-56	2.10e-57	4.78e-58	3.06e-59	2.00e-59	2.00e-59	1.62e-59	.59e-6	.31e-	2.00e-59	4.55e-50	2.41e-50

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Parathyroid Ck, designated a BOPCak I. The nucleic acid sequence of BOPCaR 1 can be used as part of the recombinant nucleic acid in the	inant nucleic acid. The present sequence represents boyine	fect the one or more CR activities in a cell not com	Ηħ	one or more activities of the calcium recept	d; (B) determining the ability of the tes	rom	t cell comprises a recombinant nuclèic acid exp	cacting a recombinant cell with a test compound, where the	ectivities of a calcium receptor (CR) comprises: (A)	has been developed	ig 47: 176pı	of compounds on calcium receptor activity	and determining	-VSUB; V88483.	119871/10.	t SC,	drin MF, Brown EM, Del Mar EG) NPS PHARM	BRIGHAM & WOM	-1994; US-35378	1994;	-1994; US-292827	-1993; US-14124	·1993; US-00938	1993; US-01712	-1992; US-93416	-1992; US-83404	·1991; US-74945	-1995; US-48075	1995; 480751	12-JAN-1999.	S58586	HOS AD	ion: anyiety	disease: Parkinson;	+113	hyperparathyroidism; seizure; stroke; epilepsy; hypoxia-induced merve cell damage: cardiac arres	arathyroid calcium receptor; inorganic ion receptor; osteoporosis	thyroid calcium receptor BoPCaR 1.	9-MAR-1999 (first entry)	W89563;	¥895	⊣

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VILCRPELNNTE

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Parkinson's
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                                                                                        WINTAPPSSYRNHELEDEIIFITCHEGSLMALGFLIGYTC-LLAAICFFF-AFKSRKLPE
                                                                                                                                                                                                                                                                                                                                                  FGISFVLCISCILVKTNRVLLVFE--AKIPTSFHRKWWGLNLQFLLVFLCTFMQIVICAI 742
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1085 AA;
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Pred. No. 2.60e-107;
234; Mismatches 273;
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Best Local
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23-AUG-1991; US-749451.
11-FEB-1992; US-834044.
21-AUG-1992; US-934161.
12-FEB-1993; US-017127.
23-FEB-1993; US-017127.
23-FEB-1993; US-00389.
22-OCT-1993; US-292827.
19-AUG-1994; US-292827.
21-OCT-1994; WO-UIZ117.
08-DEC-1994; US-353784.
(BGHM ) BRIGHAM & WOMENS (NPSP-) NPS PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The bovine parathyroid calcium receptor gene encodes a 1085 amino acid protein. The tissue from which this receptor and receptors from human parathyroid and rat kidney are derived, respond to changes, and control changes, in calcium ion concentration, e.g. parathyroid hormone regulates Ca2+ homeostasis in blood and extracellular fluid, and kidney function alters through changes in Ca2+ levels in juxtaglomerular and proximal tubule cells in the kidney. The purified receptors (produced recombinantly) can be used to screen for compounds that modulate calcium receptor activity, especially those that can be used to treat diseases associated with the receptors in these tissues. They can also be used to treat diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Brown EM, Garrett JE, Hebert WPI; 98-347412/30. N-PSDB; V26962.
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kidney; calcium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Match 20.7%;
Local Similarity 31.9%;
                                                                                                                                                                                                                                                                                                                                                                          GDIILGGLFFIHFG-VAVKDQDLKSRPESVECIRYNFRGFRWLQAMIFAIEEINSSPALL
                    QIPGFREFLQKVHPRKSVHNGFAKEFWEETFNCHLQEGAKGPLPVDTFLRGHEEGGARLS
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                                                                                           IVVFSSGPDLEPLI-KEIVRRNITGRIWLASEAWASSSLIAMPEYFHVVGGTIGFGLKAG
                                                                                                                                                                                                             HAVTTAALLSPELMPLVSYEASSVILSGKRKFPSFLRTIPSDKYQVEVIVRLLQSFGWVW
 TVLGV-A-IQ--Q-RQ-VP-GL-KEF-EESY----VQ-AVMGA-P--
                                                                                                                                                                                                                                              ISTAVANLLGLFYIPQVSYASSSRLLSNKNQFKSFLRTIPNDEHQATAMADIIEYFRWNW
                                                                                                                                                                                                                                                                                   PNITLGYELYDVCSESSNVY-ATLRVPAQQGTGHLEMQR--DLRNHSSKVVALIGPDNTD
                                                                                                                                                                                                                                                                                                                   PNMTLGYRIFDTCNTVSKALEATLSFVAQNKIDSLNLDEFCNCSEHIPSTIAVVGATGSG
                                                                                                                                        ISLVGSYGDYGQLGVQALEELATPRGICVAFKDVVPLSAQAGDPRMQRMMLRLARARTTV
                                                                                                                                                                         VGTIAADDDYGRPGIEKFREEAEERDICIDFSELISQYSDE-E-KIQQVVEVIQNSTAKV
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Pred. No. 2.60e-107;
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RTCPEG-SW-C
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activities, preferably disorders of calcium homeostasis,

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1 Bovine parathyroid cell calcium receptor 1 (BoPCaR 1).

2 Bovine parathyroid cell calcium receptor 1; BoPCaR 1;

3 Calcium homeostasis; hyperparathyroidism; osteoporosis.

4 Calcium homeostasis; hyperparathyroidism; osteoporosis.

5 Bos sp.

6 US568938-A.

7 US568938-A.

7 US-1995; 48588.

7 US-1995; US-48588.

7 US-1995; US-48588.

7 US-1995; US-34044.

7 US-1995; US-34044.

7 US-1993; US-934151.

7 US-1993; US-934151.
                                                                                                                                                             07-JUN-1995; 485588.

07-JUN-1995; US-485588.

23-AUG-1991; US-749451.

11-FEB-1992; US-934151.

12-FEB-1993; US-031451.

12-FEB-1993; US-017127.

23-FEB-1993; US-017127.

23-FEB-1993; US-017127.

23-FCB-1993; US-141248.

19-AUG-1994; US-29287.

11-CCT-1994; WO-U12117.

08-DEC-1994; US-353784.
(BGHM ) BRIGHAM & WOMENS HOSPITAL.
(NESP-) NPS PHARM INC.
Brown EM, Fuller FH, Garrett JE, HWPI; 98-008040/01.
The specification includes details of molecules that can modulate one or more inorganic ion receptor activities, and antibodies and antibody fragments targetted to inorganic ion receptor proteins. I proteins, nucleic acids and antibodies may be used to treat disorders by modulating one or more inorganic ion receptor
                                                                           DNA encoding calcium receptor polypeptide(s) - utherapeutic purposes, e.g. hyperparathyroidism a Claim 4; Columns 107-116; 174pp; English.

The present sequence is bovine parathyroid cell receptor 1 (BoPCaR 1).
                                                                                                                                                       N-PSDB; T95857
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W38272;
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                                                         NYNEAKCYTFSLLLHFVSWIAFFTM-SSIYQGSYLPAVNYLAGLATLSGGFSGYFLPKCY
                                                                                                           WLAMWIPRPIREYORFPHLVILECIEVN - - SVGFLVAFAHNILLSISTFVCSYLGKELPE
                                                                                                                                                              FSLGFAIFLSCLTIRSEQLVIIEKFSTKVPT-FYHTWAQNHGAGIFVIVSSTVHLFLCLT
                                                                                                                                                                                                                  LLIGTAGLFA-WRLHTPVVRSAGGRLCFLMLGSLVAG-SCSLYSFFGKPTVPACLLRQPL
                                                                                                                                                                                                                                                                                                                                                                            SGTCA-RGPVYPWQLLQQIYKVNFLLHK-KTVAFDDKGDPLGYYDIIAWDWNGPE-WT-F
                                                                                                                                                                                                                                                                                                                                                                                                      NGSCADIKKVEAWQVLKHLRHLNFTSNMGEQVTFDECGDLAGNYSIINWHLSPEDGSIVF
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                                                                                                                                                                                       FGISFVLCISCILVKTNRVLLVFE--AKIPTSFHRKWWGLNLQFLLVFLCTFMQIVICAI
                                                                                                                                                                                                                                                                                                                                                                                                                                 -G-TN-Q-LCRECHAFTTWNMPELGAFSMSAAYNVYEAVYAVAHGLHQLLGC----T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IVVFSSGPDLEPLI-KEIVRRNITGRIWLASEAWASSSLIAMPEYFHVVGGTIGFGLKAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ISTAVANLLGLEYIPQVSYASSSRLLSNKNQFKSFLRTIPNDEHQATAMADIIEYFRWNW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PNMTLGYRIFDTCNTVSKALEATLSFVAQNKIDSLNLDEFCNCSEHIPSTIAVVGATGSG
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272; Conservative
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                               871
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Pred. No. 2.60e-107;
234; Mismatches 273;
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RESULT
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AC WS
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W54846 standard; W54846; 01-SEP-1998 (fi

(first entry)

Protein; 1078

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Best Local (
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(BGHM ) BRIGH
(NPSP-) NPS P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The tissue from which the human parathyroid calcium receptor and receptors from bovine parathyroid and rat kidney are derived, respond to changes, and control changes, in calcium ion concentration, e.g. parathyroid hormone regulates Ca2+ homeostasis in blood and extracellular fluid, and kidney function alters through changes in Ca2+ levels in juxtaglomerular and proximal tubule cells in the kidney. The purified receptors (produced recombinantly) can be used to screen for compounds that modulate calcium receptor activity, especially those that tasses. They can also be used to raise antibodies for use in detection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antibody production
Claim 7; Fig 49; 174pp;
The tissue from which th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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Calcium receptor poly:peptide(s) useful for drug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Brown
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P-) NPS PHARM INC.
n EM, Garrett JE, Hebert SC;
98-347412/30.
                                                                                                                                                                                                             IVVFSSGPDLEPLI-KEIVRRNITGKIWLASEAWASSSLIAMPQYFHVVGGTIGFALKAG
                                                                                                                                                                                                                                                                        VGTIAADDDYGRPGIEKFREEAEERDICIDFSELISQYSDEEE--IQHVVEVIQNSTAKV
                                                                                                                                                             QIPGFREFLKKVHPRKSVHNGFAKEFWEETFNCHLQEGAKGPLPVDTFLRGHEESGDRFS
                                                                                                                                                                                         VVVFSN-RHLAGVFFRSVVLANLTGKVWIASEDWA----IS-T-YITNVPG-IQ-GI--G
                                                                                                                                                                                                                                                                                                                HAVTTAALLSPFLMPLVSYEASSVILSGKRKFPSFLRTIPSDKYQVEVIVRLLQSFGWVW
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                                                                                                                                                                                                                                                                                                                                                                          PNITLGYELYDVCSESSNVY-ATLRVPAQQGTGHLEMQR--DLRNHSSKVVALIGPDNTD 151
                                                                                                                                                                                                                                                                                                                                                                                                    PNLTLGYRIFDTCNTVSKALEATLSFVAQNKIDSLNLDEFCNCSEHIPSTIAVVGATGSG 148
                                                                                                                                                                                                                                                                                                                                                                                                                                  GDFLLAGLFSLHADCLQVRHRPLVTSCDRSDS--FNGHGYHLFQAMRFTVEEINNSTALL
            SGTCA-RGPVYPWQLLQQIYKVNFLLHK-KTVAFDDKGDPLGYYDIIAWDWNGPE-WT-F
                                        NGSCADIKKVEAWOVLKHLRHLNFTNNMGEQVTFDECGDLVGNYSIINWHLSPEDGSIVF
                                                                                                   NSSTAFRPLCTGDENISSVETPYIDYTHLRISYNVYLAVYSIAHALQDIYTCLPGRGLFT
                                                                                                                                 TVLG----VA-IQQRQ-VP-GL-KEF-EESY---VQ-AVMGA-P-----RTCPE-GSW--
                                                                                                                                                                                                                                                     ISLVGSYGDYGQLGVQALEELATPRGICVAFKDVVPLSAQAGDPRMQRMMLRLARARTTV
                                                                     -CGTN-Q-LCRECHAFTTWNMPELGAFSMSAAYNVYEAVYAVAHGLHQL---L-GC---T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   parathyroid calcium receptor 4.0 protein of ion concentration; parathyroid hormone; y; calcium receptor; detection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
271; Conser
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US-749451

US-834044

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US-934161

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US-009389

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US-292827

WO-U12117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              234;
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Pred.
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No. 3.67e-105;
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07-JUN-1995;
23-AUG-1991;
11-FEB-1992;
11-FEB-1993;
12-FEB-1993;
23-FEB-1993;
23-FEB-1993;
11--GCT-1994;
11-GCT-1994;
08-DEC-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-MAR-1999 (first entry)
Human parathyroid calcium receptor; phupCaR 4.0.
Parathyroid calcium receptor; inorganic ion receptor; osteoporosis; calcium homeostasis; hyperparathyroidism; seizure; stroke; epilepsy; spinal cord injury; hypoxia-induced nerve cell damage; cardiac arres; neonatal distress; neurodegenerative disease; Alzheimer's disease;
recombinant cell comprises a recombinant nucleic acid expressing to provided that the cell does not have functional CR expression from endogenous nucleic acid; (B) determining the ability of the test compound to affect one or more activities of the calcium receptor; (C) comparing the ability with the ability of the test compound to
                                                                            Screening for calcium receptor-active compounds - by recombin sexpression of nucleic acid encoding calcium receptor and determine effect of compounds on calcium receptor activity Claim 1; Fig 49; 176pp; English.

A method has been developed of screening for a compound able one or more activities of a calcium receptor (CR) comprises: contacting a recombinant cell with a test compound, where the
                                                                                                                                                                                                                        Balandrin MF, Brow
Hebert SC, Nemeth
                                                                                                                                                                                            N-PSDB; V82485.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
US5858684-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   depression; anxiety.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Huntington's disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NYNEAKCYTESLLLHEVSWIAFETM-SSIYQGSYLPAVNVLAGLATLSGGESGYFLPKCY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WLYTAPPSSYRNQELEDETIFITCHEGSLMALGFLIGYTC-LLAAICFFF-AFKSRKLPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LLIGTAGLEA-WRLHTPVVRSAGGRLCFLMLGSLVAG-SCSLYSFFGKPTVPACLLRQPL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              standard;
                                                                                                                                                                                                                                                           BRIGHAM & WOMENS
NPS PHARM INC.
                                                                                                                                                                                                            19871/10.
                                                                                                                                                                                                                           MF, Brown EM, Nemeth EF,
                                                                                                                                                                                                                                                                                                      480751.

US-480751.

US-749451.

US-834044.

US-934161.

US-934161.

US-009389.

US-009389.

US-141248.

US-292827.

WO-U12117.
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                                                                                                                                                                                                                           Van
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Parkinson's disease; dementia;
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                                                                                                                                                                                                                           Wagenen
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and determi
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          affect the one or more CR activities in a cell not comprising the recombinant nucleic acid. The present sequence represents human parathyroid CR, designated a phuPCaR 4.0. The nucleic acid sequence of phuPCaR 4.0 can be used as part of the recombinant nucleic acid in the method described above. The compounds identified can be used to treat diseases or disorders characterised by abnormal calcium homeostasis, e hyperparathyroidism, osteoporosis and other bone and mineral-related disorders. They can also be used for the treatment of diseases and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         409
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                           NENEAKFITESMLIFFIVWISFIPAYASTY-GKFVSAVEVIAILAASFGLLACIFFNKIY
                                                                                                                                                                                                                                                                                        FGISFVLCISCILVKINRVLLVFE--AKIPISFHRKWWGLNLQFLLVFLCIFWQIVICVI
                                                                                                                                                                                                                                                                                                                                                           LLIGTAGLFA-WRLHTPVVRSAGGRLCFLMLGSLVAG-SCSLYSFFGKPTVPACLLRQPL
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                                                                                              WLAMWTPRPTREYQREPHLVILECTEVN--SVGFLVAFAHNILLSISTFVCSYLGKELPE
                                                                                                                                                           WLYTAPPSSYRNOELEDEIIFITCHEGSLMALGFLIGYTC-LLAAICFFF-AFKSRKLPE
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                                                                                                                                                                                                                              FSLGFAIFLSCLTIRSFQLVIIFKFSTKVPT-FYHTWAQNHGAGIFVIVSSTVHLFLCLT
                                                                                                                                                                                                                                                                                                                                                                                                                     LTAFVLGVFIKFR-NTPIVKATNRELSYLLLFSLLCCFSSSLF-FIGEPQDWTCRLRQPA
   Similarity 271; Conser
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Pred. No. 3.67e-105;
234; Mismatches 274;
Length 1078;
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OCCORDED STREET STREE
                                                                                                                                                                                                                                                                                          cc gland adenoma tumour using pBoPCARI as a hybridisation probe. mRNA was consisted from a 39 year old caucasian male diagnosed with primary consisted from a 39 year old caucasian male diagnosed with primary consisted from a 39 year old caucasian male diagnosed with primary consisted from a 39 year old caucasian male diagnosed with primary consisted from a 19 year old caucasian male diagnosed with primary consisted from a 19 year old caucasian male diagnosed with primary consisted from the presence of functional calcium receptors. Both clone consisted for the presence of functional calcium receptors. Both clone consisted for the presence of functional calcium receptors as assessed by the consistence analysis of the two conversations and consistence of at the same propriate calcium receptor agonists, e.g. NPS R-467 and NPS R-568. Consequence analysis of the two conversations as a sessed by the consequence analysis of the propriation and consistence of at the sequence variation and consequence analysis of the propriation and consequence analysis of the propriation and consequence analysis of the human can gene consequence analysis of the human can gene consequence that the additional 30 bp in clone phupCaR4.0 the compared to phupCaR4.0, results from alternative mRNA splicing. This alternative encoded by pHupCaR5.2 between residues 536 and 537 of the protein encoded by pHupCaR5.2 between residues 536 and 537 of the protein concoded by pHupCaR4.0. In addition pHupCaR5.2 encodes Gln at position concoded by pHupCaR5. The human can gene encodes Gln at position and consequence analysis of the protein concoded by pHupCaR5. The human can gene encodes Gln at position concoded by pHupCaR5. The human can gene encodes Gln and protein concoded by pHupCaR5.0 between the protein professions. The human can gene encodes Gln and protein concoded by pHupCaR5.0 between the protein concoded by pHupCaR5.0 be
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from the EPO.
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The sequences given in Will888-89 represent functional calcium receptors. The cDNAs encoding these sequences were isolated from human parathyroid
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23-OCT-1995; U13704.
21-OCT-1994; WO-U12117.
08-DEC-1994; US-353784.
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18-NOV-1997.
07-JUN-1995;
07-JUN-1995;
12-AUG-1991;
11-FEB-1992;
12-FEB-1993;
12-FEB-1993;
                                                                             Human parathyroid cell calcium receptor 4.0 (HuPCaR 4.0 Human parathyroid cell calcium receptor 4.0; HuPCaR 4.0 calcium homeostasis; hyperparathyroidism; osteoporosis Homo sapiens.
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                                                                                                                                W38274 standard; Protein; 1078
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 485588.

US-485588.

US-749451.

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19-AUG-1994; US-292827.
21-OCT-1994; WO-U12117.
08-DEC-1994; US-353784.
(BGHM ) BRIGHAM & WOMENS H
(NPSP-) NPS PHARM INC.
BFOWN EM, FULLER H, Garre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is human parathyroid cell calcium receptor 4.0 (HuPCaR 4.0).

The specification includes details of molecules that can modulate one or more inorganic ion receptor activities, and antibodies and antibody fragments targetted to inorganic ion receptor proteins. The proteins, nucleic acids and antibodies may be used to treat disorders by modulating one or more inorganic ion receptor activities, preferably disorders of calcium homeostasis, e.g. sequence 1078 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA encoding calcium receptor polypeptide(s) therapeutic purposes, e.g. hyperparathyroidism Claim 20; Columns 125-134; 174pp; English.
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FGISFVLCISCILVKTNRVLLVFE--AKIPTSFHRKWWGLNLQFLLVFLCTFWQIVICVI
                                                                                                               MPCEAGTFLNTSELHTCOPCGTEEWAPEGSSACFSRTVEFLGWHEPISLVLLAANTLLLLL
                                                                                                                                                   VECPDGEYSDETDASACNKCPDDFWSNENHTSCIAKEIEFLSWTEPFGIALTLFAVLGIF
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l Similarity 31.8%;
271; Conservation
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Pred. No. 3.67e-105;
234; Mismatches 274;
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The invention relates to polynucleotide sequences encoding mammalian pheromone receptor polypeptides. The polypeptides are expressed in murine and rat vomeronasal organ. The products can be used for modifying pheromone activity, e.g. for decreasing pheromone receptor mediated signal transduction. They can be used for controlling fertility and behaviour in vertebrates and invertebrates. Compositions comprising the polypeptides are particularly useful in e.g. controlling fertility in interrupting the normal behaviours of rodents or insects by interrupting the normal behaviours of rodents or insects that result in reproduction. The present sequence represents a rat kidney extracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         calcium/polyvalent cation-sensing receptor.
Sequence 1079 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated pheromone receptor polypeptides - us products for controlling fertility and behaviour
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07-JAN-1999.
30-JUN-1998; U13680.
30-JUN-1997; US-051284
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                                                                              VVVFSN-RHLAGVFFRSVVLANLTGKVWIASEDWA----IS-T-YITNVPG-IQ-GI--G
                                                                                                                                  IVVFSSGPDLEPLI-KEIVRRNITGRIWLASEAWASSSLIAMPEYFHVVGGTIGFGLKAG
                                                                                                                                                                                            ISLVGSYGDYGQLGVQALEELATPRGICVAFKDVVPLSAQAGDPRMQRMMLRLARARTTV
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19-AUG-1994;
19-OCT-1994;
08-DEC-1994;
(BGHM ) BRIGH
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23-AUG-1991;
11-FEB-1992;
11-FEB-1992;
21-AUG-1993;
23-FEB-1993;
                                                                                                                                                                                                                                                                                                                            US5763569-A.
09-JUN-1998.
07-JUN-1995;
The tissue from which the rat kidney calcium receptor and receptors from bovine parathyroid and rat kidney are derived, respond to changes, and control changes, in calcium ion concentration, e.g. parathyroid hormone regulates Ca2+ homeostasis in blood and extracellular fluid, and kidney function alters through changes in Ca2+ levels in juxtaglomerular and
                                                                                                                                                                                                                                                                                                                                                                                        Calcium ion concentration; parathyroid calcium reconcentration;
                                                                      antibody production Claim 8; Fig 50; 174pp;
                                                                                                               WPI; 98-347412,
N-PSDB; V26965
                                                                                                                                                                                                                                                                                                                                                                                                                                        W54847 standard; W54847;
                                                                                               Calcium receptor poly:peptide(s)
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EM, Garrett JE,
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US-749451.

US-834044.

US-934161.

US-017127.

US-009389.

US-141248.

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WO-U12117.
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                                                                           NYNEAKCVTFSLLLHFVSWIAFFTM-SSIYQGSYLPAVNVLAGLATLSGGFSGYFLPKCY
                                                                                                               NENEAKFITESMLIFFIVWISFIPAYASTY-GKFVSAVEVIAILAASFGLLACIFFNKVY
                                                                                                                                                        WLAMWTPRPTREYQRFPHLVILECTEVN--SVGFLVAFAHNILLSISTFVCSYLGKELPE
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                                                                                                                                                                                                                                                                            FGISFVLCISCILVKTNRVLLVFE--AKIPTSFHRKWWGLNLQFLLVFLCTFMQILICII
                                                                                                                                                                                                                                                                                                                   LLIGTAGLFA-WRLHTPVVRSAGGRLCFLMLGSLVAG-SCSLYSFFGKPTVPACLLRQPL 638
                                                                                                                                                                                                                                                                                                                                                         LTAFVLGVFIKER-NTPIVKATNRELSYLLLESLLCCFSSSLF-FIGEPQDWTCRLRQPA 683
                                                                                                                                                                                                                                                                                                                                                                                                                                         VECPDGEYSGETDASACDKCPDDFWSNENHTSCIAKEIEFLAWTEPFGIALTLFAVLGIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KEVGYYNVYAKKGERLFINEEKILWSGFSREVPFSNCSRDCQAGTRKGIIEGEPTCCFEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SGTCA-RGPVYPWQLLQQIYKVNFLLHK-KTVAFDDKGDPLGYYDIIAWDWNGPE-WT-F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NGSCADIKKVEAWQVLKHLRHLNFTNNMGEQVTFDECGDLVGNYSIINWHLSPEDGSIVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -CGTN-Q-LCRECHAFTTWNMPELGAFSMSAAYNVYEAVYAVAHGLHQL---L-GC---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TVLGV-A-IQ--Q-RQ-VP-GL-KEF-EESY---VQ-AVMGA-P-----RTCPEGS-W--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IVVFSSGPDLEPLI-KEIVRRNITGRIWLASEAWASSSLIAMPEYFHVVGGTIGFGLKAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ISLYGSYGDYGQLGVQALEELATPRGICVAFKDVVPLSAQAGDPRMQRMMLRLARARTTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VGTIAADDDYGRPGIEKFREEAEERDICIDFSELISQYSDEEE--IQQVVEVIQNSTAKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HAVTTAALLSPFLMPLVSYEASSVILSGKRKFPSFLRTIPSDKYQVEVIVRLLQSFGWVW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PNITLGYELYDVCSESSNVY-ATLRVPAQQGTGHLEMQR--DLRNHSSKVVALIGPDNTD 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PNMTLGYRIFDTCNTVSKALEATLSFVAQNKIDSLNLDEFCNCSEHIPSTIAVVGATGSG 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GDFLLAGLFSLHADCLQVRHRPLVTSCDRSDS--FNGHGYHLFQAMRFTVEEINNSTALL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1079 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20.1%;
31.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 1282; DB 1;
Pred. No. 3.91e-104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches 280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1079;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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12-JAN-1999.
07-JUN-1995;
07-JUN-1995;
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22-OCT-1993;
19-AUG-1994;
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11-FEB-1992;
21-AUG-1992;
12-FEB-1993;
                                                                                                                                                                                                                                                                                                                                                                                                            Balandrin MF, Brown EM, De
Balandrin MF, Brown EM, De
Hebert SC, Nemeth EF, Van
WPI; 99-119871/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rat parathyroid calcium receptor pRakCaR 3A.

Parathyroid calcium receptor; inorganic ion receptor; osteoporosis;
calcium homeostasis; hyperparathyroidism; seizure; stroke; epilepsy;
spinal cord injury; hypoxia-induced nerve cell damage; cardiac arrest;
neonatal distress; neurodegenerative disease; Alzheimer's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                           (BGHM )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-DEC-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   depression; anxiety.
                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; V82486.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Huntington's disease; Parkinson's disease; dementia; muscle tension;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W89566;
19-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W89566 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-OCT-1994;
152
                  149
                                     95
                                                       89
                                                                          37
                                                                                             30
                                                                                                                        Local Similarity 31.2%;
                 VSTAVANLLGLEYIPQVSYASSSRLLSNKNQYKSFLRTIPNDEHQATAMADIIEYFRWNW 208
                                                                                             GDIILGGLFPIHFG-VAAKDQDLKSRPESVECIRYNFRGFRWLQAMIFAIEEINSSPSLL 88
HAVTTAALLSPFLMPLVSYEASSVILSGKRKFPSFLRTIPSDKYQVEVIVRLLQSFGWVW
                                                       PNMTLGYRIFDTCNTVSKALEATLSFVAQNKIDSLNLDEFCNCSEHIPSTIAVVGATGSG 148
                                                                          GDFLLAGLFSLHADCLQVRHRPLVTSCDRSDS--FNGHGYHLFQAMRFTVEEINNSTALL
                                     PNITLGYELYDVCSESSNYY-ATLRVPAQQGTGHLEMQR--DLRNHSSKYVALIGPDNTD 151
                                                                                                                                                                                                                                                                                                                                                                                                                                            BRIGHAM & WOMENS HOSPITAL NPS PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       480751.

US-480751.

US-749451.

US-834044.

US-834161.

US-017127.

US-017127.

US-017127.

US-017127.

US-02827.

WO-U12117.
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                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                          Wagenen
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                                                                                                                 240;
                                                                                                               Score 1282; DB 1; 1
Pred. No. 3.91e-104;
240; Mismatches 280;
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                                                                                                                                                                                                                                                                                                                                                                                                                          BC;
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                                                                                                                                 Length 1079;
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AC WALLACE WALLACE WALLACE WALLACE RECEIVED TO RECE
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              Rattus sp.
US568938-A.
18-NOV-1997.
18-NOV-1997.
07-JUN-1995, V8-48588.
07-JUN-1995, US-48588.
23-AUG-1991, US-74-4451.
11-FEB-1992, US-834044.
21-AUG-1992, US-934161.
12-FEB-1993, US-003389.
22-CCT-1993, US-003389.
22-CCT-1994, US-292827.
21-CCT-1994, WG-US-18714.
08-DEC-1994, WG-US-18714.
(BGHM ) BRIGHAM & WOMENS HOSPITAL.
(NPSP-) NPS PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-MAY-1998 (first entry)
Rat kidney cell calcium receptor 3A; RakCaR 3A;
Rat kidney cell calcium receptor 3A; RakCaR 3A;
calcium homeostasis; hyperparathyroidism; osteoporosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W38275 standard;
W38275;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VILCRPELNNTEHFQASIQDYT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MPCEAGTFLNTSELHTCQPCGTEEWAPEGSSACFSRTVEFLGWHEPISLVLLAANTLLLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KEVGYYNVYAKKGERLFINEEKILWSGFSREVPFSNCSRDCQAGTRKGIIEGEPTCCFEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TVLGV-A-IQ--Q-RQ-VP-GL-KEF-EESY---VQ-AVMGA-P-----RTCPEGS-W--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VVVFSN-RHLAGVFFRSVVLANLTGKVWLASEDWA----IS-T-YITNVPG-IQ-GI--G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IVVFSSGPDLEPLI-KEIVRRNITGRIWLASEAWASSSLIAMPEYFHVVGGTIGFGLKAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NYNEAKCYTFSLLLHFVSWIAFFTM-SSIYQGSYLPAVNVLAGLATLSGGFSGYFLPKCY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WLAMWTPRPTREYORFPHLVILECTEVN - - SVGFLVAFAHNILLSISTFVCSYLGKELPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WLYTAPPSSYRNHELEDEIIFITCHEGSLMALGSLIGYTC-LLAAICFFF-AFKSRKLPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FSLGFAIFLSCLTIRSFQLVIIFKFSTKVPT-FYHTWAQNHGAGIFVIVSSTVHLFLCLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FGISFVLCISCILVKTNRVLLVFE--AKIPTSFHRKWWGLNLQFLLVFLCTFMQILICII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LLIGTAGLEA-WRLHTPVVRSAGGRLCFLMLGSLVAG-SCSLYSFFGKPTVPACLLRQPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LTAFVLGVFIKFR-NTPIVKATNRELSYLLLFSLLCCFSSSLF-FIGEPQDWICRLRQPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VECPDGEYSGETDASACDKCPDDFWSNENHTSCIAKEIEFLAWTEPFGIALTLFAVLGIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EVIG--SA-SISPVHLDINKTKIQWHGKNNQVPVSVCTRDCLEGHHR-LVMGSHHCCFEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SGTCA-RGPVYPWQLLQQIYKVNFLLHK-KTVAFDDKGDPLGYYDIIAWDWNGPE-WT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NGSCADIKKVEAWQVLKHLRHLNFTNNMGEQVTFDECGDLVGNYSIINWHLSPEDGSIVF
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Best Local S
Matches 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA encoding calcium receptor polypeptide(s) - usef therapeutic purposes, e.g. hyperparathyrcidism and Claim 20; Columns 133-142; 174pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; T95860
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NFNEAKFITFSMLIFFIVWISFIPAYASTY-GKFVSAVEVIAILAASFGLLACIFFNKVY
                                                                                                                                         FGISFVLCISCILVKTNRVLLVEE--AKIPTSFHRKWWCLNLQFLLVFLCTFMQILICII
                                                                                                                                                                             LLIGTAGLEA-WRLHTPVVRSAGGRLCFLMLGSLVAG-SCSLYSFFGKPTVPACLLRQPL
                                                                                                                                                                                                 LTAFVLGVFIKFR-NTPIVKATNRELSYLLLFSLLCCFSSSLF-FIGEPQDWTCRLRQPA
                                                                                                                                                                                                                                                                                                                            EVIG--SA-SLSPVHLDINKTKIQWHGKNNQVPVSVCTRDCLEGHHR-LVMGSHHCCFEC
                                                                                                                                                                                                                                                                                                                                                            KEVGYYNVYAKKGERLFINEEKILWSGFSREVPFSNCSRDCQAGTRKGIIEGEPTCCFEC
                                                                                                                                                                                                                                                                                                                                                                                                                                  NGSCADIKKVEAWQVLKHLRHLNEINNMGEQVIFDECGDLVGNYSIINWHLSPEDGSIVF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VVVFSN-RHLAGVFFRSVVLANLTGKVWIASEDWA----IS-T-YITNVPG-IQ-GI--G
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                                 WLAMWTPRPTREYQRFPHLVILECTEVN - - SVGFLVAFAHNILLSISTFVCSYLGKELPE
                                                                   WLYTAPPSSYRNHELEDEIIFITCHEGSLMALGSLIGYTC-LLAAICFFF-AFKSRKLPE
                                                                                                       FSLGFAIFLSCLTIRSFQLVIIFKFSTKVPT-FYHTWAQNHGAGIFVIVSSTVHLFLCLT
                                                                                                                                                                                                                                                    MPCEAGTFINTSELHTCQPCGTEEWAPEGSSACFSRTVEFIGWHEPISLVLLAANTLLLL
                                                                                                                                                                                                                                                                                      VECPDGEYSGETDASACDKCPDDFWSNENHTSCIAKEIEFLAWTEPFGIALTLFAVLGIF
                                                                                                                                                                                                                                                                                                                                                                                                SGTCA-RGPVYPWQLLQQIYKVNFLLHK-KTVAFDDXSDPLGYYDIIAWDWNGPE-WT-F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -CGTN-Q-LCRECHAFTTWNKPELGAFSMSAAYNVYEAVYAVAHGLHQL---L-GC---T
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Pred. No. 3.91e-104;
240; Mismatches 280;
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                                                                                                                                                                                                              Query Match
Best Local S
Matches 26
                                                                                                                                                                                                                                                                            the expression of the aquatic PVCR activates or inhibits aquatic PVCR mediated ion transport and endocrine changes that permit fish to adapt to fresh or salt water. The method facilitates the aquaculture of marine fish and can provide for the development of marine fish that are easily adaptable to fresh water aquaculture. Sequence 1026 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W32059 standard;
W32059;
27-MAR-1998 (fir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated Aquatic polyvalent cation sensing receptor - used to develop products for increasing or decreasing the salinity tolerat of fish for use in aquaculture Claim 9; Fig 5A-B; 57pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 97-489640/45.
N-PSDB; T89290.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Region
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Calcium receptor related
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  polycation-sensing receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (BGHM ) BRIGHAM & WOMENS HOSPITAL.
Brown E, Harris HW, Hebert S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-OCT-1997.
27-MAR-1997;
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                                 ISTAVANLLGLEYIPQVSYASSSRLLSNKNEYKAFLRTIPNDEQQATAMAEIIEHFQWNW : : | | | | | | : : : | | | |
                                                                                                                                              GDFLLAGLFSLHADCLQVRHRPLVTSCD--RSDSFNGHGYHLFQAMRFTVEEINNSTALL
                                                                                                                                                                            GDIILGGLFPIHFG-VAAKDQDLKSRPEATKCIRYNFRGFRWLQAMIFAIEEINNSMTFL
                                                                                                             PNITLGYRIFDTCNTVSKALEATLSFVAQNKIDSLNLDEFCNCSDHIPSTIAVVGATGSG
                                                                                                                                                                                                                               Similarity
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larity 31.0%;
Conservative :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "region in extracellular domain that is highly divergent from mammalian PVCR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                lcium receptor related protein (SKCaR-RP)
d protein; CaR-RP; dogfish shark; SKCaR-R
ptor; aquaculture; fish farming;
                                                                               -ATLRVPAQQGTGHLEMQR--DLRNHSSKVVALIGPDNTD
                                                                                                                                                                                                            Score 1204; DB 1;
Pred. No. 7.44e-97;
237; Mismatches 273
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                                                                                                                                                                                                                                           Length 1026;
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11-FEB-1992;
21-AUG-1993;
12-FEB-1993;
23-FEB-1993;
23-FEB-1993;
22-CCT-1994;
21-CCT-1994;
08-DEC-1994;
                                                                                                                                                                                                                                                        08-MAY-1998 (first entry)
Human parathyroid cell calcium receptor 5.2 (HuPCaR Human parathyroid cell calcium receptor 5.2; HuPCaR calcium homeostasis; hyperparathyroidism; osteoporos Homo sapiens.
             (BGHM )
                                                                                                                                                                                                                                                                                                                          w38273 standard; Protein; 1088
w38273;
08-MAY-1998 (first entry)
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07-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QPAFGISFVLCISCILVKTNRVLLVFE--AKIPTSLHRKWVGLNLQFLLVFLCILVQIVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FECMPCEAGTFLNTSELHTCQPCGTEEWAPEGSSACFSRTVEFLGWHEPISLVLLAANTL
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             BRIGHAM & WOMENS
NPS PHARM INC.
                                                         485588.

US-749451.

US-749461.

US-834044.

US-934161.

US-934161.

US-009389.

US-009389.

US-141248.

US-292827.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence is human parathyroid cell calcium receptor 5.2 (Hupcar 5.2).

The specification includes details of molecules that can modul one or more inorganic ion receptor activities, and antibodies antibody fragments targetted to inorganic ion receptor proteir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA encoding calcium receptor polypeptide(s) - useful for therapeutic purposes, e.g. hyperparathyroidism and osteoporosis Claim 20; Columns 117-126; 174pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98-008040/01.
                                    STVHLFLCLTWLAMWTPRPTREYQRFPHLVILECTEVN--SVGFLVAFAHNILLSISTFV
                                                                       TFMQIVICVIWLYTAPPSSYRNQELEDEIIFITCHEGSLMALGFLIGYTC-LLAAICFFF
                                                                                                              VPACLLRQPLFSLGFA1FLSCLTIRSFQLVIIFKFSTKVPT-FYHTWAQNHGAGIFVIVS
                                                                                                                                               DWTCRLRQPAFGISFVLCISCILVKTNRVLLVFE--AKIPTSFHRKWWGLNLQFLLVFLC
                                                                                                                                                                                       LLAANTLLLLIGTAGLFA-WRLHTPVVRSAGGRLCFLMLGSLVAG-SCSLYSFFGKPT
                                                                                                                                                                                                              LTLFAVLGIFLTAFVLGVFIKFR-NTPIVKATNRELSYLLLFSLLCCFSSSLF-FIGEPQ
                                                                                                                                                                                                                                                             MGSHHCCFECMPCEAGTFLNTSELHTCQPCGTEEWAPEGSSACFSRTVEFLGWHEPISLV
                                                                                                                                                                                                                                                                                                EGEPTCCFECVECPDGEYSDETDASACNKCPDDFWSNENHTSCIAKEIEFLSWTEPFGIA
                                                                                                                                                                                                                                                                                                                                    EVIG--SA-SLSPVHLDINKTKIQWHG--KN----N--QVPVSVCTRDCLEGHHR-LV
                                                                                                                                                                                                                                                                                                                                                                       KEVGYYNVYAKKGERLFINEEKILWSGFSREPLTFVLSVLQVPFSNCSRDCLAGTRKGII
                                                                                                                                                                                                                                                                                                                                                                                                                                               NGSCADIKKVEAWQVLKHLRHLNFINNMGEQVTFDECGDLVGNYSIINWHLSPEDGSIVF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IVVFSSGPDLEPLI-KEIVPRNITGKIWLASEAWASSSLIAMPQYFHVVGGTIGFALKAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HAVTTAALLSPFLMPLVSYEASSVILSGKRKFPSFLRTIPSDKYQVEVIVRLLQSFGWVW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VSTAVANLLGLFYIPQVSYASSSRLLSNKNQFKSFLRTIPNDEHQATAMADIIEYFRWNW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GDFLLAGLFSLHADCLQVRHRPLVTSCDRSDS--FNGHGYHLFQAMRFTVEEINNSTALL
-AFKSRKLPENFNEAKFITFSMLIFFIVWISFIPAYASTY-GKFVSAVEVIAILAASFGL
                                                                                                                                                                                                                                                                                                                                                                                                            SGTCA-RGPVYPWQLLQQIYKVNFLLHK-KTVAFDDKGDPLGYYDIIAWDWNGPE-WT-F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PNLTLGYRIFDTCNTVSKALEATLSFVAQNKIDSLNLDEFCNCSEHIPSTIAVVGATGSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -CGTN-Q-LCRECHAFTTWNMPELGAFSMSAAYNVYEAVYAVAHGLHQL---L-GC---T
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l Similarity 31.6%;
272; Conservative
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cches 272;
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RESULT 14

RESULT 14

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Best Local :
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07-JUN-1995; US-484565.
23-AUG-1991; US-749451.
11-FEB-1992; US-834044.
21-AUG-1992; US-934161.
12-FEB-1993; US-0077127.
23-FEB-1993; US-009389.
22-OCT-1994; US-141248.
19-AUG-1994; US-292827.
21-OCT-1994; US-35784.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Calcium receptor poly:peptide(s) - useful for drug screening or antibody production
Claim 5; Fig 48; 174pp; English.
The tissue from which the human parathyroid calcium receptor and receptors from bovine parathyroid and rat kidney are derived, respond to changes, and control changes, in calcium ion concentration,
e.g. parathyroid hormone regulates Ca2+ homeostasis in blood and extracellular fluid, and kidney function alters through changes in Ca2+ levels in juxtaglomerular and proximal tubule cells in the kidney. The purified receptors (produced recombinantly) can be used to screen for compounds that modulate calcium receptor activity, especially those that tissues. They can also be used to raise antibodies for use in detection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             calcium receptor; detection Homo sapiens. US5763569-A.
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N-PSDB; V26963
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07-JUN-1995;
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VVVFSN-RHLAGVFFRSVVLANLTGKVWIASEDWA---
                                                     IVVFSSGPDLEPLI-KEIVRRNITGKIWLASEAWASSSLIAMPQYFHVVGGTIGFALKAG
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                                                                                                           {\tt ISLVGSYGDYGQLGVQALEELATPRGICVAFKDVVPLSAQAGDPRMQRMMLRLARARTTV}
                                                                                                                                                                 VGTIAADDDYGRPGIEKFREEAEERDICIDFSELISQYSDEEE--IQHVVEVIQNSTAKV
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-) NPS PHARM INC.

EM, Garrett JE, Hebert
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Pred. No. 1.42e-96;
235; Mismatches 272;
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IS-T-YITNVPG-IQ-GI--G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human parathyroid calcium receptor pHuPCaR 5.2.

Parathyroid calcium receptor; inorganis ion receptor; osteoporosis;

calcium homeostasis; hyperparathyroidism; seizure; stroke; epilepsy;

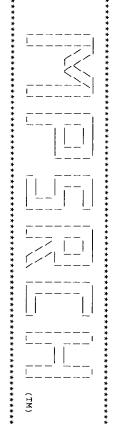
spinal cord injury; hypoxia-induced nerve cell damage; cardiac arrest;

neonatal distress; neurodegenerative disease; Alzheimer's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W89564 standard;
                                                        Balandrin MF, Brown El
Hebert SC, Nemeth EF,
WPI; 99-119871/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          depression; anxiety
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                                   N-PSDB;
                                                                                                                                    (BGHM )
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                                                                                                         BRIGHAM & WOMENS HOSPITAL NPS PHARM INC.
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                                                                                                            Garrett
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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A method has been developed of screening for a compounds of screening for a compound of s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     contacting a recombinant cell with a test compound, where the recombinant cell comprises a recombinant nucleic acid express.
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LTLEAVLGIFLTAEVLGVFIKER-NTPIVKATNRELSYLLLESLLCCFSSSLF-FIGEPQ | : | : | : | : | : | : | : | : | | : | | |
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                                                                                                        MGSHHCCFECMPCEAGTFLNTSELHTCQPCGTEEWAPEGSSACFSRTVEFLGWHEPISLV
                                                                                                                                                   EGEPTCCFECVECPDGEYSDETDASACNKCPDDFWSNENHTSCIAKEIEFLSWTEPFGIA
                                                                                                                                                                                                                                                                                         KEVGYYNVYAKKGERLFINEEKILWSGFSREPLTFVLSVLQVPFSNCSRDČLAGTRKGII
                                                                                                                                                                                                                                                                                                                                                                                       SGTCA-RGPVYPWQLLQQIYKVNFLLHK-KTVAFDDKGDPLGYYDIIAWDWNGPE-WT-F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IVVFSSGPDLEPLI-KEIVRRNITGKIWLASEAWASSSLIAMPQYFHVVGGTIGFALKAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                           NGSCADIKKVEAWQVLKHLRHLNFTNNMGEQVTFDECGDLVGNYSIINWHLSPEDGSIVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -CGTN-Q-LCRECHAFTTWNMPELGAFSMSAAYNVYEAVYAVAHGLHQL---L-GC---T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ISLVGSYGDYGQLGVQALEELATPRGICVAFKDVVPLSAQAGDPRMQRMMLRLARARTTV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PNITLGYELYDVCSESSNVY-ATLRVPAQQGTGHLEMQR--DLRNHSSKVVALIGPDNTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PNLTLGYRIFDTCNTVSKALEATLSFVAQNKIDSLNLDEFCNCSEHIPSTIAVVGATGSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 272;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -GL-KEF-EESY---VQ-AVMGA-P----
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Pred. No. 1.42e-96;
235; Mismatches 272;
                                                                                                                                                                                                                                                     -N--QVPVSVCTRDCLEGHHR-LV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CR)
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Mar 17 13:31:21 2000; MasPar time 105.23 Seconds 511.946 Million cell updates/sec

Tabular output not generated

Description: Perfect Score:

Sequence: >US-09-361-652-3 (1-777) from US09361652.pep 5838 1 RSCSFNEHGYHLFQAMRLGV.....NSTEHFQASIQDYTRRCGST 777

Scoring table: PAM 150 Gap 11

Searched: 225878 seqs, 69334122 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

sptrembll2
1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human
5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle
9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified
13:sp_vertebrate 14:sp_virus

Statistics: Mean 51.690; Variance 98.585; scale 0.524

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

20	18	17	16	15	14	13	12	11	10	9	8	7	6	5	4	ω	2	1	Result
718	756	765	771	838	844	915	946	994	1066	1197	1216	1217	1271	1270	1286	1293	1848	4587	Score
12.3	12.9	•	13.2		14.5	15.7	16.2	17.0	18.3	20.5	20.8	20.8	21.8	21.8	22.0	22.1	31.7	78.6	Query Match 1
803	908	408				779	855							864	868	α	843	840	Length
11	4.	13	11	13	1	11	11	11	13	13	13	13	13	13	13	13	11	11	DB.
035191	095945	093558	035189	093555	Q62916	035269	070409	070410	073640	073638	073635	093552	073639	073637	073636	093553	Q9Z0R7	Q9Z0R8	ID
PUTATIVE PHEROMONE REC	-3	PUTATIVE ODORANT RECEP	PUTATIVE PHEROMONE REC	PUTATIVE ODORANT RECEP	METABOTROPIC GLUTAMATE	PUTATIVE PHEROMONE REC	PUTATIVE PHEROMONE REC	PUTATIVE PHEROMONE REC	PHEROMONE RECEPTOR.	PHEROMONE RECEPTOR.	CALCIUM2+ SENSING RECE	PUTATIVE ODORANT RECEP	PHEROMONE RECEPTOR.	PHEROMONE RECEPTOR.	PHEROMONE RECEPTOR.	PUTATIVE ODORANT RECEP	PUTATIVE TASTE RECEPTO	PUTATIVE TASTE RECEPTO	Description
4.10e-121 2.35e-118	٠	2.42e-128	1.28e-129	. 2		1.79e-160	3.72e-167			1.20e-221	8.51e-226	5.15e-226	. 07	1.33e-237	4.21e-241	1.23e-242	0.00e+00	0.00e+00	Pred. No.

45	44	43	42	41	40	39	<u>د</u> 8	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21
477	479	480	476	479	484	483	488	490	498	504	503	505	521	584	619	638	643	644	648	676	703	699	711	714
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19	652	654	σ	651	3556	64	653	3645	655	3564	363	364	647	411	194	9	193	413	192	35272	266	556	5267	265
PUTATIVE PHEROMONE REC	PHEROMONE RECEPTOR (FR	PHEROMONE RECEPTOR (FR	PHEROMONE RECEPTOR (FR	PHEROMONE RECEPTOR (FR	_	PHEROMONE RECEPTOR (FR	PHEROMONE RECEPTOR (FR	×	E RECEPTOR (F45H11.4 PROTEIN.	CALCIUM SENSING RECEPT	$^{\circ}$	PHEROMONE RECEPTOR (FR	PHEROMONE	PUTATIVE PHEROMONE REC	PUTATIVE PHEROMONE REC	PHEROMONE	PUTATIVE PHEROMONE REC	E PHEROMONE	E PHEROMONE	PUTATIVE PHEROMONE REC	PUTATIVE ODORANT RECEP	PUTATIVE PHEROMONE REC	PUTATIVE PHEROMONE REC
	.66e-6	1.04e-68	.81e-6	.66e-6	.58e-6	.53e-6	.41e-7	9.38e-71	.15e-	.27e-7	.03e-	9e-	.03e-	3.54e-90	.72e-	1.79e-101	.59e-	.80e-	-10	.79e-10	.53e-	.47e-	Ļ	1.65e-117

ALIGNMENTS

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Best Local S
Matches 29
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01-MAY-1999 (TrEMBLrel. 10, C.
01-MAY-1999 (TrEMBLrel. 10, L.
01-MAY-1999 (TrEMBLrel. 10, L.
101-MAY-1999 (TrEMBLrel. 10, L.
PUTATIVE TASTE RECEPTOR TR2 (...
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
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Cell
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                                                                                                                              SEQUENCE
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                                                                                                                                                                                                                                       STRAIN-WISTAR;
                                                                                                                                                                                                                                                                     Eutheria;
                                                                                                                                                                      "Putative mammalian taste receptors: a class with distinct topographic selectivity."; Cell 96:541-551(1999).
                                                                                                                                                                                                      ZUKER C.
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                                     GYHLFQAMRLGVEEINNSTALLPNITLGYQLYDVCSDSANVYATLRVLSLPGQHHIELQG
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DLLHYSPTVLAVIGPDSTNRAATTAALLSPFLV-HISYAASSETLSVKRQYPSFLRTIPN
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                                                                                              Similarity
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843 AA;
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llarity 37.5%;
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95799 MW;
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193; |
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(FRAGMENT).
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Pred. No. 0.
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O93553;
O1-NOV-1998 (TrEMBLrel. 08, C
O1-NOV-1998 (TrEMBLrel. 08, L
O1-NOV-1999 (TrEMBLrel. 12, L
PUTATIVE ODORANT RECEPTOR.
CAO Y., OH B.C., STRYER L.;
"Cloning and localization of two multigene recepto
goldfish olfactory epithelium.";
Proc. Natl. Acad. Sci. U.S.A. 95:11987-11992(1998)
EMBL; AF083081; AAC64076.1; -.
PFAM; PF00003; 7tm_3; 1.
PFAM; PF01004; ANF_RECEPTOT; 1.
PRINTS; PR00248; GPCRMGR.
                                                                                                                                                                                                 GFB8.
                                                                                                                                               Carassius auratus (Goldfish).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Neopterygii; Teleostei; Euteleostei; Ostariophysi; C
Cyprinoidea; Cyprinidae; Cyprininae; Carassius.
                                                                                                                        SEQUENCE FROM N.A
                                                                                                MEDLINE;
                                                                                                             TISSUE-OLFACTORY
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SO

SEQUENCE

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RESULT 4
ID 073636;
AC 073636;
DT 01-AUG-1998 (TIEMBLIFE1 0)
DT 01-NOY-1999 (TIEMBLIFE1 1)
DT 01-NOY-1999 (TIEMBLIFE1 1)
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Best Local S
Matches 24
CA02.1.
Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
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Similarity 31.4%;
247; Conservative
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Pred. No. 1.23e-242;
194; Mismatches 309;
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Query Match
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Matches 239; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE; 98226788.
NAITO T., SAITO Y., YA
NAKANISHI S., BRENNER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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Petraodontiformes; Tetraodontoidei; Tetraccontidae; Fugu.
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                                                                                                                                                                               VFFHHRTSPIVRANNSELSFILLFSLTILCFLCSLTFIGAPSHLSCMLRHTAFGITFVLCI
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LLFNFVS-WIAFFTTASVYDGKYLPAANMMAGLSSLSSGFGGY-FLPKCYVILCRPDLNS
                                                     VRNLTTYKERIILECALGSSYGFWAVLGYIGLLAAVCLVLAVLARKLPDNENEAKMITFS
                                                                                                           SCLTVRSFQLIIIFKFSTKVPTFYHA-WVQNHGAGLFVMISSAAQLLICLTWLVVWTPLP
                                                                                                                        SCYLGKT--VVYLMAFRATLPGSNYMKWFGPPQQRMTVVTFTSIQVLICIVWLVVNPPFP
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
Reloostei; Euteleostei; Acanthopterygii; Percomorpha;
Tetraodontiformes; Tetraodontoidei; Tetraodontidae; Fugu.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pheromone.
SEQUENCE
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NAKANISHI S., BRENNER S.;
"Putative pheromone receptors rel
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Local Similarity 30.6%;
les 243; Conservation
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KDIMPFSAQVGDERMQCLMRHLAQAGATVVVVFSSR-QLARVFFESVVLTNLTGKVWVAS
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                                                                                                                                      SFIRTIPNDKYQVETMVILIQKFGWTWISLVGSSDDYGQLGVQALENQALVR-GI-CIAF
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                                     VCCFDCLLCSEGKISNTIDSMECTSCPEDFWSSPQRDHCVPKKTEFLSYHEPLG-ICLTA
                                                                                                                                                                                        EYSFQCKFGASGSAEACTGDENIQQVDAEFLDVSNLRPEYNIYKAVYALAYALDDMLQCE
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                                                                                                                                                                                                                                                                                                                                                                                                EEAFALQGGCAG-SPPVLGIVGDSLSTFTIASASVLGLYKIPMVSYFATCSCLTNRQRFP 192
                                                                        PKWT-FTVLGSSTWSPV---QLNINETKIQWHGKNHQVPKSVCSSDCLEGHQRVVT-GFH
                                                                                                                         AS-E-L---
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ASLLGTVISVVVLGIFIHHRSTPVVRANNSELSFLLLVSLKLCFLCSLL-FIGRPRLWTC
                     HCCFECVPCGAGTFLNKSELYRCQPCGTEEWAPEGSQTCFPRTVVFLALREHTSWVLLAA
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PF00003; 7tm_3; 1.
PF01094; ANF_receptor;
S; PR00248; GPCRMGR.
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                                                                                                                                                                          -SNQLCRE-C--QAFMAHTMPK-LKAFSMSSAYNAYRAVYAVAHGLHQLLGC-
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Pred. No. 1.33e-237;
216; Mismatches 287;
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Last sequence update)
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RESULT 6
ID 073639;
AC 073639;
DT 01-AUG-1998 (
DE PHEROMONE REC
GN CA13.
OS FUGU rubripes
OC Eukaryota; M
OC Neopterygii;
OC Tetraodontifc
RN [1]
OC Tetraodontifc
RN [1]
The SEQUENCE FROM
RX MEDLINE; 9822
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Best Local :
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MEDLINE; 98226788.
NAITO T., SAITO Y., YAM
NAKANISHI S., BRENNER S
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Rigu rubripes (Japanese pufferfish) (Takifugu rubripes).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;

Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorpha;

Tetraodontiformes; Tetraodontoidei; Tetraodontidae; Fugu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proc. Natl. Acad. Sci. U.S.A.
EMBL, AB008861; BAA56126.1; -
PFAM, PF00003; 7'm_3; 1.
PFAM, PF01094; ANT_receptor;
PRINTS; PR00248; GPCRMGR.
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VFQCSLDPHGHSEAKRPCSGTEELRSVKNIYSDVSQLRISYNVYKAVYALAYAIKAMRSC
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                                                                       AWALSRHITGVPGIQRIGM-VLGVAIQKRAVPGLKAFE-EAY-ARAD-KEAP--RPCHKG
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(TrEMBLrel. 07, Last sequence update)
(TremBLrel. 12, Last annotation updat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21.8%; Score 1271; DB larity 30.6%; Pred. No. 8.07e-Conservative 214; Mismatches
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VER S.;
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Pred. No. 8.07e-238;
214; Mismatches 298;
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01-NOV-1998 (TrEMBLrel.
01-NOV-1998 (TrEMBLrel.
01-NOV-1999 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                     PFAM; PF00003; 7tm_3; 1.
PFAM; PF01094; ANF_receptor; 1.
PRINTS; PR00248; GPCRMGR.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes;
Cyprinoidea; Cyprinidae; Cyprininae; Carassius.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Cloning and localization of two multigene receptor goldfish olfactory epithelium.; Proc. Natl. Acad. Sci. U.S.A. 95:11987-11992(1998).
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TISSUE=OLFACTORY EPITHELIUM;
                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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QHHIELQGDLLHYSPTVLAVIGPDSTNRAATTAALLSPFLVH-ISYAASSETLSVKRQYP
                                                    SQDFG-PGNICNGHSPLHAIIGESETSATVILSRTTGPFKIPVISHSSSCECLSNRKNYP 183
                                                                                                               SCS-FNEHGYHLFQAMRLGVEEINNSTALLPNITLGYQLYDVCSDSANVYATLRVLSLPG
                                                                                                                                                     SCSSVNLRDFRLAQTMIFAIQEINKNEILLPNISIGYIIYDTCGSRLST-MTA-TMGLMN 124
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08, Last sequence update)
12, Last annotation updat
                                                                                                                                                                                                                                         209;
                                                                                                                                                                                                                                  Score 1217; DB 13;
Pred. No. 5.15e-226;
209; Mismatches 312;
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  Query Match
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EMBL; AB008857; BAA26122.1; -.
PFAM; PF00003; 7tm_3; 1.
PFAM; PF01094; ANF_receptor; 1.
PRINTS; PR00248; GPCRMGR.
PRINTS; PR00592; CASENSINGR.
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01-AUG-1998 (Tremstrel. 07, Last sequence update)
01-AUG-1998 (Tremstrel. 12, Last sequence update)
01-NOV-1999 (Tremstrel. 12, Last annotation update)
CALCIUM2+ SENSING RECEPTOR.
Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorpha;
Tetraodontiformes; Tetraodontoidei; Tetraodontidae; Fugu.
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                                                                                                                                                                                                                                                                     Fugu."
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NAKANISHI S., BRENNER
"Putative pheromone re
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RESULT 9
ID 073638
AC 073638;
DT 01-AUG-1998
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DT 01-NOV-1999
DE PHEROMONE REC
GN CA12.
OS Fugu rubripe:
OC Eukaryota; M
OC Neopterygii;
OC Tetraodontif
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RP SEQUENCE FROJ
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorpha;
Tetraodontiformes; Tetraodontoidei; Tetraodontidae; Fugu.
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SEQUENCE
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NAITO T., SAITO Y., YAMAMOTO J., NOZAI
NAKANISHI S., BRENNER S.;
"Putative pheromone receptors related
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                                          VVGNYDASQPNGRQFTMNNINITWAARLQKRPLSVCSQSCIPGFRQAVIKGKPICCFTCV
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                     LILKPEKNTKKH
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
Neopterygii; Teleostei; Euteleostei; Raanthopterygii; Percomorpha;
Tetraodontiformes; Tetraodontoidei; Tetraodontidae; Fugu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proc. Natl. Acad. Sci. U.S.A. EMBL; AB008852; BAA56127.1; -. PFAM; PF00003; 7Tm_3: 1. PFAM; PF01094; ANF_Teceptor; 1 PRINTS; PR00248; GPCRMGR.
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MEDLINE; 98226788.
NAITO T., SAITO Y., YAMAHOTO J.,
NAKANISHI S., BRENNER S.;
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                                                 LILGTA-GLFAWHLDTPVVRSAGGRLCFLMLGSLAAGSGSLYGFFGEPTRPACLLRQALF
                                                                                               VVTTAVFVVFLHYRHTPMVRANNSELSFLLLLSLKLCFLCSLVFIGRPSVWSCRFQQAAF
                                                                                                                                                VPCGAGTFLNKSELYRCQPCGTEEWAPEGSQTCFPRTVVFLALREHTSWVLLAANTLLLL
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RESULT 11

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Matches 23
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RYBA N.J.P., TIRINDELLI R.;
Submitted (MAR-1998) to the EMBL,
EMBL; AF053986; AAC08413.1; -.
PFAM; PF00003; 7tm.3; 1.
PFAM; PF01094; ANE_receptor; 1.
PFAM; PF01094; GPCRMGR.
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les 231; Conservative
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                                                                                                                                                                                            AWITSALIAKPEYFPYFGGTIGFATPRSVIPGLKEFLYDVHPNKDPNDVLTIEFWQTAFN
                                                -SWC-SS---N--Q---LC-RECQAF-MA-H--T----MPKLK-AF-SMS-
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224; 1
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Pred. No. 1.59e-177;
224; Mismatches 291;
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thi; Muridae;
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we: Murinae;
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                                                -SAYNAYR-
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                                                                                                                                                     Matches
                                                                                                                                                                  Query Match
Best Local
                                                                                                                                                                                                         RYBA N.J.P., TIRINDELLI R.;
Submitted (MAR-1998) to the EM
EMBL; AF053985; AAC08412.1; -.
PFAM; PF000003; 7tm_3; 1.
PFAM; PF01094; ANE_receptor; 1
SEQUENCE 855 AA; 96215 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     070409;
070409;
01-AUG-1998;
01-AUG-1998;
01-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                             TISSUE-VOMERONASAL NEURONS; MEDLINE; 97436753.
RYBA N.J., TIRINDELLI R.;
                                                                                                                                                                                                                                                                                           TISSUE-VOMERONASAL NEURONS;
                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PUTATIVE PHEROMONE RECEPTOR
                                                                                                                                                                                                                                                                                                                                     Neuron
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                                                                   138
           198 TAALYQ-GIVQLLLY-FTWIWVGLVVPDDMRGELYLRDITKEMISHGICFAFAEKVTEYS
                                           69
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                                                                                                                        79
                                                                                                                                                                                                                                                                                                                                  BA N.J., TIRINDELLI R.;
new multigene family of putative
uron 19:371-379(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LYNGLLSISAFACSYLGKDLPENYNEAKCYTFSLLFNFVSWIAFFTTASVYDGKYLPAAN
                                                                CRPEKTDKLVAVIGGISTSISIQISRVLSLYNVPQISYAPFDQILGTRVQLQSPYQFSMH 197
                                                                                                                        YOHILAMVFAIEKINKDPNILFNKSLGFFLFNVNFIEMKAAEGSMAL-LSGESPPIPNYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MMAGLSSLSSGFGGY-FLPKCYVILCRPDLNSTE 761
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S-GSLYGFFGEPTRPACLLRQALFALGFTIFLSCLTVRSFQLIIIFKFSTKVPTFYHAWV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VLSSLL-FIGKPCNWSCMARQITLALGFCLCLSSILGKTISLFFAYRISVSKTRLI-S-M
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                                                                                             YHLFQAMRLGVEEINNSTALLPNITLGYQLYDVCSDSANVYATLRVLSLPGQ-HHIELQG
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                                                                                                                                                                 h 16.2%;
Similarity 28.3%;
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(TrEMBLIEL. 07,
(TrEMBLIEL. 10,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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W.
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Pred.
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Last sequence update)
Last annotation updat
V2R1.
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                                                                                                                                                  re 946; DB 11;
11. No. 3.72e-167;
Mismatches 313;
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Indels 49;
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RESULT 13
ID 035269
AC 035269
AC 035269
AC 035269
AC 01-JAN-1998 (TIEMBLIEL 05, L2
DT 01-JAN-1998 (TIEMBLIEL 05, L2
DE PUTATIVE PHEROMONE RECEPTOR.
GN GO-VNS.
OS RATUS ONTYPEGICUS (RAT).
OC EUKHATYOTA; Metazoa; Chordata;
OC EUKHATIA; RODANLEY;
RN [1]
RP SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
RN SEQUENCE FROM N.A.
RA HERRADA G., DULAC C.;
RA HERRADA G., 
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Query Match
Best Local Similarity
                                                                                                     MEDLINE; 97433086.

HERRADA G., DULAC C.;

"A novel family of putative pheromone receptors in mammals with topographically organized and sexually dimorphic distribution."; cell 90:763-773(1997).

EMBL; AFO16182; AAC53329.1; -.

PFAM; PF00003; 7tm_3; 1.

PFAM; PF01094; ANF_receptor; 1.
                                                                                                                                                                                                                                                                                                                                                                                               GO-YND.

Rattus norvegicus (Rat).

Rukaryota; Metazoa; Chordata; Craniata; Vertebrata;

Eukaryota; Metazoa; Criuroqnathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            638
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RESULT IN RESULT OF ACCORD OF COLUMN ACCORD RESULT OF 
 SEQUENCE FROM N.A.

O'HARA P.J.;
Submitted (JAN-1996) to the EMBL/GenBank EMBL;
EMBL; U47331; AAA88788.1;
PROSITE; PS00980; G_PROTEIN_RECEP_F3_3;
PROSITE; PS009979; G_PROTEIN_RECEP_F3_1;
                                                                                                                                        RATHUS NOTVEGICUS (Rat).
RATHUS NOTVEGICUS (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eukaryota; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                              LT 14
062916 PRELIMINARY: PRT; 983 AA.
062916;
01-NOV-1996 (TREMBLrel. 01, Created)
01-NOV-1996 (TREMBLrel. 01, Last sequence up
01-NOV-1999 (TREMBLE) 112, Last annotation
METABOTROPIC GLUTAMATE RECEPTOR 4B.
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Best Local
Matches 2
 093555
093555;
093555;
01-NOV-1998
01-NOV-1998
01-MAY-1999
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PFAM; PF01094; ANF_receptor; 1
PRINTS; PR00248; GPCRMGR.
PRINTS; PR00593; MTABOTRODICR.
SEQUENCE 983 AA; 109276 MW;
                                                                                                                                                                                              832
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                                                                                                                                                                                                                                                                                                                                                                                                              RIFLGLGMSISYAALLTKINRIYRIFBQGKRSVSAPRFISPASQLAITFILIS--LQLLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VVGIAATLFVVVTFVRYNDTPIVKASGRELSYVLLAGIFLCYATTFLMIAEPDLGTCSLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WHCEPC-TG-YQYQVDRYTCXTCPYDMRPTENRTSCQPIPIVKLE-WD-SPWAVLPLFLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QSVKIPREPKTGEFDKI--IKRLLETSNARGIIIFANEDDIRRVLEAARRANQTGHFFWY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NEHGYHLFQAMRLGVEEINNSTALLPNITLGYQLYDVCS-DSANVYATLR-VLSLPGQHH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KEKGIHRLEAMLFALDRINNDPDLLPNITLGARILDTCSRDTHALEQSLTFVRALIEKDG
                                                                                                                                                        SGFGGYFLPKCYVIL
                                                                                                                                                                                              VSLGMLYMPKVYIIL
                                                                                                                                                                                                                                                          IKTRGVPETFNEAKPIGFTMYTTCIVWLAFIPIFFGTSQSADKLYIQTTTLTVSVSLSAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TLLLLLLGTAGLFAWHLDTPVVRSAGGRLCFLMLGSLAAGSGSLYGFFGEPTRPACLLR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -G-CAS--ELCSR-GRVYPWQLLEQIHKVHFL-LHKDTVAFNDNRDPLSSYNIIAWD-WN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RDLCPGRVGLCPRMDPVDGTQLLKYIRNVNFSGIAGNPVTFNENGDAPGRYDIYQYQLRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FKDIMPFSAQVGD-ERWQCLMRHLAQAGATVVVVFSSRQLARVFFESVVLINLTGKV-WV
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                                                                                                                                                                                                                                  YLGKDLPENYNEAKCVTFSLLFNFVSWIAF
                                                                                                                                                                                                                                                                                                                             ICV-WFVVDPSHSVVDFQDQRTLDPRFARGVLKC-DISDLSLICLLGYSKLLMVTCTVYA
                                                                                                                                                                                                                                                                                                           ICLTWLVVWTPLPAREXQ--R-F-PHLV--MLECTETNSLGFILAFLYNGLLSISAFACS
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 (TrEMBLrel.) (TrEMBLrel.)
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larity 27.3%;
Conservative
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d. No. 3.21e-145;
Mismatches 287;
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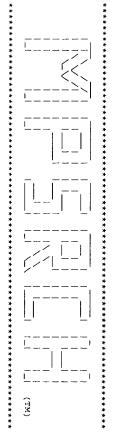
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Search completed: Fri Mar 17 13:35:21 2000 Job time: 240 secs.
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Best Local S
Matches 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Cloning and localization of two multigene receptor families goldfish olfactory epithelium.";
Proc. Natl. Acad. Sci. U.S.A. 95:11987-11992(1998).
EMBL; AF083084; AAC64079.1; -.
PFAM; PF00003; 7tm_3; 1.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
Neopterygii; Teleostei; Eutaleostei; Ostariophysi; Cypriniformes;
Cyprinoidea; Cyprinidae; Cyprininae; Carassius.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE 458 AA; 51119 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAO Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-OLFACTORY EPITHELIUM; MEDLINE; 98426265.
                                                                                                                                                                                                                                                                                                                                361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                324 NAYRAYYAYAHGLHQLLGCASEL-CSRG-RYYPWQLLEQIHKYHFLLH-KDTVAFNDNRD 380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14.48;
Local Similarity 30.98;
les 139; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 NVYKAVYAVAHSLHSLLNCKEQTGCEKSLTIQPKHVVEALKKVNFTVKFGDHVWFDSTGG 62
                                                                                                                                                                                                                                                                                              AGLFVMISSAAQLLICLTWLVVWTPLPAREYQRFPHLVMLECTETNSLGFILAFLYNGLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LALREHTSWVLLAANTLLLL-LLLGTAGLFAWHLDTPVVRSAGGRLCFLMLGSLAAGSGS 554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CPPGTRKAAQKGRPVCCYDCIPCAEGEISNETDSINCKQCPGEYWPNAEKNKCVLKAVEF 182
                                                                                                                                                                                           AS-SFGLLFCIFAPKCYIILLKSDQNTKQH 448
                                                                                                                                                                                                                                                                                                                                                                                                                                      QRFSVLAFTLIQVLICLLWLTISPPYPHKNMKYYKEKIIIECSLRSTLGFWAVLGYVGLL 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LYGFFGEPTRPACLLRQALFALGFTIFLSCLTVRSFQLIIIFKFSTKVPTFYHAWVQNHG 614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SLTFIGRPTEWSCMLRHTAFGITFVLCISCILGKTMVVLMAFK-ATLPGSNVMKWFGPAQ 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLEGHQRVV-TGFHHCCFECVPCGAGTFLNKSELYRCQPCGTEEWAPEGSQTCFPRTVVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AVAHYEVVNWQQDSNRSLQFKPVGYFDTSLPPDQSFMLKTENVIWAGGQLEKPRSVCSES 122
                                                                                                                          SSLSSGFGGY-FLPKCYVILCRPDLNSTEH
                                                                                                                                                                                                                                                            SISAFACSYLGKDLPENYNEAKCYTFSLLFNFVS-WIAFFTTASVYDGKYLPAANMMAGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Score 838; DB 13;
; Pred. No. 6.20e-144;
119; Mismatches 177;
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tabular output not generated. Fri Mar 17 13:29:20 2000; MasPar time 43.87 Seconds 528.906 Million cell updates/sec

Description: Perfect Score: >US-09-361-652-3 (1-777) from US09361652.pep 5838 1 RSCSFNEHGYHLFQAMRLGV...

Sequence: RSCSFNEHGYHLFQAMRLGV.....NSTEHFQASIQDYTRRCGST 777

Scoring table: PAM 150 Gap 11

Searched: 82229 seqs, 29854865 residues

Post-processing: Minimum Match 0\$ Listing first 45 summaries

Database: swiss-prot38 1:swissprot

Statistics: Mean 53.443; Variance 92.251; scale 0.579

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	œ	7	o	ر. د	4	ω	2	L	Result
150	333	452	674	675	714	718	731	729	757	761	768	772	787	789	796	796	798	846	856	1158	1160	1170	Score
2.6	5.7	7.7					12.5							13.5			13.7				19.9		Query Match 1
986	999	976	915	915	877	879	877	871	806	872	908	908	1194	872	1212	1199	1203	912	912	1079	1078	1085	Length
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CYGR_ARBPU	MGR1_CAEEL	MGR_DROME	MGR7_RAT	MGR7_HUMAN	MGR3_HUMAN	MGR3_RAT	MGR6_HUMAN	MGR6_RAT	MGR8_HUMAN	MGR2_HUMAN	MGR8_RAT	MGR8_MOUSE	MGR1_HUMAN	MGR2_RAT	MGR5_HUMAN	MGR1_RAT	MGR5_RAT	MGR4_HUMAN	MGR4_RAT	CASR_RAT	CASR_HUMAN	CASR_BOVIN	ID
RESACT RECEPTOR PRECUR	PROBABLE METABOTROPIC	METABOTROPIC GLUTAMATE		METABOTROPIC GLUTAMATE	EXTRACELLULAR CALCIUM-	EXTRACELLULAR CALCIUM-	EXTRACELLULAR CALCIUM-	Description															
_	.05e-	2.	4.50e-12	2.64e-12	: 2.18e-	2.54e-130	2.32e-	6.82e-13	1.90e-13	2.19e-14	4.99e-	5.74e-14	1.72e-14	5.82e-14	1.31	1.31e-14	4	2.13e-16		.09e-23	- 2.67e-235	1.05e-237	Pred. No.

44	43	42	41	40	39	38	37	36	35	34	ω ω	32	31	30	29	28	27	26	25	24
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TRANSCRIPTION-REPAIR C INOSITOL 1,4,5-TRISPHO		EPITHIN (EC 3.4.21).	SPORULATION-SPECIFIC S	TRANSMEMBRANE PROTEIN	ARSENICAL PUMP MEMBRAN	ARSENICAL PUMP MEMBRAN	EPS I POLYSACCHARIDE E	BISPHOSPHOGLYCERATE MU	NADH-UBIQUINONE OXIDOR	NADH-UBIQUINONE OXIDOR	NACH-UBIQUINONE OXIDOR	CHITIN SYNTHASE 1 (EC	HYPOTHETICAL AMINO-ACI	C-C CHEMOKINE RECEPTOR	INOSITOL 1,4,5-TRISPHO	HYPOTHETICAL 61.2 KD P	GLUTAMATE [NMDA] RECEP	GLUTAMATE [NMDA] RECEP	GLUTAMATE [NMDA] RECEP	SPERACT RECEPTOR PRECU
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G-protein coupled receptor; Transmembrane; Glycoprotein; Signal. SIGNAL 1 19 POTENTIAL.	E; PS00981; G_PROTEIN_RECEP_F3_3; PE01004; 7tm_3; 1.	PS00980; G_PROTEIN_RECEP_F3_	-	40476; S40476.	S67307; AAB29171.1;	or send an email to license@isb-sib.ch).	license agreement (See http://w	ified and this statement is not removed. Usage by and for commerc	use by non-profit institutions as long as its content is in no way	veen the Swiss Institute of Bioinformatics and the EMBL outstatic	uced throug	1	!- SIMILARITY: BELONGS TO FAMILY 3 OF G-PRO	-!- SUBCELLULAR IOCATION: INTEGRAL MEMBRANE PROTEIN.	MESCRUCER SYSTEM	MILCIAC TACHLOCHENAL BARROUGH CHILL AND CHILL STORY OF THE STORY OF TH	THE EXTRACELLULAR CONCENTRATION	ure 366:575-580(1993).	from bovine parathyroid	rization of	LYTTON J., HEBERT S.C.;	BROWN E. M. GAMBA G. RICCARDI D. LOMBARDI M. BUTTERS R. KIFOR O.	TISSUE=PARATHYROID;	SEQUENCE FROM N.A.		Bos.	Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae;	Wotaraa Chambata Canadata Wastabata	R OR PCAR1.	ENSING RECEPTOR).	AR CALCIUM-SENS	(Rel. 34, Last	U1-JUN-1994 (Rel. 29, Created) O1-JUN-1994 (Rel. 29, Last sequence update)		CASR_BOVIN STANDARD; PRT; 1085 AA.	P

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MEDLINE; 95179179.

POLLAK M.R., BROWN E.M., EST
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"Autosomal dominant hypocalc
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                                                                                                                                   POLLAK M.R., BROWN E.M., CHOU Y.H., HEBERT S.C., STEINMANN B., LEVI T., SEIDMAN C.E., SEIDMAN J.C. "Mutations in the human Ca(2+)-sensing receptor hypocalciuric hypercalcemia and neonatal severe hyperparathyroidism."; Cell 75:1297-1303(1993).
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PEARCE S.
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J. Biol. Chem. 270:12919-12925(1995).
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GARRETT J.E., CAPU
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HEBERT S.C., NEMETH E.F., FULLER F.;
"Molecular cloning and functional expression
calcium receptor CDNAs";
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Hum. Mutat. 10:233-235(1997).
-!- FUNCTION: SENSE CHANGES IN THE EXTRACELLULAR CONCENTRATION OF
CALCIUM IONS. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY A
G-PROTEIN THAT ACTIVATES A PHOSPHATIDYLINOSITOL-CALCIUM SECOND
MESSENGER SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BARON J., WINER K.K., YANOVSKI J.A., CUNNINGHAN ZIMMERNAN D., CUTLER G.B. JR.;
"Mutations in the Ca(2+)-sensing receptor gene dominant and sporadic hypoparathyroidism.";
Hum. Mol. Genet. 5:601-606(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE; 95243222.
CHOU Y.-H.W., POLLAK M.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE; 96292
PEARCE S.H.S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Calcium-sensing receptor mutations and neonatal hyperparathyroidism.";
J. Clin. Invest. 96:2683-2692(1995).
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J. Clin. Endocrinol. Metab. 80:2594-2598(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WARD B.K., STUCKEY B.G.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VARIANT FHH ARG-174.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VARIANTS NSHPT LEU-227 AND TYR-598.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 1-61 FROM N.A., AND VARIANT FHH ALA-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEIDMAN C.E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         novel mutation (L174R) in the Ca2+-sensing
                                                                                                                                                                                                                                                                                                                                                                TISSUE SPECIFICITY: FOUND IN KIDNEY, BUT NOT IN BRAIN, LUNG, LIVER, HEART, SKELETAL MUSCLE, OR PLACENTA.

DISEASE: DEFECTS IN CASR ARE A CAUSE OF FAMILIAL HYPOCALCIURIC PROPERCALCEMIA (FH) AND NEONATAL SEVERE HYPERPARAHYROLDISM (NSPT), TWO INHERITED CONDITIONS CHARACTERIZED BY ALTERED CALCIUM HOMEOSTASIS. THE MUTATIONS REDUCE THE ACTIVITY OF THE RECEPTOR. FHH AFFECTED INVITUDALS EXHIBIT MILD OR MODEST HYPERCALCEMIA, RELATIVE HYPOCALCIURIA, AND INAPPROPRIATELY NORMAL PTH LEVELS. IN CONTRAST, NSHPT IS A RARE AUTOSOMAL RECESSIVE LIFE-THREATENING DISORDER CHARACTERIZED BY VERY HIGH SERUM CALCIUM CONCENTRATIONS, SKELETAL DEMINERALIZATION, AND BARATHYROID HYPERPLASIA. IN SOME INSTANCES NSHPT HAS BEEN DEMONSTRATED TO BE THE HOMOZYGOUS FORM OF
DISEASE: DEFECTS IN PCAR1 ARE ALSO THE CAUSE OF AUTOSOMAL DOMINANT HYPOPARATHYROIDISM (ADHP). ADHP IS CHARACTERIZED BY HYPOCALCEMIA AND HYPERPHOSPHATEMIA DUE TO INADEQUATE SECRETION OF PARATHYROID HORMONE. SYMPTOMS ARE SEIZURES, TETANY AND CRAMPS.

SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                 FHH.
DISEASE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN ALTERNATIVE PRODUCTS: TWO ISOFORMS SEEM TO BE PARTICULAR OF THE PROPULATION OF 
                                                                                                                                                                                CA(2+) LEVELS.
DISEASE: DEFECTS
                                                                                                                                                                                                                                                                HYPOCALCEMIA
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Genet. 8:303-307(1994)
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                                                                                                                                                                                                                                                                                                 DEFECTS
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                                                                                                                                                                                                                                                       ECTS IN CASR ARE ALSO THE CAUSE (ADH) IN WHICH THE RECEPTOR IS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                D.
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PATERSON C.R.,
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PROSITE; PS00979; G_PROTEIN_RECEP_F3_1; PROSITE; PS00980; G_PROTEIN_RECEP_F3_2; PROSITE; PS00981; G_PROTEIN_RECEP_F3_3;
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7745
7745
7769
7969
805
805
807
805
                                      66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   I (POTENTIAL).
CYTOPLASMIC (PO
II (POTENTIAL).
EXTRACELLULAR (
III (POTENTIAL)
                                                                                                                                                                                                                                                                                                                              Transmembrane; Glycoprotein; Signal; ve splicing; Polymorphism.
                                                                                                                                                                                                                            IV (POTENTIAL).
EXTRACELLULAR (1
V (POTENTIAL).
                                             /FTId=VAR_003585.
R -> M (IN MILD F)
/FTId=VAR_003586.
                                                                                                       POTENTIAL.
POTENTIAL.
POTENTIAL.
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                                                                                                                                                                 POTENTIAL.
      /FTId=VAR_003588
E -> A (IN ADH).
                                                                                                                                                                                                  VI (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                    CYTOPLASMIC
                                                                                                                                                                                                                                                      CYTOPLASMIC
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                                                                                                                                                                                                                                                                                                                EXTRACELLULAR CALCIUM-SENSING RECEPTOR
                      R -> C (IN FHH).
/FTId=VAR_003587
A -> T (IN ADHP)
                                                                                        POTENTIAL
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                                                                                                                                                                                   CYTOPLASMIC
                                                                                                                                                                                            VII (POTENTIAL
                                                                        -> EPLTFVLSVLQ
-> A (IN FHH).
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                                                                                SECOND ISOFORM).
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Note: remainder of annotations omitted.

SWISS-PROT entry is copyright.

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produced through a collaboration

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Matches 26
                             01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
EXTRACELULAR CALCIUM-SENSING RECEPTOR PRECURSOR
CELL CALCIUM-SENSING RECEPTOR).
CASR OR PCARL.
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chor
                                                                                                                                           CASR_RAT
                                                                                                                                                                                                         718
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C-SFNEHGYHLFQAMRLGVEEINNSTALLPNITLGYQLYDVCSDSANVYATLRVLSLPGQ
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                                                                                                                                                                                                         VYDGKYLPAANMMAGLSSLSSGFGGY-FLPKCYVILCRPDLNSTE
                                                                                                                                                                                                                                                                                                                                                                                                                LLLFSLLCCFSSSLF-FIGEPQDWTCRLRQPAFGISFVLCISCILVKTNRVLLVFE--AK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GEQVTFDECGDLVGNYSIINWHLSPEDGSIVFKEVGYYNVYAKKGERLFINEEKILWSGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HHIE-LQ-GDLLHYS---PTVLAVIGPDSTNRAATTAALLSPFLV-HISYAASSETLSVK
                                                                                                                                                                                                                                     TY-GKEVSAVEVIAILAA-SEGLLACIFENKIYIILEKPSRNTIE
                                                                                                                                                                                                                                                                    SLGFILAFL--YNGLLSISAFACSYLGKDLPENYNEAKCVTFSLLFNFVSWIAFFTT-AS
                                                                                                                                                                                                                                                                                                  SL-MALGELIGYTCLLAAICFFFAFKSRKLPENFNEAKFITFSMLIFFIVWISFIPAYAS
                                                                                                                                                                                                                                                                                                                                   VPT-FYHAWVQNHGAGLFVMISSAAQLLICLTWLVVWTPLPAREYQRFPHLVMLECT
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                                                                                                                                                                                                                                                                                                                                                                                              LMLGSLAAG-SGSLYGFFGEPTRPACLLRQALFALGFTIFLSCLTVRSFQLIIIFKFSTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                             GSQTCFPRTVVFLALREHTSWVLLAANTLLLLLLLG-TAGLFAWHLDTPVVRSAGGRLCF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NHTSCIAKEIEFLSWTEPFG-IALTLFAVLGIFLTAFVLGVFIKFRNTPIVKATNRELSY 652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NHQVPKSVCSSDCLEGHQR-VVTGFHHCCFECVPCGAGTFLNKSELYRCQPCGTEEWAPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EAYA-R-ADKE-APRPCH---KGSWCSSNQLCRECQAF--M-A--HTMPKLKA----FS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ETFNCHLQEGAKGPLPYDTFLRGHEESGDRFSNSSTAFRPLCTGDENISSVETPYIDYTH 413
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AFKDIMP-FSAQVGDERMQCLMRHLAQAGATVVVVFSS-RQLARVFFESVVLTNLTGKVW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DFSELISQYSDE--EE-IQHVVEVIQNSTAKVIVVFSSGPDLEPLIKE-IVRRNITGKIW 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RQYPSFLRTIPNDKYQVETMVLLLQKFGWTWISLVGSSDDYGQLGVQALENQALVRGICI 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NQFKSFLRTIPNDEHQATAMADIIEYFRWNWVGTIAADDDYGRPGIEKFREEAEERDICI 237
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263; Conser
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larity 31.9%;
Conservative
                                                                                                                                           STANDARD;
Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               232;
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Pred. No. 2.67e-235;
232; Mismatches 250;
Craniata;
                                                                                                                                           PRT;
                                                                                                                                         1079
Vertebrata;
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                                                            (CASR) (PARATHYROID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                       870
Mammalia;
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                                                                                            CARBOHYD
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CARBOHYD
CARBOHYD
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SIGNAL
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TRANSMEM
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RUAT M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eutheria;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE: PS00979; G_PROTEIN_RECEP_F3_1; PROSITE: PS00980; G_PROTEIN_RECEP_F3_2; PROSITE: PS00981; G_PROTEIN_RECEP_F3_3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proc. Natl. Ac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Calcium sensing receptor: molecular cloning in to nerve terminals.";

proc Na+1 "--"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RICCARDI D., PARK J., LEE W., GAMBA G., BROWN E "Cloning and functional expression of a rat kidi calcium/polyvalent cation-sensing receptor."; Proc. Natl. Acad. Sci. U.S.A. 92:131-135(1995).
                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                   PFAM; PF00003; 7tm_3; 1.
PFAM; PF01094; ANF_receptor; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U10354; AAC52149.1; -. EMBL; U20289; AAC52195.1; -.
                                              SEQUENCE
                                                                                                                                                                                                              TRANSMEM
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                                                                                                                                                                                                                                                                                                      TRANSMEM
                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                          GCRDB; GCR_1449; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-SPRAGUE-DAWLEY;
                                                                                                                                                                                       TRANSMEM
                                                                                                                                                                                                  DOMAIN
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                                                                                                                                                                                                                                                          TRANSMEM
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                                                                                                                                                                                                                                   CRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NOC. Natl. Acad. Sci. U.S.A. 92:3161-3165(1995).
FUNCTION: SENSE CHANGES IN THE EXTRACELULAR CONCENTRATION OF CALCIUM IONS. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY A G-PROTEIN THAT ACTIVATES A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM.
SUBCELLULAR IOCATION: INTEGRAL MEMBRANE PROTEIN.
SUBCELLULAR IOCATION: INTEGRAL MEMBRANE PROTEIN.
              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95116508
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638
650
671
682
701
  arity 31.4%;
Conservative
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769
792
805
828
836
836
1079
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612
635
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670
681
700
724
                         19.8%;
                                               120867
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  Pred.
233; 1
                                               MW;
Score 1158; DB 1;
Pred. No. 8.09e-235;
233; Mismatches 261;
                                                                                                                                                                                                                                                                                                                                                                       Transmembrane;
                                                                     POTENTIAL.
                                                                                           POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                         POTENTIAL.
                                                                                                                                                                                                                                                                      CYTOPLASMIC
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                                                           POTENTIAL
                                                                                                                                                                           CYTOPLASMIC
                                                                                                                                                                                                  VI (POTENTIAL)
EXTRACELLULAR
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                                                                                                                                                                                                                                                                                                      II (POTENTIAL).
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                                               34118BE9 CRC32;
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                                                                                                                                                                                                                                                                                                                                                   CALCIUM-SENSING RECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                        Glycoprotein; Signal
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                                                                                                                                                                                                                                                                                          (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                        (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    kidney
                      Length 1079;
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262;

Indels

78;

Gaps

55;

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В 20 Вb 20 B

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RESULT
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                                                                                                                                                                                                                                                             MGR4_RAT STANDARD;
P31423;
01_JUL-1993 (Rel. 26, Cr
01_JUL-1993 (Rel. 26, La
15_JUL-1999 (Rel. 38, La
METABOTROPIC GLUTAMATE R
TISSUE=BRAIN;
MEDLINE; 92110002
                                                                                                                                                                                                                                     GRM4 OR MGLUR4
                                                                                                                                                                                                  Rattus
                                                                                                                                    Eutheria; Rodentia;
                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            719
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          601
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ota; Metazoa;
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TAMATE RECEPTOR '
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a coefficient the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              O'HARA P.J., SHEPPARD P.O., THOGERSEN H., VENEZIA D., HALDEMAN MCGRANE V., HOUMED K.M., THOMSEN C., GILBERT T.L., MULVIHILL E "The ligand binding domain in metabotropic glutamate receptors related to bacterial periplasmic binding proteins.";
Neuron 11:41-52(1993).
-!- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEIS MEDIATED BY A G-PROTEIN THAT INHIBITS ADENYLATE CYCLASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TANABE Y., MASU M., ISHII T., SHIGEMOTO R., NAKA "A family of metabotropic glutamate receptors."; Neuron 8:169-179(1992).
                                                                                                                                                                                                                                                                                               G-protein
Multigene
                                                                                                                                                                                                                                                                                                                            PROSITE; PS00981; G_PROTEIN_RECEP_PFAM; PF00003; 7tm_3; 1.
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EMBL; M90518;
                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                        TRANSMEM
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TISSUE SPECIFICITY: IS WIDELY DISTRIBUTE IN THE CNS.
EXPRESSION IS SEEN IN THE GRANULE CELLS OF THE CEREBEI
SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED I
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KEKGIHRLEAMLFALDRINNDPDLLPNITLGARILDTCSRDTHALEQSLTFVQALIEKDG
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                             Similarity
                                                                                                                                                                                                                                                                                               fami
                                                                           JH0563.
                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                               -; NOT_ANNOTATED_CDS.
AAA93190.1; -.
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CYTOPLASMIC (PC
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EXTRACELLULAR
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Q -> R (IN R
W; 95F3E7D6
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I (POTENTIAL).
CYTOPLASMIC (PI
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IV (POTENTIAL)
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01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-DEC-1999 (Rel. 39, Last annotation update)
METABOTROPIC GLUTAMATE RECEPTOR 4 PRECURSOR.
                       MEDLINE; 96346635.

MAROFF A., LELCHUK R., OXER M.,

"Molecular characterization and
glutamate receptor type 4.";
                                                                                                                                                                                                                                   Eutheria; Primates;
                                                                                                                                                                                                                                                        Homo sapiens (Human)
Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MGR4_HUMAN
                                                                                                                                               TISSUE-BRAIN;
                                                                                                                                                                       SEQUENCE FROM N.A.
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-G-CAS--ELCSR-GRVYPWQLLEQIHKVHFL-LHKDTVAFNDNRDPLSSYNIIAWD-WN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YLGKDLPENYNEAKCVTFSLLFNFVSWIAF - - - FTTASVYDGK - YLPAANMAGLS - SLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ICV-WFVVDPSHSVVDFQDQRTLDPRFARGVLKC-DISDLSLICLLGYSMLLMVTCTVYA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GPKWTFTVLGSSTWSPVQLNINETKIQWHGKNHQVPKSVCSSDCLEG-HQRVVTGFHHCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ICLTWLVVWTPLPAREYQ--R-F-PHLV--MLECTETNSLGFILAFLYNGLLSISAFACS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                             Chordata; Craniata; Vertebrata; Mammalia; Catarrhini; Hominidae; Homo.
  Res.
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                                                     HARRINGTON K., I localization of
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                                                        metabotropic
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[2]
SEQUENCE FROM N.A.
MEDLINE; 98141892.
WU S., WRIGHT R.A.,
                                                                        TRANSMEM
DOMAIN
TRANSMEM
          CARBOHYD
CARBOHYD
                               CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                    G-protein
Multigene
                                                                                                                                                                                                                                                                                                         PROSITE;
                                                                                                                                TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE; 95342351.
FLOR P.J., LUKIC S., RUEEGG D., LEONHARDT T., KNOEPFEL T., KUHN R., "Molecular cloning, functional expression and pharmacological characterization of the human metabotropic glutamate receptor type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ROSTECK P.R. JR., JOHNSON B.G., SCHOEPP D.D., BELAGAJE "Group III human metabotropic glutamate receptors 4, 7 molecular cloning, functional expression, and compariso pharmacological properties in RGT ceils.", Brain Res. Mol. Brain Res. 53:88-97(1998).
                                                                                                                                                                                                                                                                        PFAM; PF01094; ANF_receptor; 1.
                                                                                                                                                                                                                                                                                                                                                            EMBL; X80818;
EMBL; U92457;
SEQUENCE
                                                     CARBOHYD
                                                                                                                                                                           DOMAIN
                                                                                                                                                                                     TRANSMEM
                                                                                                                                                                                                           TRANSMEM
                                                                                                                                                                                                                                                                                               PROSITE;
                                                                                                                                                                                                                                                                                                                                MIN;
                                                                                                                                                                                                                                                                                                                                       GCRDB; GCR_2069; -
                                                                                                                                                                                                                                                                                                                                                   GCRDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Neuropharmacology 34:149-155(1995).
                                                               DOMAIN
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                                                                                                                    TRANSMEM
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                                                                                                                                                                                                                                          SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SÜBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
TISSUE SPECIFICITY: STRONGLY EXPRESSED IN THE CEREBELUM.
EXPRESSED AT LOW LEVELS IN HIPPOCAMPUS, HYPOTHALAMUS AND
THALAMUS. NO EXPRESSION DETECTED IN LIVER.
SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
STRONGEST, TO MGLURG.
                                                                                                                                                                                                                                                                                                                                604100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIATED BY
                                                                                                                                                                                                                                                                                            PS00979; G_PROTEIN_RECEP_F3_1;
PS00980; G_PROTEIN_RECEP_F3_2;
PS00981; G_PROTEIN_RECEP_F3_3;
                                                                                                                                                                                                                                                    coupled receptor;
family.
                                                                                                          588
611
625
646
657
657
700
721
751
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AAB51762.1;
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           ROCKEY P.K.,
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                                                                                                                                                                                                                                                               Transmembrane;
          POTENTIAL.
                              POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                              EXTRACELLULAR (POTENTIAL) VII (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                       EXTRACELLULAR V (POTENTIAL)
                                                                                                                                                                                                CYTOPLASMIC
                                                                                                                                                     CYTOPLASMIC
                                                                                                                                                                 EXTRACELLULAR III (POTENTIA:
                                                                                                                                                                                                           EXTRACELLULAR I (POTENTIAL)
                                                                                                VI (POTENTIAL)
                                                                                                           CYTOPLASMIC
                                                                                                                                           IV (POTENTIAL)
                                                                                                                                                                                                                                METABOTROPIC GLUTAMATE RECEPTOR
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                                                                                                                    (POTENTIAL)
                                                                                                                                                                                     (POTENTIAL)
740D9054
                                                                                                                                                                 (POTENTIAL
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 CRC32;
                                                                                                                                                    (POTENTIAL).
                                                                                                         (POTENTIAL).
                                                                                                                                                                                               (POTENTIAL).
                                                                                                                               (POTENTIAL)
                                                                                                                                                                                                                                                               Glycoprotein;
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and 8:
                                                                                                                                                                                                                                                               Signal;
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Query

Match

Score

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DB

Length

912;

MIZUNO N., NAKANISHI

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RECEPTORS IBOTENATE

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Matches
                                                                                                         MGR5_RAT STANDARD;
P31424;
01-JUL-1993 (Rel. 26, Cr
01-NOV-1995 (Rel. 32, La
15-DEC-1999 (Rel. 39, La
METABOTROPIC GLUTAMATE R
                                                                           Rattus norvegicus (Rat).
                                          Eutheria;
                                                         Eukaryota;
       SEQUENCE
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                                                                                                                                                                                                                                                                         GFGGYFLPKCYVILCRPDLN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LLLLLLGTAGLFAWHLDTPVVRSAGGRLCFLMLGSLAAGSGSLYGFFGEPTRPACLLRQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W-EDNFHCKLSRHALKKGSHVKKCTNRERIGQDSAYEQEGKVQFVIDAVYAMGHALHAMH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KEKGIHRLEAMLFALDRINNDPDLLPNITLGARILDTCSRDTHALEQSLTFVQALIEKDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ECVPCGAGTFLNKSELYRCQPCGTEEWAPEGSQTCFPRTVVFLALREHTSW-VL-LAANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -G-CAS--ELCSR-GRVYPWQLLEQIHKVHFL-LHKDTVAFNDNRDPLSSYNIIAWDWNG
       FROM
                                      ; Metazoa;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -SK-IAPVLHLEEVAEG-AVTILPKRMS-VRGFDRYFSSRTLDNNRRNIWFAEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -GDL-LHYSPT-VLAVIGPDSTNRAATTAALLSPFLV-HISYAASSETLSVKRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               larity 27.0%;
Conservative
       N.
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                                                                                                                                                                                                     STANDARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -QAFM--AHTMP-KLKA-FSMSSAYN--A---Y-R-AVYAVAHGLHQLL
                                                                                          26, Createa)
32, Last sequence update)
39, Last annotation update)
AMATE RECEPTOR 5 PRECURSOR.
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                                    Sciurognathi;
                                                         Chordata;
                                                                                                                                                                                                                                                                                                            852
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                                                       Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             No. 2.13e-160;
Mismatches 298;
                                        Muridae;
                                                                                                                                                                                                   1203
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                                                         Mammalia;
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       CARBOHYD
CARBOHYD
                                                                        CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                  DOMAIN
TRANSMEM
DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                            TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                             SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                              G-protein
Multigene
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"A variant of metabotropic glutamate receptor subtype 5: an evolutionally conserved insertion with no termination codon.";

Biochem. Biophys. Res. Commun. 194:522-627(1993).

-!- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR MEDIATED BY A G-PROTEIN THAT ACTIVATES A PHOSPHATIDYLINOSITOL-
                                                       CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00979; G_PROTEIN_RECEP_F3_1; PROSITE; PS00980; G_PROTEIN_RECEP_F3_2; PROSITE; PS00981; G_PROTEIN_RECEP_F3_3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; D10891; -; NOT_ANNOTATED_CDS
EMBL; S64315; AAB27666.1; -.
PIR; A42916; A42916.
                                                                                                           DOMAIN
                                                                                                                             TRANSMEM
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                                                                                                                                                                                                                                                                                                                                          TRANSMEM
                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                              PFAM; PF01094; ANF_receptor; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PFAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCRDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE; 93343913
MINAKAMI R., KATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       transduction.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABE T., SUGIHARA H., NAWA H., 1
"Molecular characterization of receptor mGluR5 coupled to ino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE; 92317054.
ABE T., SUGIHARA F
                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=BRAIN;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CENTRAL NERVOUS SYSTEM.

MISCELLANEOUS: ACTIVATED BY QUISQUALATE > GLUTAMATE
TRANS-1- AMINCCYCLOPENTYL-1,3-DICARBOXYLATE.
SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRODUCED BY ALTERNATIVE SPLICING. THEY 32 RESIDUES.
TISSUE SPECIFICITY: WIDELY DISTRIBUTED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR ALTERNATIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRONGEST, TO MGLUR1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHLORIDE CURRENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CALCIUM SECOND MESSENGER SYSTEM AND GENERATES A CALCIUM-ACTIVATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chem. 267:13361-13368(1992).
                                                                                                                                                                                                                                                                                                                                                                                                            family; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                               coupled receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0444;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 859-923
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: INTEGRAL MEMBRANE PROTEIN.
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 FROM N.A.,
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VE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  H., SHIGEMOTO R., MIZUNO N
n of a novel metabotropic
inositol phosphate/Ca2+ s
                                                                                                                                                                                                                                                                                                                                                                                                                               Transmembrane;
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VI (POTENTIAL).
EXTRACELLULAR (
VII (POTENTI
CYTOPLASMIC
POTENTIAL.
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POTENTIAL.
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V (POTENTIAL).
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PLICING. THEY
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METABOTROPIC GLUTAMATE I
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    PROSITE; PS00979; G_PROTEIN_RECEP_F3_1; 1
PROSITE; PS00980; G_PROTEIN_RECEP_F3_2; 1
PROSITE; PS00981; G_PROTEIN_RECEP_F3_3; 1
PFAM; PF000003; 7tm_3; 1.
G-protein coupled receptor; 1.
G-protein coupled receptor; Transmembrane; Multigene family; Alternative splicing.
SIGNAL 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIN J.-P., WAEBER C., PREZEAU L., BOCKAERT J., HEINEMANN S.F.;

"Alternative splicing generates metabotropic glutamate receptors inducing different patterns of calcium release in xenopus oocytes.";

Proc. Natl. Acad. Sci. U.S. A. 89:10331-10335(1992).

-!- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR MEDIATED BY A G-PROTEIN THAT ACTIVATES A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM. MAY PARTICIPATE IN THE CENTRAL ACTION OF GLUTAMATE IN THE CNS, SUCH AS LONG-TERM POTENTIATION I THE HIPPOCAMENES AND LONG-TERM DEPRESSION IN THE CEREBELLUM.

-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

-!- ALTERNATIVE PRODUCTS: THREE ISOFORMS; 1A (SHOWN HERE), 1B AND 1C ARE PRODUCED BY ALTERNATIVE SPLICING. 1B AND 1C ARE C-TERMINALLY
                                                                                                                                                                                                                                                            use by modified
                                                                                                                                                                                                                                                                                                      This SWI
between
                                                                                                                                     PIR; S15362; S15362.
PIR; A41939; A41939.
                                                                                                                                                                  EMBL; X57569; CAA40799.1;
EMBL; M61099; AAA19497.1;
EMBL; S48085; AAB24138.1;
                                                                                                                                                                                                                              entities requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Cloning, expression, and gene structure glutamate receptor from rat brain."; Science 252:1318-1321(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HOUAMED K.M., KUIJPER J.L., GILBERT T. MULVIHILL E.R., ALMERS W., HAGEN F.S.;
                                                                                                                         GCRDB; GCR_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE; 93066232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-BRAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 349:760-765(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MASU M., TANABE Y., TSUCHIDA K., SHIGEMOTO Sequence and expression of a metabotropic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NABE Y., MASU M., ISHII family of metabotropic uron 8:169-179(1992).
                                                                                                                                                                                                                                                                                                                                                              TISSUE SPECIFICITY: IS PREDOMINANTLY EXPRESSED IN CE PURKINJE CELLS, CA2-CA3 PYRAMIDAL CELLS OF THE HIPPO MITRAL AND TUFTED CELLS OF THE OLFACTORY BULB. MISCELLANEOUS: ACTIVATED BY QUISQUALATE > GLUTAMATE TRANS-1- AMINOCYCLOPENTYL-1,3-DICARBOXYLATE; INHIBI 2-AMINO- 3-PHOSPHONOPROPIONATE. SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED
                                                                                                                                                                                                                                                          European Bioinformatics Institute. There by non-profit institutions as long as ified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ARE PRODUCED BY ALTERNATIVE TRUNCATED FORMS OF 1A.
                                                                                                                                                                                                                                                                       SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EW European Bioinformatics Institute. There are no restr by non-profit institutions as long as its content
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TANABE Y.,
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in Xenopus oocytes.";
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Submitted
                                  This SWISS-PROT entry is copyright. It is produced through a c between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
           EMBL;
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G-protein coupled receptor;
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                                    AHGLHQL-LG-CAS-E-LCSRGR-VYPWQLLEQIHKVHFL-LHKDTVAFNDNRDPLSSYN
                                                AYGLHNMQMSLCPGYAGLCDAMKPIDGRKLLESLMKTNFTGYSGDTILFDENGDSPGRYE
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IIAWDWNGPKWTFTVLGSSTWSPVQLNINETKIQWHGKNHQVPKSVCSSDCLEGHQRVV-
                 IMNFKEMGKDY-FDYINVGSWDNGELKMDDDEV-W-SKKSNIIRSVCSEPCEKGQIKVIR
                                                                            EAPRPCHKGSWCSSNQLCR-E--CQ--A-F-MA-HTMPKLKAFSMSSAYNAY--RAVYAV
                                                                                              NHRNPWFQEFWQHRFQ-CRLEGFPQENSKYNKTCNSSLTLKTHHVQDSKMGFVINAIYSM
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GCR_1002;
GCR_1003;
GCR_1317;
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204; Mismatches
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         PROSITE; PS00979; G_PROTEIN_RECEP_F3_1; PROSITE; PS00980; G_PROTEIN_RECEP_F3_2; PROSITE; PS000981; G_PROTEIN_RECEP_F3_3; PFAM; PF00003; 7tm_3; 1.

PFAM; PF01094; ANF_receptor; 1.
                                                                                                               EMBL;
                                                                                                                                     This SWISS-PROT entry is copyright. It is produced the between the Swiss Institute of Bioinformatics and the European Bioinformatics Institute. There are no use by non-profit institutions as long as its con modified and this statement is not removed. Usage bentities requires a license agreement (See http://www.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus (Rat).
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eurtheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MGR2_RAT
P31421;
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                                                                          GCRDB; GCR_
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 coupled receptor;
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(Rel. 26, Last sequence update)
(Rel. 38, Last annotation update)
CGLUTAMATE RECEPTOR 2 PRECURSOR.
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195; Mismatches 322;
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GCRDB; GCR_1983; -.
PROSITE; PS00979; G_PROTEIN_RECEP_F3_1; 1
PROSITE; PS00980; G_PROTEIN_RECEP_F3_2; 1
PROSITE; PS0091; G_PROTEIN_RECEP_F3_3; 1
PFAM; PF00003; 7tm_3; 1.
PFAM; PF01094; ANF_receptor; 1.
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G13255; Q13256; Q14757; Q14758;
Q1-NOV-1997 (Rel. 35, Created)
Q1-NOV-1997 (Rel. 35, Last sequence up
15-DEC-1999 (Rel. 39, Last annotation
METABOTROPIC GLUTAMATE RECEPTOR 1 PREC
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Homo sapiens (Human).
---- Metazoa; Chordata;
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                                                                                                                                                                                                                               tities requires a license agreement (S send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                     TOPDAIRMACOLOGY 35:1649-1650(1996).

FUNCTION: RECEPTOR FOR GLUTAWATE. THE ACTIVITY OF THIS RECEPTOR MEDIATED BY A G-PROTEIN THAT ACTIVATES A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM. MAY PARTICIPATE IN THE CENTRAL ACTION OF GLUTAMATE IN THE CNS, SUCH AS LONG-TERM POTENTIATION THE HIPPOCAMEUS AND LONG-TERM DEPRESSION IN THE CEREBELLUM. SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

ALTERNATIVE PRODUCTS: TWO ISOFORMS; ALDEA (SHOWN HERE) AND BETA ARE PRODUCED BY ALTERNATIVE SPLICING.

SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
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U31216; AAA87844.1; -.
L76627; AAB05337.1; -.
L76631; AAB05338.1; -.
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1: mRNA distribution,
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                                                                                                                                                                                                                                     MRRLGVVGEFSLIGSDGWA-DRDEV-IEGYE-VEANGGIII-KLQSPEVRSFDDYFLKLR
: | ::|:| | :::|:: |
                                                                           RYDIMNLQYTEANR-YDYVHVGTWHEGVLNIDDYKIQ-MNKS-GVVRSVCSEPCLKGQIK
                                                                                                         YAVAHGIHQIL-G-CASE--LCSRGR-VYPWQLLEQIHKVHFL-LHKDTVAFNDNRDPLS
                                                                                                                          YAMAHGIQNMHHALCPGHVGLCDAMKPIDGSKLLDFLIKSSFIGVSGEEVWFDEKGDAPG
                                                                                                                                                                 ADKEAPRPCHKGSWCSSNQLCRECQAFWAHT-MPKL-KAF-SMSSAY--NA---Y--RAV
                                                                                                                                                                                            LDTNTRNPWFPEFWQHRFQ-CRLPGHLLENPNFKRICTGNESLEENYVQDSKMGFVINAI
                                                                                                                                                                                                                     VVLTNLTGKVW-VASEAWALSRHITGVPGIQRIGMVLGVAIQKRAVPGLKAFEEAYA--R
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                                                                                                                                                                                                                                                                                                   KELAAQEGLCIAHSDKI-YSN-AGEKSFDRLLRKLRERLPKARVVVCFCEGMTVRGLLSA
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                                                                                                                                                                                                                                                                                                                                                                                   -VL-SLPGQHH-IE--L-QGDLLHYSPT---VLAVIGPDSTNRAATTAALLSPF-LVHIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                       RSCS-FNEH-GYHLFQAMRLGYEEINNSTALLPNITLGYQLYDVCSDSA-NVY-AT--LR
                             VIRKGEVSCCWICTACKENEYVQ-DE-FTCKACDLG-WWPNADLTGCEPIPVRYLEWSNI
                                                        SYNIIAWDWNGPKWTFTVLGSSTWSPVQLNINETKIQWHGKNHQVPKSVCSSDCLEGHQR
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  VV-TGFHHCCFECVPCGAGTFLNKSELYRCQPCGTEEWAPEGSQT-CFPRTVVFLALREH
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ilarity 26.9%;
Conservative
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211; M
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Pred. No. 1.72e-146;
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EXTRACELLULAR ()
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CYTOPLASMIC (POTENTIAL).
IV (POTENTIAL)
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CYTOPLASMIC (POTENTIAL)
GLN/PRO-RICH.
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CYTOPLASMIC (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NSNGKSVSWSEPGGGQVPKG -> KKRQPEFSPSSQCPSAH
AQL (IN ISOFORM BETA).
MISSING (IN ISOFORM BETA).
NSNGKSVSWSEPGGGQVPKG -> KKRQPEFSPTSQCPSAH
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ASP/GLU-RICH
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EXTRACELLULAR (POTENTIAL)
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P47743;
01-FEB-1996
  TRANSMEM
DOMAIN
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DOMAIN
                                                                                                                      GCRDB; GCR_1712; -.

MGD; MGI:109600; GRM8.

PROSITE; PS00979; G_PROTEIN_RECEP_F3_1;

PROSITE; PS00980; G_PROTEIN_RECEP_F3_3;

PROSITE; PS00981; G_PROTEIN_RECEP_F3_3;
                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a coll between the Swiss Institute of Bioinformatics and the EMBL out the European Bioinformatics Institute. There are no restriction use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for centitles requires a license agreement (See http://www.isb-sib.ch/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                           J. Neurosci. 15:3075-3083(1995).
-!- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECIS MEDIATED BY A G-PROTEIN THAT INHIBITS ADENYLATE CYCLASE
                                                                    G-protein
Multigene
                                                                                                                                                                                                                                                                                                                                                                      + +
                                                                                                                                                                                                                                                                                                                                                                                                                                                "A novel metabotropic olfactory bulb.";
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15-JUL-1998
                                                                                            PFAM; PF01094;
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                                                      SIGNAL
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                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
TISSUE SPECIFICITY: STRONGLY EXPRESSED IN OLFACTORY BULB,
ACCESSORY OLFACTORY BULB, AND MAMMILLARY BODY. WEAKER EXF
IN THE RETINA, AND IN SCATTERED CELLS IN THE CORTEX AND I
SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECE
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                                                     coupled receptor; family; Olfaction 1 33
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Rodentia;
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(Rel. 33, Last sequence up
(Rel. 36, Last annotation
                                                                                                                                                                                            AAA68149.1;
                                                                                                          7tm_3;
                                                                                            ANF_receptor;
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METABOTROPIC GLUTAMATE RECEPTOR EXTRACELLULAR (POTENTIAL). I (POTENTIAL). CYTOPLASMIC (POTENTIAL).
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                                                LVVWTPLPAREY--QR-F-P-HL-VMLECTETNSLGFILAFLYNGLLSISAFACSYLGKD
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Mismatches 31
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SAUGSTAD J.A., KII
WESTBROOK G.L.;
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PFAM; PF00004; ANF_receptor;
G-protein coupled receptor; '
Multigene family; Olfaction.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U63288; AAB09537.1; GCRDB; GCR_1411; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Mol. Pharmacol. $1:119-125(1997).
-i-FUNCTION: RECEPTOR FOR GLUTHANTE. THE ACTIVITY
IS MEDIATED BY A G-PROTEIN THAT INHIBITS ADENYI
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SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
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01-NOV-1997 (Rel. 35, I
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METABOTROPIC GLUTAMATE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NEHGYHLFQAMRLGVEEINNSTALLPNITLGYQLYDVCS-DSANVYATLR-VLSLPGQH- 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KEKGIHRLEAMLYAIDQINKDPDLLSNITLGVRILDTCSRDTYALEQSLTFVQALIEKDA 128
                                                                                                                                                                                                       GKDLPENYNEAKCVTFSLLFNFVSW--
                                                                                                                                                                                                                               TRGVPETFNEAKPIGFTMYTTCIIWLAFIPIFFGTAQSAEKMYIQTTTLTVSMSLSASVS
                                                                                                                                                                                                                                                                                                                                               IFLGLGMCFSYAALLTKTNRIHRIFEQGKKSVTA-PKFI-SPASQLVITFSLISVQLLGV
                                                                                                                                                                                                                                                                                                                                                                            LLLLLGT-AGL-FAWHLDTPVVRSAGGRLCFLMLGSLAAGSGSLYGFFGEPTRPACLLRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                HCERCEGYNY-QVDEL-SCELCPLDQRPNINRTGC-QR-IPIIKLEWHSPWAVVPVFIAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KSTEYKIIGH--WTN-QLHLKVEDMQWANREHTHPASVCSLPCKPGERKKTVKGVP-CCW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WCSSNQLCR-ECQAFM-AHTMP-K-LKAFSMSSAYN--A---Y-R-AVYAVAHGLHQLL-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YDFFSRVVPPDSYQAQAMVDIVTALGWNYVSTLASEGNYGESGVEAFTQISREIGGVCIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SDVKCANGDPPIFTKPDKISGVIGAAASSVSIMVANILRLFKIPQISYASTAPELSDNTR 188
                                                                                                                                              FGGYFLPKCYVILCRPDLN
                                                                                                                                                                                                                                                                                                                      ALFALGFTIFLSCLTVRSFQLIIIFKFSTKVPTFYHAWVQNHGAGLFVMIS-SAAQLLIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              210;
 MGLUR2
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908
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ilarity 26.3%;
Conservative
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                                                                                     STANDARD;
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565
101866
          Created)
Last sequence update)
Last annotation update
E RECEPTOR 2 PRECURSOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 768; DB 1;
Pred. No. 4.99e-14
219; Mismatches 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
POTENTIAL.
7; 5043FF81 CRC32;
                                                                                      PRT;
                                                                                     872
                            update)
                                                                                     B
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305;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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밁 δÃ B

114

54 g

Similarity

Conservative

Indels

58;

Gaps

113

NEHRGIQRLEAMLFALDRINRDPHLLPGVRLGAHILDSCSKDTHALEQALDFVRASLSRG

ADGSRHICPDGSYATHGDAPTAITGVIGGSYSDVSIQVANLLRLFQIPQISYASTSAKLS 173 NEH-GYHLFQAMRLGVEEINNSTALLPNITLGYQLYDVCSDSANVYA-TL---RV-LSL-

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Query Match
Best Local S
Matches 21
                                                          CARBOHYD
CARBOHYD
CARBOHYD
                                                                                       TRANSMEM
DOMAIN
CARBOHYD
                                                                                                                                                                                TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                         G-protein
Multigene
                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                 CARBOHYD
                                                                                                                    DOMAIN
                                                                                                                                                            DOMAIN
                                                                                                                                                                                                            TRANSMEM
                                                                                                                                                                                                                                                                                             PFAM; PF00003; 7tm_3; 1.
PFAM; PF01094; ANF_receptor;
                                                                                                                                                                                                                                                                                                             PROSITE; PS00979; G_PROTEIN_RECEP_F3_1; PROSITE; PS00980; G_PROTEIN_RECEP_F3_2; PROSITE; PS00981; G_PROTEIN_RECEP_F3_3;
                                                                                                                                                                                                                                                                                                                                             GCRDB; GCR_1
MIM; 604099;
                                                                                                                                                                                                                                                                                                                                                              EMBL; L35318;
                                                                                                                                                                                                                                                                                                                                                                                                                          the
                                                                                                                                                                                                                                                                                                                                                                                                                                  between
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Molecular cloning,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE; 95346007.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
                                       SEQUENCE
                                                                                                                                 TRANSMEM
                                                                                                                                         DOMAIN
                                                                                                                                                  TRANSMEM
                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                        DOMAIN
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                                                                                                                                                                                                                                                     CHAIN
                                                                                                                                                                                                                                                               SIGNAL
                                                                                                                                                                       PRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . J. Neurosci. 7:622-629(1995).

FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR MEDIATED BY A G-PROTEIN THAT INHITIST ADENYLATE CYCLASE ACTIVITY MAY MEDIATE SUPPRESSION OF NEUROTIFANSMISSION OR MAY BE INVOLVED SYNAPTOGENESIS OR SYNAPTIC STABILIZATION.

SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

TISSUE SPECIFICITY: WIDELY EXPRESSED IN DIFFERENT REGIONS OF THE
                                                                                                                                                                                                                                                                                                                                                                                                             SWISS-PROT entry is copyright. It is produced through wen the Swiss Institute of Bioinformatics and the EM European Bioinformatics Institute. There are no restr by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADULT BRAIN AS WELL AS IN FETAL BRAIN.
SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRONGEST, TO MGLUR3
                                                                                                                                                                                                                                                                         coupled family.
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5688
5911
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2033
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                                       Ą
                                                                                                                                                                                                                                                                                  receptor;
                                                            13.0%;
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the human r
                                        95507
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PUTTNER
                                       XX;
Score 761; DB 1; L
Pred. No. 2.19e-140;
200; Mismatches 320;
                                                                                                                                                                                                                                                                                  Transmembrane;
                                                 POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                  METABOTROPIC G
EXTRACELLULAR
I (POTENTIAL).
                                                                                        CYTOPLASMIC POTENTIAL.
                                                                                                                    VI (POTENTIAL)
EXTRACELLULAR
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                                                                                                                                                                       IV (POTENTIAL)
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                                                                                                                                                                                        (POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RUEGG
                                       CRC32;
                                                                                                                                                                                                                                                                                                                (POTENTIAL).
                                                                                                  (POTENTIAL)
                                                                                                                                         (POTENTIAL).
                                                                                                                                                                                                                        (POTENTIAL).
                                                                                                                                                                                                                                         GLUTAMATE RE
R (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        D.,
                                                                                                                                                            (POTENTIAL)
                                                                                                                                                                                                                                                                                  Glycoprotein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           glutamate
                                                                                                                     (POTENTIAL)
                                                                                                                                                                                                    (POTENTIAL)
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                 Length 872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        s.,
                                                                                                                                                                                                                                                     RECEPTOR
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                                                                                                                                                                                                                                                                                  Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                    a collaboration -
MBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E ACTIVITY.
INVOLVED IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           type
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RESULT ACCORDANCE OF THE PROPERTY OF THE PROPE
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MEDLINE; 98141892.

WU S., WRIGHT R.A., ROCKEY P.K., BURGETT S.G., ARNOLD J ROSTECK P.R. JR., JOHNSON B.G., SCHOEPP D.D., BELAGAJE: "Group III human metabotropic glutamate receptors 4, 7; molecular cloning, functional expression, and compariso pharmacological properties in RGT cells."; Brain Res. Mol. Brain Res. 53:88-97(1998).
                                                                                                                                                                                                                                                                                                                                                      GRM8
                                                                                                                                                                                                                                                                                                                                                                            MGR8_HUMAN STANDARD; PRT; 908 AA. 000222; 015403; 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 15-DEC-1999 (Rel. 39, Last annotation update) METABOTROPIC GLUTAMATE RECEPTOR 8 PRECURSOR.
                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                        Eutheria;
                                                                                                                                                                                                                                                                                                    Eukaryota;
                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         748
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and for entitles requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
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MEDLINE: 97446143.

SCHERER S.W., SODER S., DUVOISIN R.M., HUIZENGA J.J.,

"The human metabotropic glutamate receptor 8 (GRM8) ged
disproportionately large gene located at 7q31.3-q32.1.

Genomics 44:232-236(1997).
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PROSITE: PS00979; G_PROTEIN_RECEP_F3_1;
PROSITE: PS00980; G_PROTEIN_RECEP_F3_2;
PROSITE: PS00981; G_PROTEIN_RECEP_F3_3;
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U95025; AAB72040.1;
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METABOTROPIC GLUTAMATE
                                              phosphonobutyrate.";
J. Biol. Chem. 268:1
                                                                                                                             SEQUENCE FROM N.A.
STRAIN-SPRAGUE-DAWLEY;
MEDLINE; 93280152.
NAKAJIMA Y., IWAKABE H.
                                                                                                                 NAKANISHI S.;
                                                                                                                                                                                                                 Eutheria;
                                                                                                                                                                                                                                                Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                  01-JUN-1994
                                                                              receptor mGluR6 with a
                                                                              Molecular characterization receptor mGluR6 with a high
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                                            Chem. 268:11868-11873(1993).
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Rodentia; Sciurognathi;
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    AMATE RECEPTOR 6 PRECURSOR

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CARBOHYD
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                              LTNLTGK-VWVASEAWALSRHITGVPGIQRIGMVLGVAI-QKRAVPGLKAFEEAY-ARAD
                                         QANLTGHFLWVGSDSWG-SK-ISPILNLEEEA-VGAITILPKRA--SIDGFDQYFMTRSL
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                                                                   NQAL-VRGICIAFKDIMPFSAQVGDERMQCLMRHLAQAGATVVVVFSSRQLARVFFESVV
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                                                          672 GLLSISAFACSYLGKDLPENYNEAKCYTFSLLFNFVSWIAF----FTTASVYDGKYLPAA 727
                                                                             753 LLLMVTCTVYAIKARGVPETFNEAKPIGFTMYTTCIIWLAFVPIFFGTAQSAEKIYIQTT 812
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ALIGNMENTS

Db 356 1	Db 296 <i>I</i> Qy 235 <i>I</i>	Db 239 I Qy 176 <i>I</i>	Db 179 I Qy 116 I	Db 119 1 Qy 62 1	Db 61 (Qy 3 (Query Match Best Local Matches 2	REFERENCE #authors #journal #title #cross-ref #accession ##statue ##molecc ##resid	RESOLT ENTRY TITLE ORGANISM DATE
TFNCHLQEGAKGPLPVDTFLRGHEDGGARLSNSPTAFRPLCTGEENISSVBTPYMDYTHL 415	ASEAWASSSLIAMPEYFHYVGGTIGFGLKAGQIPGFREFLQKVHPRKSVHNGFAKEFWEE 355	DFSE-L-ISOYSDEEKIQQVVEVIONSTAKVIVVFSSGPDLEPLIKE-IVRRNITGRIWL 295 : : : : : : :	NQFKSFLRTIPNDEHQATAMADIIEYFRWNWVGTIAADDDYGRPGIEKFREEAEERDICI 238 	NKIDSLNLDEFCNCSEHIPSTIAVVGATGSGISTAVANLLGLFYIPQVSYASSSRLLSNK 178 :	CIRYNFRGFRWLQAMIFAIEEINSSPALLPNMTLGYRIFDTCNTVSKALEATLSFVAQ 118	tch 20.0%; Score 1170; DB 2; Length 1085; al Similarity 31.9%; Pred. No. 5.20e-203; 263; Conservative 227; Mismatches 256; Indels 78; Gaps 56;	s referention atus lecule_sidues	F

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                                                                                                                                                                                                                                                  #authors Pollak, M.R.; Brown, E.M.; Chou, Y.H.; Hebert, S.C.; Marx, S.J.; Steinmann, B.; Levi, T.; Seidman, C.E.; Seidman, Cell (1993) 75:1297-1303
#title familial hypocalciuric hypercalcemia and neonatal severe hyperparathyroidism.
#cross-references MUID:94094324
#accession A49419
                                  ##note
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               preliminary
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289-303 ##label
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SL-MALGELIGYTCLLAAICEFFAFKSRKLPENFNBAKFITFSMLIFFIVWISFIPAYAS
                                           VPT-FYHAWVQNHGAGLEVMISSAAQLLICLTWLVVWTPLPAREYQRFPHLVMLECTETN 660
                                                                            IPTSFHRKWWGLNLQFLLVFLCTFMQIVICVIWLYTAPPSSYRNQELEDEIIFITCHE-G
                                                                                                                        LMLGSLAAG-SGSLYGFFGEPTRPACLLRQALFALGFTIFLSCLTVRSFQLIIIFKFSTK 601
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#length 1078 #molecular-weight 120672 #checksum 8159
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hyperparathyroidism
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Pred. No. 1.42e-201;
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SLGFILAFL--YNGLLSISAFACSYLGKDLPENYNEAKCVTFSLLFNFVSWIAFFTT-AS

B

TY-GKFVSAVEVIAILAA-SFGLLACIFFNKIYIILFKPSRNTIE

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ACCESSIONS
REFERENCE
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #authors
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RDS glycoprotein; receptor; transmembrane protein

#length 1078 #molecular-weight 120573 #chec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60 CIRYNFRGFRWLQAMIFAIEEINSSPALLPNLTLGYRIFDTCNTVSKALEA--TLSFVAQ 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VYDGKYLPAANMMAGLSSLSSGFGGY-FLPKCYVILCRPDLNSTE
LLLFSLLCCFSSSLF-FIGEPQDWTCRLRQPAFGISFVLCISCILVKTNRVLLVFE--AK
                                   GSQTCFPRTVVFLALREHTSWVLLAANTLLLLLLLG-TAGLFAWHLDTPVVRSAGGRLCF
                                                                                                                                             SREVPFSNCSRDCLAGTRKGIIEGEPTCCFECVECPDGEYSDETDASACNKCPDDFWSNE
                                                                                                                                                                                                                GEQVTFDECGDLVGNYSIINWHLSPEDGSIVFKEVGYYNVYAKKGERLFINEEKILWSGF
                                                                                                                                                                                                                                                    MSSAYNAYRAVYAVAHGLHQLLGC-AS-EL----CS-RGRVYPWQLLEQIHKVHFLLHK
                                                                                                                                                                                                                                                                             LRISYNVYLAVYSIAHALQDIYTCLPGRGLFTNGSCADIKKVEAWQVLKHLRHLNFTNNM
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                                                                                                                                                                                                                                                                                                                                                                                                                                 LASEAWASSSLIAMPQYFHVVGGTIGFALKAGQIPGFREFLKKVHPRKSVHNGFAKEFWE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AFKDIMP-FSAQVGDERMQCLMRHLAQAGATVVVVFSS-RQLARVFFESVVLTNLTGKVW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DFSELISOYSDE--EE-IQHVVEVIQNSTAKVIVVFSSGPDLEPLIKE-IVRRNITGKIW 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NKIDSLNLDEFCNCSEHIPSTIAVVGATGSGVSTAVANLLGLFYIPQVSYASSSRLLSNK 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C-SFNEHGYHLFQAMRLGVEEINNSTALLPNITLGYQLYDVCSDSANVYATLRVLSLPGQ 61
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                                                                   NHTSCIAKEIEFLSWTEPFG-IALTLFAVLGIFLTAFVLGVFIKFRNTPIVKATNRELSY
                                                                                                                                                                                -DTVAFNDNRDPLSSYNIIAWDWNGPK-WT-FTVLGS-STWSP-VQ-LNINETKIQWHGK
                                                                                                                                                                                                                                                                                                                            EAYA-R-ADKE-APRPCH---KGSWCSSNQLCRECQAF--M-A--HTMPKLKA----FS-
                                                                                                                                                                                                                                                                                                                                                              ETFNCHLQEGAKGPLPVDTFLRGHEESGDRFSNSSTAFRPLCTGDENISSVETPYIDYTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RQYPSFLRTIPNDKYQVETMVLLLQKFGWTWISLVGSSDDYGQLGVQALENQALVRGICI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HHIE-LQ-GDLLHYS---PTVLAVIGPDSTNRAATTAALLSPFLV-HISYAASSETLSVK 115
                                                                                                       NHQVPKSVCSSDCLEGHQR-VVTGFHHCCFECVPCGAGTFLNKSELYRCQPCGTEEWAPE
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Garrett,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Garrett, J.E.; Capuano, I.V.; Hammerland, L.G.; Brown, E.M.; Hebert, S.C.; Nemeth, E.F.; Full J. Biol. Chem. (1995) 270:12919-12925 Molecular cloning and functional expression of parathyroid calcium receptor cDNAs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A56715 #type complete
calcium receptor (clone phPCaR-4.0) - humar
#formal_name Homo sapiens #common_name man
19-Oct-1995 #sequence_revision 19-Oct-1995
17-Mar-1999
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Pred. No. 5.86e-201
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KEYWORDS
FEATURE
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187-212
613-635
650-670
683-700
725-744
770-790
806-828
841-860
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##cross-references EMBL:U20289;
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                                                                                                                                                                                                                                                                                                                                                ##experimental_source kidney
Calcium; glycoprotein;
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                                                                                                                                                                                                                                                                                                                                                                                                    ##molecule_type mRNA
               60
                                                      Local
CIRYNFRGERWLQAMIFAIEEINSSPSLLPNMTLGYRIFDTCNTVSKALEA--TLSFVAQ 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IPTSFHRKWWGLNLQFLLVFLCTFMQIVICVIWLYTAPPSSYRNQELEDEIIFITCHE-G
                                         262;
                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                            Proc. Natl. Acad. Sci. U.S.A. (1995) 92:131-135
Cloning and functional expression of a rat kidney
extracellular calcium/polyvalent cation-sensing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Riccardi, D.; Park,
Hebert, S.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       159362 #type complete calcium/polyvalent cation-sensing receptor precursor - recalcium/polyvalent cation-sensing receptor precursor - reformal_name Rattus norvegicus #common_name Norway rat 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
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159362; A5559
                                                                                              #length
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                                           Conservative
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                                                                                                          kinase C) #status predicted\
#binding_site phosphate (Ser) (covalent) (by protein kinase A) #status predicted
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#domain
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transmembrane #status predicted
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                                                                                                                                                                                                                       transmembrane #status
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                                                                                              #molecular-weight 120867
                                           233;
                                                      Score 1158;
Pred. No. 1.
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                                           Mismatches
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                                                      ) DB 2;
1.51e-200;
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Indels 90;

Gaps

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#checksum

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RESULT
ENTRY
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ORGANISM
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#authors
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#title
                                                                                       #cross-references MUID:95279439
#accession B56715
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Garrett, J.E.; Capuano, I.V.; Hammerland, L.G.; Hung, Brown, E.M.; Hebert, S.C.; Nemeth, E.F.; Fuller, F. J. Biol. Chem. (1995) 270:12919-12925
Molecular cloning and functional expression of human parathyroid calcium receptor cDNAs.
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NDS glycoprotein; receptor; transmembrane protein
%Y #length 1088 #molecular-weight 121799 #chec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62
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Local Similarity 31.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ω
                                                                                                                                                                                                                                                                                          WISFIPAYASTY-GKFVSAVEVIAILAA-SFGLLACIFFNKIYIILFKPSRNTIE
||:|: || ||:||::| |:: ||: ||:| |:| |:|
WIAFFTT-ASVYDGKYLPAANMMAGLSSLSSGFGGY-FLPKCYVILCRPDLNSTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                 IIFITCHE-GSL-MALGFLIGYTCLLAAICFFFAFKSRKLPENFNEAKFITFSMLIFFIV 827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LRISYNVYLAVYSIAHALQDIYTCLPGRGLFTNGSCADIKKVEAWQVLKHLRHLNFTNNM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VASEAWA---L-S--R--HITGVP-GIQ-RIGMVLGV-A-IQK---R-AVP-GL-KAF-E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DFSELISQYSDE--EE-IQHVVEVIQNSTAKVIVVFSSGPDLEPLIKE-IVRRNITGKIW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RQYPSFLRTIPNDKYQVETMVLLLQKFGWTWISLVGSSDDYGQLGVQALENQALYRGICI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NQFKSFLRTIPNDEHQATAMADIIEYFRWNWVGTIAADDDYGRPGIEKFREEAEERDICI 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NKIDSLNLDEFCNCSEHIPSTIAVVGATGSGVSTAVANLLGLFYIPQVSYASSSRLLSNK 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C-SFNEHGYHLFQAMRLGVEEINNSTALLPNITLGYQLYDVCSDSANVYATLRVLSLPGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CIRYNFRGFRWLQAMIFAIEEINSSPALLPHLTLGYRIFDTCHTVSKALEA--TLSFVAQ 117
                                                                                                                                                                                                                                                                                                                                                                                                                LYMLECTETNSLGFILAFL--YNGLLSISAFACSYLGKDLPENYNEAKCYTFSLLFNFVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LITIFKFSTKVPT-FYHAWVQNHGAGLFVMISSAAQLLICLTWLVVWTPLPAREYQRFPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VLLVFE--AKIPTSFHRKWWGLNLQFLLVFLCTFMQIVICVIWLYTAPPSSYRNQELEDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VRSAGGRICFLMLGSLAAG-SGSLYGFFGEPTRPACLLRQALFALGFTIFLSCLTVRSFQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PCGTEEWAPEGSQTCFPRTVVFLALREHTSWVLLAANTLLLLLLG-TAGLFAWHLDTPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -DTVAFNDNRDPLSSYNIIAWDWNGPK-WT-FTVLGS-STWSP-VQ-LNINETKIQWHG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GEQVTFDECGDLVGNYSIINWHLSPEDGSIVFKEVGYYNVYAKKGERLFINEEKILWSGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MSSAYNAYRAVYAVAHGLHQLLGC-AS-EL----CS-RGRVYPWQLLEQIHKVHFLLHK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ETFNCHLQEGAKGPLPVDTFLRGHEESGDRFSNSSTAFRPLCTGDENISSVETPYIDYTH 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LASEAWASSSLIAMPQYFHVVGGTIGFALKAGQIPGFREFLKKVHPRKSVHNGFAKEFWE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HHIE-LQ-GDLLHYS---PTVLAVIGPDSTNRAATTAALLSPFLV-HISYAASSETLSVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KCPDDFWSNENHTSCIAKEIEFLSWTEPFG-IALTLFAVLGIFLTAFVLGVFIKFRNTPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SREPLIFVLSVLQVPFSNCSRDCLAGTRKGIIEGEPTCCFECVECPDGEYSDETDASACN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EAYA-R-ADKE-APRPCH---KGSWCSSNQLCRECQAF--M-A--HTMPKLKA----FS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -KNH------QVPKSVCSSDCLEGHQR-VVTGFHHCCFECVPCGAGTFLNKSELYRCQ
                                                      metabotropic glutamate receptor 4 precursor -
#formal_name Rattus norvegicus #common_name Nc
30-Jun-1992 #sequence_revision 30-Jun-1992 #te
13-Sep-1998
   JH0561
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231; Mismatches 250;
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                                                                                    #common_name Norway rat
30-Jun-1992 #text_change
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98,301,454,484,
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751-772
786-807
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#title
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870
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 596
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ##molecule_type mRNA
                                    453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          132 TEVRCGSGGPPIITKPERVVGVIGASGSSVSIMVANILRLFKIPQISVASTAPDLSDNSR 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72 KEKGIHRLEAMLFALDRINNDPDLLPNITLGARILDTCSRDTHALEQSLTFVQALIEKDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6
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                                                          WHCEPC-TG-YQYQVDRYTCKTCPYDMRPTENRTSCQPIPIVKLE-WD-SPWAVLPLFLA
                                                                                                                                                                                               RDLCPGRVGLCPRMDPVDGTQLLKYIRNVNFSGIAGNPVTFNENGDAPGRYDIYQYQLRN
                                                                                                                                                                                                                                                                      W-EDNFHCKLSRHALKKGSHIKKCTNRERIGQDSAYEQEGKVQFVIDAVYAMGHALHAMH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YDFFSRVVPSDTYQAQAMVDIVRALKWNYVSTLASEGSYGESGVEAFIQKSRENGGVCIA
                                 FECVPCGAGTFLNKSELYRCQPCGTEEWAPEGSQTCFPRTVVFLALREHTSW-VL-LAAN
                                                                                                                                         GSA-EYKVIGS--WTD-HLHLRIERMQWPGSGQQLPRSICSLPCQPGERKKTVKGMA-CC
                                                                                                                                                                                                                                                WCSSNQLCREC-QAFM--AHTMP-KLKA-FSMSSAYN--A---Y-R-AVYAVAHGLHQLL
                                                                                                                                                                                                                                                                                                                    ASEAWALSRHITGVPGIQRIGMVLGVAIQKRAVPGLKAFEEAYA-RADKEAPRPC-HKGS
                                                                                                                                                                                                                                                                                                                                                       GSDSWG-SKS-APVLRLEEVAEG-AVTILPKRMS-VRGFDRYFSSRTLDNNRRNIWFAEF
                                                                                                                                                                                                                                                                                                                                                                                          FKDIMPFSAQVGD-ERMQCLMRHLAQAGATVVVVFSSRQLARVFFESVVLTNLTGKV-WV
                                                                                                                                                                                                                                                                                                                                                                                                                         QSVKIPREPKTGEFDKI--IKRLLETSNARGIIIFANEDDIRRVLEAARRANQTGHFFWM
                                                                                                                                                                                                                                                                                                                                                                                                                                                              YPSFLRTIPNDKYQVETMVLLLQKFGWTWISLVGSSDDYGQLGVQALENQALVRG-ICIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IELQ--
VVGIAATLEVVVTEVRYNDTPIVKASGRELSYVLLAGIFLCYATTELMIAEPDLGTCSLR
                                                                                                        GPKWTFTVLGSSTWSPVQLNINETKIQWHGKNHQVPKSVCSSDCLEG-HQRVVTGFHHCC
                                                                                                                                                                            -G-CAS--ELCSR-GRVYPWQLLEQIHKVHFL-LHKDTVAFNDNRDPLSSYNIIAWD-WN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NEHGYHLFQAMRLGVEEINNSTALLPNITLGYQLYDVCS-DSANVYATLR-VLSLPGQHH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This protein is coupled to a G protein and evokes a variety functions by mediating intracellular signal transduction.
#superfamily metabotropic glutamate receptor 4
G protein coupled receptor; glycoprotein; phosphoprot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             219;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          h 14.7%;
Similarity 27.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ·GDL-LHYSPT-VLAVIGPDSTNRAATTAALLSPFLV-HISYAASSETLSVKRQ
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A family of metabotropic glutamate nces_MUID:92110002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #length
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predicted #label MET`
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Pred. No. 4.92e-139;
225; Mismatches 289;
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                                                                                                                                                                                                                                                                                                              TEVRCGSGGPPIITKPERVVGVIGASGSSVSIMVANILRLFKIPQISYASTAPDLSDNSR 191
                                                                                                                                                                                                                                                                                                                                                    NEHGYHLFQAMRLGVEEINNSTALLPNITLGYQLYDVCS-DSANVYATLR-VLSLPGQHH 63
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   WCSSNQLCREC-QAFM--AHTM2-KLKA-FSMSSAYN--A--
                                W-EDNFHCKLSRHALKKGSHIKKCTNRERIGQDSAYEQEGKVQFVIDAVYAMGHALHAMH
                                                                    ASEAWALSRHITGVPGIQRIGMVLGVAIQKRAVPGLKAFEEAYA-RADKEAPRPC-HKGS
                                                                                                       GSDSWG-SKS-APVLRLEEVAEG-AVTILPKRMS-VRGFDRYFSSRTLDNNRRNIWFAEF
                                                                                                                                        FKDIMPFSAQVGD-ERMQCLMRHLAQAGATVVVVFSSRQLARVFFESVVLTNLTGKV-WV
                                                                                                                                                                          QSVKIPREPKTGEFDKI--IKRLLETSNARGIIIFANEDDIRRVLEAARRANQTGHFFWM
                                                                                                                                                                                                            YPSFLRTIPNDKYQVETMVLLLQKFGWTWISLVGSSDDYGQLGVQALENQALVRG-ICIA
                                                                                                                                                                                                                                         YDFFSRVVFSDTYQAQAMYDIVRALKWNYVSTLASEGSYGESGVEAFIQKSRENGGVCIA 251
                                                                                                                                                                                                                                                                                IELQ---GDL-LHYSPT-VLAVIGPDSTNRAATTAALLSPFLV-HISYAASSETLSVKRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VSLGMLYMPKVYIILFHPEQN 852
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                                                                                                                                                                                                                                                                                                                                                                                                                        219;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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Neuron (1993) 11:41-52
The ligand-binding domain in metabotropic glutamate receptors is related to bacterial periplasmic binding proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         #superfamily metabotropic glutamate receptor 4
neurotransmitter receptor
#length 912 #molecular-weight 101846 #checksum
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metabotropic glutamate receptor - rat
#formal_name Rattus norvegious #common_name Norway rat
26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change
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                                                                                                                                                                                                                                                                                                                                                                                                                        225;
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Pred. No. 1.25e-138;
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NID:g205400;
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   -Y-R-AVYAVAHGLHQLL
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                                                                                                                                                                                                                                                                                                                                                    ##molecule_type mRNA
##residues 1-1171 ##label ABE
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Local Similarity 26.4%;
hes 212; Conservative
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                                                                                                      RSC-SFNEH-GYHLFQAMRLGVEEINNSTALLPNITLGYQLYDVCSDSANVYA-TLR-VL 56
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                                                                                                                                         RKCGAVREQYGIQRVEAMLHTLERINSDPTLLPNITLGCEIRDSCWHSAVALEQSIEFIR 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YLGKDLPENYNEAKCYTFSLLFNFVSWIAF - - - FTTASVYDGK - YLPAANMMAGLS - SLS
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                                                                  DSLISSEEEEGLVRCVDGSSSFRSKKPIVGVIGPGSSSVAIQVQNLLQLFNIPQIAYSAT 174
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SMDLSDKTLFKYFMRVVPSDAQQARAMVDIVKRYNWTYVSAVHTEGNYGESGMEAFKDMS
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                                 -SL-PGQHHIEL-Q-GD-LLHY-SPT-VLAVIGPDSTNRAATTAALLSPFLV-HISYAAS
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                                                                                                                                                                                                                                                   G protein-coupled receptor; transmembrane #length 1171 #molecular-weight 128289 #c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Abe, T.; Sugihara, H.; Nawa, H.; Shigi
Nakanishi, S.
J. Biol. Chem. (1992) 267:13361-13368
Molecular characterization of a novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A42916 #type complete
metabotropic glutamate receptor mGluR5 - rat
#formal_name Rattus norvegicus #common_name Norway rat
04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change
29-Jan-1999
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NCBIP:107750)
                                                                                                                                                                                                                                                                                                                                                                                             preliminary
                                                                                                                                                                             Score 798; DB 2; Le
Pred. No. 2.38e-127;
207; Mismatches 329;
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#accession JC2132
                                                                                                                                                                                                                                                                                                                       #authors
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                                                                                                  s 1-1180 ##label MIN
protein is coupled to guanine nucleotide binding
glycoprotein; neurotransmitter; receptor; transm
                                                                                                                                                                                                                                        Biochem. Biophys. Res. Commun. (1994) 199:1136-1143 Molecular cloning and the functional expression of isoforms of human metabotropic glutamate receptor
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metabotropic glutamate receptor 5 A - humar
#formal_name Homo sapiens #common_name man
28-aug-1985 #sequence_revision 07-Oct-1994
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A41939 #type complete
G protein-coupled glutamate receptor -
#formal_name Rattus norvegicus #common_
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#length 1180 #molecular-weight 129053 #checksum 237
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#authors Houamed, K.Y.; Kuijper, J.L.; Gilbert, T.L.; Haldeman, O'Hara, P.J.; Mulvihili, E.R.; Almers, W.; Hagen, F. science (1991) 252:1318-1321

#title Cloning, expression, and gene structure of a Generating, expression, and gene structure of a Generating protein-coupled glutamate receptor from rat brain.

#cross-references MUID:92022526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #title Sequence and expression #cross-references MUID:91156047 #accession $15362
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#1-1199 ##1_abel MAS
##residues 1-1199 ##1_abel MAS
##cross-references = EX3L:N37359; N*D:g55645; PID:g55647
##cross-references = EX3L:N37359; N*D:g55647; PID:g55647
##cross-references = EX3L:N37359; N*D:g55645; PID:g55647; PID:
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##molbecule_type nucleic acid

##residues 1-1199 ##label HOU

##cross-references GB:M61099; NID:
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##note sequence extracted from
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YAMAHGLQNMHHALCPGHVGLCDAMKPIDGRKLLDFLIKSSFVGVSGEEVWFDEKGDAPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -VI-SLPGQHH-IE--L-QGDLHYSPT---VLAVIGPDSINRAATTAALLSPF-LVHIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RKCGEIREQYGIQRVEAMFHTLDKINADPVLLPNITLGSEIRDSCWHSSVALEQSIEFIR 124
TSWVLLAANTLLLLLLGTAGLFAWHLDTPVVRSAGGRLCFLMLGSLAAGSGSLYGFFGE
                                                                                  ESITATAFSCLGILVTLFVTLIFVLYRDTPVVKSSSRELCYTILAGIFLGYVCPFTLIAK
                                                                                                                                                                                                                                                          VIRKGEVSCCWICTACKENEFVQ-DE-FTCRACDLG-WWPNAELTGCEPIPVRYLEWSDI
                                                                                                                                                                                                                                                                                                                                            SYNIIAWDWNGPKWTFTVLGSSTWSPVQLNINETKIQWHGKNHQVPKSVCSSDCLEGHQR
                                                                                                                                                                                                                                                                                                                                                                                                                                   RYDIMNLQYTEANR-YDYVHVGTWHEGVLNIDDYKIQ-MNKSGMV-RSVCSEPCLKGQIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YAVAHGLHQLL-G-CASE--LCSRGR-VYPWQLLEQIHKVHFL-LHKDTVAFNDNRDPLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADKEAPRPCHKGSWCSSNQLCRECQAFMAHT-MPKL-KAF-SMSSAY--NA---Y--RAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LDTNTRNPWFPEFWQHRFQ-CRLPGHLLENPNFKKVCTGNESLEENYVQDSKMGFVINAI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MRRLGVVGEFSLIGSDGWA-DRDEV-IEGYE-VEANGGITI-KLQSPEVRSFDDYFLKLR
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Nature (1991) 349:750-755
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larity 27.1%;
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Pred. No. 6.00e-127;
210; Mismatches 318;
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Matches 21
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#title
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##molecule_type mRNA
##residues 1-1212 ##label MIN
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                                                                                                                                                                                                     TSMDLSDKTLFKYFMRVVPSDAQQARAMVDIVKRYNWTYVSAVHTEGNYGESGMEAFKDM 234
                                                                                                                                                                                                                                                                                                                                                      RKCGAVREQYGIQRVEAMLHTLERINSDPTLLPNITLGCEIRDSCWHSAVALEQSIEFIR 114
                                                                                                                                                                                                                                                                                           DSLISSEEEEGLVRCVDGSSSSFRSKKPIVGVIGPGSSSVAIQVQNLLQLFNIPQIAYSA 174
                                                                                                                                                                                                                                                                                                                               RSC-SFNEH-GYHLFQAMRLGVEEINNSTALLPNITLGYQLYDVCSDSANVYA-TLR-VL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ILISVQLTLVVTLIIMEPPMPILSYPSIKE-VYLIC-NTSNLGVVAPVGYNGLLIMSCTY 769
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NHRNPWFQEFWQHRFQ-CRLEGFPQENSKYNKTCNSSLTLKTHHVQDSKMGFVINAIYSM
                                  TNLTGK-VWVASEAWALSRHITGVPGIQRIGMVLGVAIQKRAVPGLKAFEEAYA--RADK
                                                                    LGLAGEFILLGSDGWA-DRYDV-TDGYQREA-VGGITI-KLQSPDVKWFDDYYLKLRPET
                                                                                                          ALVRGICIAFKDIMPFSAQVGDERMQCLMRHLA-Q-AGATVVVVVFSSRQLARVFFESVVL
                                                                                                                                            SAKEGICIA-HSYKIYSN-AGEQSFDKLLKKLTSHLPKARVVACFCEGMTVRGLLMAMRR 292
                                                                                                                                                                               SSETLSVKRQYPSFLRTIPNDKYQVETMVLLLQKFGWTWISLVGSSDDYGQLGVQALENQ
                                                                                                                                                                                                                                                         -SL-PGQHHIEL----QGDLLHY-SPT-VLAVIGPDSTNRAATTAALLSPFLV-HISYAA
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llarity 26.7%;
Conservative
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Biochem. Biophys. Res. Commun. (1994) 199:1136-1143

Molecular cloning and the functional expression of two
isoforms of human metabotropic glutamate receptor subtype
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#formal_name Homo sapiens #common_name man
28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change
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Pred. No. 6.00e-127;
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203,286,338,402,
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#accession JH0561
     601,675,827,837,
843
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##experimental_source brain
## This protein is coupled to a G protein and evokes a variety
functions by mediating intracellular signal transduction.

### IFICATION #superfamily metabotropic glutamate receptor 4

RDS G protein-coupled receptor; glycoprotein; phosphoprote
transmembrane protein
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Neuron (1992) 8:169-179
A family of metabotropic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WTFTVLGSSTWSPVQLNINETKIQWHGKNH-QVPKSVCSSDCLEGHQRVVTGFHHCCFEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R-YRYQKVGYWAEG-LTLDTSFIPWASPSAGPLPASRCSEPCLQNEVKSVQPGEVCCWLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ELCSRGR-VYPWQLLEQ-IHKVHF-L-LHK-DT---VAFNDNRDPLSSYNIIAWDWNGPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HLCDAMRPVNGRRLYKDFVLNVKFDAPFRPADTDDEVRFDRFGDGIGRYNIFTYLRAGSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EFWEERFH-CSFRORDCAAHSLRAV-PFEQESKIMFVVNAVYAMAHALHNMHRALCPNTT 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WVASEAWALSRHITGVPGIQRIGMVLGVAIQKRAVPGLKAFEEAYARADK-EAPR-PCHK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WVASDGWG-ALE-SYVAGSERAAEG-AITIELASYP-ISDFASYFQSLDPWNNSRNPWFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CIAFKDIMPFSAQVGDERMQCLMRHLAQ-AGATVVVVFSSRQLARVFFESVVLTNLTGKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CVATSEKVG-RA-MSRAAFEGVVRALLQKPSARVAVLFTRSEDARELLAATQRLN-ASFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DKSRYDYFARTVPPDFFQAKAMAEILRFFNWTYVSTVASEGDYGETGIEAFELEARARNI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NEH-GYHLFQAMRLGVEEINNSTALLPNITLGYQLYDVCSDSANVYA-TL---RV-LSL- 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
          metabotropic glutamate receptor 8 - mouse
#formal_name Mus musculus #common_name hous
02-Jul-1996 #sequence_revision 02-Jul-1996
13-Sep-1998
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                                                                                I49142
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larity 27.8%; Pred. No. 1.53e-125;
Conservative 195; Mismatches 322;
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                                                                              #type complete
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                                             house
                          #text_change
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Best Local S
Matches 20
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#journal
#title
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#accession I49142
              688
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ##molecule_type mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ##residues
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                                           VPETFNEAKPIGFTMYTTCIIWLAFIPIFFGTAQSAEKMYIQTTTLTVSMSLSASVSLGM
                                                                                                                                                                                                                AS--ELCSR-GRVYPWQLLEQIHKVHFLLHKDT-VAFNDNRDPLSSYNIIAWDWNGPKWT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HEHGYHLFQAMRIGVEEINNSTALLPNITLGYQLYDVCS-DSANVYATLR-VLSLPGQH-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KEKGIHRLEAMLYAIDQINKDPDLLSNITLGVRILDTCSRDTYALEQSLTFVQALIEKDA
            LPENYNEAKCVTESLLENEVSW---IA-FETTASVYDGKYLPAANNMAGLS-SLSSGFGG
                                                                                                                                                                               GLGMCFSYAALLTKTNRIHRIFEQGKKSVTA-PKFI-SPASQLVITFSLISVQLLGVFVW
                                                                                                                                                                                                                                          IATTFVIVTFVRYNDTPIVRASGRELSYVLLTGIFLCYSITFLMIAAPDTIICSFRRIFL
                                                                                                                                                                                                                                                                                 PCGAGTFLNKSELYRCQPCGTEEWAPEGSQTCFPRTVVFLALREHTSWVLLAANTLLLLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                    PGYIGLCPRMVTIDGKELLGYIRAVNFNGSAGTPVTENENGDAPGRYDIFQYQINN-KST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GSW-C-SSNQLCRECQAFMAHTMPKL-K--AFSMSSAYN-AYRAVYAVAHGLHQLL-G-C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GNFGCKSGSEGKRNSHIKKCTGLERIARDSSYEQEGKVQFVIDAVYSMAYALHNMHKELC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ASEAWALSREITGVPGIQRIGMVIGVAIQKRA-VPGL-KAFEEAYARADKEAPR-P-CHK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GSDSWG-SK-IAPVYQQEEIAEGAVTILPKRASIDGFDRYFRSRTLANNRRNVWFAEFSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QSQKIPREPRPGEFEKI---IKRLLETPNARAVIMFANEDDIRGILEAAKKLNQSGHFLWI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YPSFLRTIPNDKYQVETMVLLLQKFGWTWISLVGSSDDYGQLGVQALENQAL-VRGICIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -HIE-LOGDLLHYS-P-TVLAVIGPDSTNRAATTAALLSPFLV-HISYAASSETLSVKRO
                                                                              LVVWTPLPAREY -- QR-F-P-HL-VMLECT
                                                                                                          FVVDPPHTIIDYGEQRTLDPENARGVLKC-DISDLSLICSLGYSILLMVTCTVYAIKTRG
                                                                                                                                             ALGETIFLSCLTVRSFQLIIIFKFSTKVPTFYHAWVQNHGAGLFVMIS-SAAQLLICLTW
                                                                                                                                                                                                                                                                                                               RCEGYNY-QVDEL-SCELCPLDQRPNINRTGC-QR-IPIIKLEWHSPWAVVPVLIAILGI
                                                                                                                                                                                                                                                                                                                                                - FTVLGSSTWSPVQLNINETKIQWHGKNHQVPKSVCSSDCLEG-HQRVVTGFHHCCFECV
                                                                                                                                                                                                                                                                                                                                                                                 EYKIIGH--WTN-QLHLKVEDMQWANREHTHPASVCSLPCKPGERKKTVKGVP-CCWHCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FKDIMPFSAQVGD-ERMQCLMRHLAQAGATVVVVFSSRQLARVFFESVVLTNLTGK-VWV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SDVKCANGDPPIFTKPDKISGVIGAAASSVSIMVANILRLFKIPQISYASTAPELSDNTR
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Similarity 25.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #superfamily metabotropic glutamate receptor 4
neurotransmitter receptor
#length 908 #molecular-weight 101413 #checksum
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A novel metabotropic glutamate receptor retina and olfactory bulb.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 3.95e-122;
221; Mismatches 311;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 772; DB 2; I
Pred. No. 3.95e-122;
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                                                                              TETNSLGF ILAFLYNGLLS ISAFACSYLGKD
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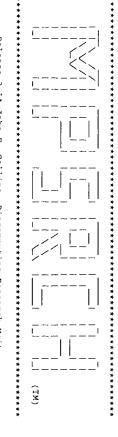
833 LYMPKVYIIIFHPEON

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KEYWORDS
FEATURE
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796-817
826-850
104,233,403,525,
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Best Local Similarity
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640-660
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717-737
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#cross-references MUID:96354880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #journal
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                                                                    459
                                                                                                                                         399
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                                                                                                                                                                                                                                                                                                                                                                                                         166 IAGVIGPGSSSVAIQVQNLLQLFNIPQIAYSATSIDLSDKTLFKYFLRVVPSDTLQARAI 225
 518
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                                                                                                                                                                                                                                                                                                                                      LDIVKRYNWTYVSAVHTEGNYGESGMEAFKELASQEGLCIAHSDKI-YSN-AGEKHFDRL 283
                                                                                                                                                                                                                                                                                                                                                                                   VLAVIGPDSTNRAATTAALLSPELV-HISYAASSETLSVKRQYPSELRTIPNDKYQVETM 135
                                                                                                                                                                                                         QEA-VGGITVKLHS-EEVTSFDDYFLKLRLNTNTRNPWFPEFWQHRFQ-CRIPGHPLENM
                                                                                                                                                                                                                                                                                LRKLRERLPKARVVVCFCEGMTVRGLLMAMRRLGVAGEFLLIGSDGWA-DRDEV-VEGYE 341
DDYMMQ-INRSDMVL-SYCSEPCSKGEIKVIRKGEVSCCWICTACKDNEIVQ-DE-FTCT
                                QLLEQIHKVHFL-LHKDTVAFNDNRDPLSSYNIIAWDWNGPKWTFTVLGSSTWSPVQLNI
                                                                 QLLEFLMRTSFTGVSGEDVWFDENGDTPGRYEIMNLQYVEPG-AFDYINVGSWHEGQLSI 517
                                                                                                                                        NYRKNCSGYESLEDNYVQDSKMGFVINAIYAMAQGLHDMHSHLCPGHVGLCKAMDPIDGS 458
                                                                                                                                                                        RIGMVLGVAIQKRAVPGLKAFEEAYA--RADKEAPRPCHKGSWCSSNQLCREC-QAFMAH
                                                                                                                                                                                                                                             MRHL-AQ-AGATYYVVVFSSRQLARVFFESVVLTNLTGK-VWVASEAWALSRHITGVPGIQ
                                                                                                                                                                                                                                                                                                              VLLLQKFGWTWISLVGSSDDYGQLGVQALENQALVRGICIAFKDIMPFSAQVGDERMQCL 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YFLPKCYVILCRPDLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kubokawa, K.; Miyashita, T.; FEBS Lett. (1996) 392:71-76 Cloning and characterization receptor activated by both
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S71376
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#formal_name Oncorhynchus masou #common_name cherry salmon
11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                     12.9%; Score 755; DB 2; Identity 26.2%; Pred. No. 1.01e-118; Conservative 199; Mismatches 279;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-May-1998
                                                                                                     -SMSSAY - -NA - - -Y - -RAVYAVAHGLHQLLG - -CASE - -LC -SRGRVYPW
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kinase C) #status predicted\
#binding_site phosphate (Thr) (covalent) (by
kinase C) #status predicted\
#binding_site phosphate (Ser) (covalent) (by
cAMP-dependent kinase) #status predicted
jth 1218 #molecular-weight 136838 #checksum
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166
                                  229
                                                                     106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ##status preliminary
##molecule_type nucleic acid
##residues 1-871 ##label NAK
##cross-references GB:D13963; NID:g391856; PID:d1003572; PID:g391857
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NQAL-VRGICIAFKDIMPFSAQVGDERMQCLMRHLAQAGATVVVVFSSRQLARVFFESVV
                                QISREAGGVCIAQSIKIPREPKPGEFHK-VIRRLMETPNARGIIIFANEDDIRRVLEATR 287
                                                                     AASSETLSVKRQYPSFLRTIPNDKYQVETMVLLLQKFGWTWISLVGSSDDYGQLGVQALE 165
                                                                                                                                           SL---PGQ-HHIELQ--GDL--LHYSPT--VLAVIGPDSTNRAATTAALLSPFLV-HISY 105
                                                                                                                                                                             ALIRGRGDGDEASVRCPGGVPPLRSAPPERVVAVVGASASSVSIMVANVLRLFAIPQISY 168
                                                                                                                                                                                                                 RSC-SFN-EHGYHLFQAMRLGVEEINNSTALLPNITLGYQLYDVCS-DSANVYATLR-VL 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FPHLVMLECTETNSLGFILAFLYNGLLSIS-AFACSYLGKDLPENYNEAKCVTFSLLFNF
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                                                                                                                                                                                                                                                                                                            Similarity
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G protein-coupled receptor; transmembrane protein
#length 871 #molecular-weight 95088 #checksum 3942
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Molecular characterization of a novel reglutamate receptor mGluR6 with a high
for L-2-amino-4-phosphonobutyrate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               metabotropic glutamate receptor, mGluR6 - rat #formal_name Rattus norvegicus #common_name Norway rat 21-Sep-193 #sequence_revision 18-Nov-1994 #text_change 29-Jan-1999
                                                                                                                                                                                                                                                                                       12.5%;
larity 26.5%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R.; Mizuno, N.; Nakanishi,
                                                                                                                                                                                                                                                                                                                                                                                                                  sequence extracted from NCBI backbone (NCBIN:133246, NCBIP:133250)
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                                                                                                                                                                                                                                                                                         Score 729; DB 2; L
Pred. No. 1.59e-113;
219; Mismatches 308;
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                                                                                                                                                                     694 ITEGLTSLQVVGVIAWLGAQPPHSVIDYEEQRTVDPEQARGVLKC-DMSDLSLIGCLGYS 752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    343 ENNRRNIWFAEFW-EENFNCKLTSSGGQSDDSTRKCTGEERIGQDSAYEQEGKVQFVIDA 401
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NMMAGLS-SLSSGFGGYFLPKCYVILCRPDLN 758
                                                                                          LLLMVTCTVYAIKARGVPETFNEAKPIGFTMYTTCIIWLAFVPIFFGTAQSAEKIYIQTT 812
                                                                                                                                                                                                                                                                               HTSWVLLAAN-TLLLLLLGTA-GLFAWHLDTPVVRSAGGRLCFLMLGSLAAGSGSLYGF 558
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                                                                                                                                                                                                             FGEPTRPACLLRQALFALGFTIFLSCLTVRSFQLIIIFKFSTKVPTFYHAWVQNHGAGLF 618
                                                                                                                                                                                                                                                                                                     -SPWAALPLLLAVLGIMATTTIMATFMRHNDTPIVRASGRELSYVLLTGIFLIYAITFLM 635
                                                                                                                                                                                                                                                                                                                                                                                 RKKMVKGVP-CCWHCEACDGYRF-QVDE-FTCEACPGDMRPTPNHTGCRPTPVVRLT-WS 576
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Search completed: Fri Mar 17 13:29:01 2000 Job time: 47 secs.



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Run on: MPsrch_pp protein - protein database search, using Smith-Waterman algorithm Fri Mar 17 13:35:28 2000; MasPar time 93.42 Seconds 864.499 Million cell updates/sec

Tabular output not generated

Sequence: Description: Perfect Score: >US-09-361-652-3 (1-777) from US09361652.pep 5838 1 RSCSFNEHGYHLFQAMRLGV.....NSTEHFQASIQDYTRRCGST 777

Searched 666290 seqs, 103942017 residues Scoring table:

PAM 150 Gap 11

Post-processing: Minimum Minimum Match 0% Listing first 45 summaries

Database:

a-pending 1:P9 2:U60 3:U7 4:U80 5:U81 5:U82 7:U83 8:U84A 9:U84B 10:U85 11:U86 12:U87 13:U88 14:U89 15:U90 16:U91 17:U92 18:U93 19:U94 20:NEWP 21:NEWU5 22:NEWU8 23:NEWU9

Statistics: Mean 42.646; Variance 177.023; scale 0.241

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	6	U	4	w	2	<u>_</u>	Result	
1160	1163	1170	1170	1170	1170	1170	1170	1182	1233	1464	1509	1797	1848	4483	4483	4587	4587	4587	5838	5838	Score	
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100.0%; Local Similarity 100.0%; nes 777; Conservation

Score 5838; DB 23; Pred. No. 0.00e+00; 0; Mismatches 0;

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Sequence 3, Application US/09361652 GENERAL INFORMATION: APPLICANT: Zuker, Charles S. APPLICANT: Adler, Jon Elliot APPLICANT: Adler, Jon Elliot APPLICANT: Hoon, Mark APPLICANT: The Regents of the University of California TITLE OF INVENTION: Involved in Sensory Transduction FILE REFERENCE: 02307E-088610US CURRENT FILING DATE: 1999-07-27 CURRENT FILING DATE: 1999-07-27 EARLIER APPLICATION NUMBER: US/09/351,652 CURRENT FILING DATE: 1998-07-28 NUMBER OF SEQ ID NOS: 8 SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 3 LENGTH: 777 TYPE: PRT ORGANISM: Homo sapiens FEATURE: OTHER INFORMATION: human G-protein coupled receptor B3 (GPCR-B SEQUENCE 777 AA; 86285 MW; 3230984 CN;	S	ALIGNMENTS	2 1160 19.9 1078 2 US-60-172- Sequence 6, Applicatio 2. 1160 19.9 1078 9 US-08-84- Sequence 7, Applicatio 2. 1160 19.9 1078 9 US-08-84- Sequence 7, Applicatio 2. 1160 19.9 1078 1 PCT-US99-1 Sequence 12, Applicatio 2. 1160 19.9 1078 2 US-60-172- Sequence 7, Applicatio 2. 1160 19.9 1078 2 US-60-172- Sequence 8, Applicatio 2. 1158 19.8 1079 1 PCT-US8-1 Sequence 8, Applicatio 3. 1158 19.8 1079 1 US-08-484- Sequence 8, Applicatio 3. 1158 19.8 1079 1 US-08-484- Sequence 8, Applicatio 3. 1158 19.8 1079 1 US-08-484- Sequence 8, Applicatio 3. 1158 19.8 1079 2 US-08-484- Sequence 8, Applicatio 3. 1158 19.8 1079 2 US-08-1484- Sequence 8, Applicatio 3. 1158 19.8 1079 2 US-08-1484- Sequence 8, Applicatio 3. 1158 19.8 1079 2 US-60-172- Sequence 10, Applicatio 3. 1158 19.8 1079 2 US-60-172- Sequence 10, Applicatio 3. 1158 19.8 1079 2 US-60-172- Sequence 10, Applicatio 3. 1158 19.8 1079 2 US-60-172- Sequence 11, Applicatio 3. 1158 19.8 1079 2 US-60-172- Sequence 12, Applicatio 1. 1158 19.8 1079 2 US-60-172- Sequence 13, Applicatio 1. 1158 19.8 1079 2 US-60-172- Sequence 13, Applicatio 1. 1158 19.8 1079 2 US-60-172- Sequence 13, Applicatio 1. 1158 19.8 1079 2 US-60-172- Sequence 13, Applicatio 1. 1158 19.8 1079 2 US-60-172- Sequence 13, Applicatio 1. 1158 19.8 1079 107-US97-0 Sequence 2, Applicatio 1. 1158 19.8 1088 9 US-08-484- Sequence 6, Applicatio 1. 1158 19.8 1088 9 US-08-484- Sequence 6, Applicatio 1. 1158 19.8 1088 9 US-08-484- Sequence 6, Applicatio 1. 1158 19.8 1088 9 US-08-484- Sequence 6, Applicatio 1. 1158 19.8 1088 9 US-08-484- Sequence 6, Applicatio 1. 1158 19.8 1088 9 US-08-484- Sequence 6, Applicatio 1. 1158 19.8 1088 9 US-08-484- Sequence 6, Applicatio 1. 1158 19.8 1088 9 US-08-484- Sequence 6, Applicatio 1. 1158 19.8 1088 9 US-08-484- Sequence 6, Applicatio 1. 1158 19.8 1088 9 US-08-484- Sequence 6, Applicatio 1. 1158 19.8 1088 9 US-08-484- Sequence 6, Applicatio 1. 1158 19.8 1088 9 US-08-484- Sequence 6, Applicatio 1. 1158 19.8 1088 9 US-08-484- Sequence 6, Applicatio 1. 1158 19.8 1088 9 US-08-484- Sequence 6
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ORGANISM: Homo sapiens FEATURE: OTHER INFORMATION: human G-protein coupled receptor B3 (GPCR-B3) SEQUENCE 777 AA; 86285 MW; 3230984 CN; Sequence 3, Application US/09361652 GENERAL INFORMATION: APPLICANT: Zuker, Charles S. APPLICANT: Adler, Jon Elliot APPLICANT: Lindemeier, Juergen APPLICANT: Hoon, Mick APPLICANT: Hoon, Mark APPLICANT: The Regents of the University of California APPLICANT: The Regents of the University of California TITLE OF INVENTION: Nucleic Acids Encoding a G-Protein Coupled Receptor TITLE APPLICANT: INVOLVED in Sensory Transduction FILE REFERENCE: 02307E-088610US CURRENT APPLICATION NUMBER: US/09/351,652 CURRENT FILING DATE: 1999-07-27 EARLIER APPLICATION NUMBER: US 50/094,465 EARLIER FILING DATE: 1998-07-28 NUMBER OF SEQ ID NOS: 8 SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 3 LENGTH: 777 TYPE: PRT

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       GENERAL INFORMATION:
APPLICANT: Zuker, Charles S.
APPLICANT: Zuker, Charles S.
APPLICANT: Lindemeier, Juergen
APPLICANT: Lindemeier, Juergen
APPLICANT: Hoon, Mark
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Nucleic Acids Encoding a G-Protein Cou
TITLE OF INVENTION: Involved in Sensory Transduction
FILE REFERENCE: 02307E-088610PC
CURRENT APPLICATION NUMBER: PCT/US99/17099
CURRENT FILING DATE: 1999-07-27
EARLIER APPLICATION NUMBER: US 60/094,465
EARLIER FILING DATE: 1998-07-28
NUMBER OF SEQ ID NOS: 8
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TYPE: PRT
ORGANISM: HOMO SAPIENS
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SOFTWARE: FastSEQ for Windows V.
SEQ ID NO 5
LENGTH: 840
TYPE: PRT
ORGANISM: UNKNOWN
FEATURE:
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GENERAL INFORMATION:
APPLICANT: BONAZZI, VIVIEN
TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN CCUPLED
TITLE OF INVENTION: RECEPTOR, NUCLEIC ACID MOLECULES
TITLE OF INVENTION: PROTEIN, AND USES THEREOF
FILE REFERENCE: CL000178
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                          QGSYLPAVNVLAGLTTLSGGFSGYFLPKCYVILCRPELNNTEHFQASIQDYTRRCGTT
                                                                                                                    NSVGFLLAFTHNILLSISTFVCSYLGKELPENYNEAKCVTFSLLLLNFVSWIAFFTMASIY
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Pred. No. 0.00e+00;
99; Mismatches 93;
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TITLE OF INVENTION: Involved in Sensory Transduction
FILE REFERENCE: 03307E-088610US
CURRENT APPLICATION NUMBER: US/09/361,652
CURRENT FILING DATE: 1999-07-27
EARLIER APPLICATION NUMBER: US 60/094,465
EARLIER FILING DATE: 1999-07-28
EARLIER FILING DATE: 1998-07-28
UNDBER OF SEQ ID NOS: 8
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APPLICANT: Ryba, Nick
APPLICANT: Hoon, Mark
APPLICANT: The Regents of the University of California
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TYPE: PRT
ORGANISM: Rattus sp.
EEATURE:
OTHER INFORMATION: rat G-protein
QUENCE 840 AA; 93496 MW; 3932001
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                CRECHTFTTRNMPTLGAFSMSAAYRVYEAVYAVAHGLHQLLGCTSEICSRGPVYPWQLLQ
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QWHGKNHQVPKSVCSSDCLEGHQRVVTGFHHCCFECVPCGAGTFLNKSELYRCQPCGTEE
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Pred. No. 0.00e+00;
99; Mismatches 93;
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APPLICANT: Adler, Jon Elliot
APPLICANT: Adler, Jon Elliot
APPLICANT: Lindemeter, Juergen
APPLICANT: Ryba, Nick
APPLICANT: Hoon, Mark
APPLICANT: Heon, Mark
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Involved in Sensory Transduction
FILE REFERENCE: 02307E-088610PC
CURRENT APPLICATION NUMBER: PCT/US99/17099
CURRENT ETLING DATE: 1999-07-27
EARLIER APPLICATION NUMBER: US 60/094,465
EARLIER FILING DATE: 1998-07-28
NUMBER OF SEQ. ID NOS: 8
NUMBER: Date: 1998-07-28
                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Rattus sp.
FEATURE:
FEATURE:
OTHER INFORMATION: rat G-protein coupled receptor B3 (GPCR-B3)
SEQUENCE 840 AA; 93496 MW; 3932001 CN;
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LENGTH: 840
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                                                                                               PRHIEIQKDLRNHSSKVVAFIGPDNTDHAVTTAALLGPFLMPLVSYEASSVVLSAKRKFP 182
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                                              SFLRTVPSDRHQVEVMVQLLQSFGMVWISLIGSYGDYGQLGVQALEELAVPRGICVAFKD 242
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             IVPFSARVGDPRMQSMMQHLAQARTTVVVVFSNRHLARVFFRSVVLANLTGKVWVASEDW
                                SELRTIPNDKYQVETMVLLLQKFGWTWISLVGSSDDYGQLGVQALENQALVRGICIAFKD
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ilarity 75.2%;
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Pred. No. 0.00e+00,
99; Mismatches 9;
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                                                                                                           APPLICANT: Zuker, Charles S.
APPLICANT: Adler, Jon Elliot
APPLICANT: Lindemeier, Juergen
APPLICANT: Lindemeier, Juergen
APPLICANT: Ryba, Nick
APPLICANT: Hoon, Mark
APPLICANT: Hoon, Mark
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Nucleic Acids Encoding a G-Protein Cou
TITLE OF INVENTION: Involved in Sensory Transduction
FILE REFERENCE: 02307E-088610PC
CURRENT APPLICATION NUMBER: PCT/US9/17099
CURRENT FILING DATE: 1999-07-27
EARLIER APPLICATION NUMBER: US 60/094,465
EARLIER FILING DATE: 1998-07-28
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                                                                                    NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.1
OTHER INFORMATION: mouse G-protein coupled receptor B3 puence 842 AA; 93455 MW; 3909917 CN;
                               ORGANISM: Mus sp.
                         FEATURE:
                                                  TYPE: PRT
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                                e 2, Application US/09361652 INFORMATION:
: Zuker, Charles S.
   Adler, Jon Elliot
   Lindemeier, Juergen
   Ryba, Nick
   Hoon, Mark
                                                  Application
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larity 74.2%;
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                                                   US/09361652
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Pred. No. 0.00e+00;
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APPLICANT: The Regents of the University of California TITLE OF INVENTION: Nucleic Acids Encoding a G-Protein Coutified of Invention: Involved in Sensory Transduction FILE REFERENCE: 023075-088610US
CURRENT APPLICATION NUMBER: US/09/361.652
CURRENT FILING DATE: 1999-07-27
EARLIER APPLICATION NUMBER: US 60/094.465
EARLIER FILING DATE: 1998-07-28
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 842
TYPE: PRT
ORGANISM: Mus sp.
TKVPTFYHTWAQNHGAGIFVIVSSTVHLFLCLTWLAMWTPRPTREYQRFPHLVILECTEV
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                                                                            TKVPTFYHAWVQNHGAGLFVMISSAAQLLICLTWLVVWTPLPAREYQRFPHLVMLECTET
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CURRENT FILING DATE: 1999-07-27
EARLIER APPLICATION NUMBER: US 60/095,464
EARLIER FILING DATE: 1998-07-28
EARLIER APPLICATION NUMBER: US 60/112,747
EARLIER FILING DATE: 1998-12-17
NUMBER OF SEQ ID NOS: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Adler, Jon Elliot
APPLICANT: Lindemeier, Juergen
APPLICANT: The Regents of the University of California
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Nucleic Acids Encoding a G-Protein Coupled Receptor
TITLE OF INVENTION: Involved in Sensory Transduction
FILE REFERENCE: 02307E-088720US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Match 31.7%;
Local Similarity 37.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 843
TYPE: PRT
ORGANISM: Rattus sp.
                                                                                                                                                                                                                                                                                                                                                                                                             9
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               -NVSWYTPNNTVPVSMCSKSCQPGQMKKSVGLHPCCFECLDCMPGTYLNRSADEFNCLSC
                                                                                                                                                                                           AIDPVLHNLTELRHTGTFLGVTIQRVSIPGFSQFR---VRRDKPGYPVPNTTNLRTTCNQ
                                                                                                                                                                                                                                                    SQVMRSEEQRQLDNILDKLRRTSARVVVVFSP-ELSLYSFFHEVLRWNFTGFVWIASESW
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TKIQWHGKNHQVPKSVCSSDCLEGHQRVVTGFHHCCFECVPCGAGTFLNKS-ELYRCQPC
                                                                                                                                           DCDACLN-TTKSFNNILILSGERVVYSVYSAVYAVAHALHRLLGCNRVRCTKQKVYPWQL
                                                                                                                                                                         ALSRHITGVPGIQRIGMVLGVAIQKRAVPGLKAFEEAYARADKEA-PRPCHKGSWCSSNQ 298
                                                                                   LREIWHVNFTLLGNRLFFDQQGDMPML-LDIIQWQWDLSQNPFQSIASYSPTSKRLTYIN
                                                                                                               LCRECQAFMAHTMPKLKAFSMSSA-YNAYRAVYAVAHGLHQLLGCASELCSRGRVYPWQL
                                                                                                                                                                                                                                  AQV--GDE-R-MQCLMRHLAQAGATVVVVFSSRQLAR-VFFESVVLTNLTGKVWVASEAW 239
                                                                                                                                                                                                                                                                                                                     ATHHIEAMVQLMVHFQWNWIVVLVSDDDYGRENSHLLSQRLTKTSDICIAFQEVLPIPES
                                                         LEQIHKVHFLLHKDTVAFNDNRD-PLSSYNIIAWDWNGPKWTFTVLGSSTWSPVQLNINE
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Pred. No. 1.65e-169;
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Best Local S
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OTHER INFORMATION: mouse G-protein coupled receptor (GPCR)
OTHER INFORMATION: acid sequence
SEQUENCE 843 AA; 95752 MW; 3996656 CN;
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CURRENT FILLING DATE: 1999-07-27
EARLIER APPLICATION NUMBER: US 60/095,464
EARLIER FILLING DATE: 1998-07-28
EARLIER APPLICATION NUMBER: US 60/112,747
EARLIER FILLING DATE: 1998-12-17
EARLIER FILLING DATE: 1998-12-17
NUMBER OF SEQ ID NOS: 10
                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Zuker, Charles S.
APPLICANT: Adler, Jon Elliot
APPLICANT: Lindemeter, Juergen
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Nucleic Acids Encoding a G-Protein
TITLE OF INVENTION: Involved in Sensory Transduction
EILE REFERENCE: 0.3307E-08872005
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                                                                                                           71 GYNLMQAMREAVEEINNCSSLLPGVLLGYEMVDVCYLSNNIQPGLYFLSQIDDFLPILK-
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                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Mus sp.
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ATHHIEAMVQLMVHFQWNWIVVLVSDDDYGRENSHLL-SQRLTNTGDICIAFQEVLPVPE
                           DLLHYSPTVLAVIGPDSTNRAATTAALLSPFLV-HISYAASSETLSVKRQYPSFLRTIPN
                                                 DYSQYRPQVVAVIGPDNSESAITVSNILSYFLVPQVTYSAITDKLQDKRRFPAMLRTVPS 189
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                                                                                                                                      Score 1797; DB 18;
Pred. No. 2.77e-164;
191; Mismatches 275;
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APPLICANT: Zuker, Charles S.
APPLICANT: Adler, Jon Elliot
APPLICANT: Adler, Jon Elliot
APPLICANT: Lindemeier, Juergen
APPLICANT: The Regents of the University of California
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: INCOLVEd in Sensory Transduction
FILE REFERENCE: 02307E-088720US
CURRENT APPLICATION NUMBER: US/09/361,631
CURRENT APPLICATION NUMBER: US/09/3644
EARLIER APPLICATION NUMBER: US 60/095,464
EARLIER APPLICATION NUMBER: US 60/112,747
EARLIER APPLICATION NUMBER: US 60/112,747
EARLIER FILING DATE: 1998-07-28
EARLIER FILING DATE: 1998-12-17
NUMBER OF SEQ ID NOS: 10
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                                                                                                                                                                      Sequence 7, Application US/09361631 GENERAL INFORMATION:
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Query Match 25.8%;
Best Local Similarity 36.1%;
Matches 246; Conservative
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SEQ ID NO 7
LENGTH: 669
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              US/60172600
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Pred. No. 7.45e-135;
162; Mismatches 248;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: BODAZZI, VIVIEN
TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
TITLE OF INVENTION: RECEPTOR, NUCLEIC ACID MOLECULES
TITLE OF INVENTION: PROTEIN, AND USES THEREOF
FILE REFERENCE: CLO00178
CURRENT APPLICATION NUMBER: US/60/172,600
CURRENT FILING DATE: 1999-12-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 2
LENGTH: 822
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 25.1%;
Local Similarity 33.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: HUMAN
QUENCE 822 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AREYQREPHLVMLECTETNSLGFILAFLYNGLLSISAFACSYLGKDLPENYNEAKCVTFS
                                                                                                                                                                           VRSEQLIIIEKESTKVPTEYHAWVQN--HGA-G-LFVMISSAAQLLICLTW-LVVWTPLP
                                                                                                                                                                                                              TLFLQAAEIF-VESELPLSWADRLSGCLRGPWAWLVVLLAMLVEVALC-TWYLVAFPPEV
                                                                                                                                                                                                                                                LDTPVVRSAGGRL-CFLMLGSLAAGSGSLYGFFGEPTRPACLLRQALFALGFTIFLSCLT
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                                  LLFNFVSWIAFFTTASVYDGKYLPAANMMAGLSSLSSGFGGYFLPKCYVILCRPDLNSTE
                                                                                                                                                                                                                                                                                RDSPLVQASGGPLACF-GLVCLGLVCLSVLLFPGQPSPARCLAQQPLSHLPLT---GCLS 619
                                                                                                                                                                                                                                                                                                                                                    DDIACTFCGQDEWSPERSTRCFRRRSRFLAWGEPAVLLLLLLSLALGLVLAALGLFVHH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CS-FNEHGYHLFQ-AMRLGVEEINNSTALLPNITLGYQLYDVCSDSA-NVYATLRVLSLP 59
                                                                  MLAYFITWVSFVPLLANVQVVLRPAVQMGALLLCVLGILAAFHLPRCYLLMRQPGLNTPE
                                                                                                                                        VTDWHMLPTEALVHCRTRSWVSFGLAHATNATLAFLCFLGTFLVRSQPGRYNRARGLTFA 737
                                                                                                                                                                                                                                                                                                                     ELYRCQPCGTEEWAPEGSQTCFPRTVVFLALREHTSWVLLAANTLLLLLLLGTAGLFAWH
                                                                                                                                                                                                                                                                                                                                                                                         SPVQLNINETKIQWHGKNHQVPKSVCSSDCLEGHQRVVTGFHHCCFECVPCGAGTFLNKS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EAWLTSDLVMGLPGMAQMGTVLGF-LQ-RGAQ-LHEFPQ-YVKTHLALATDPAFCSALGE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90342 MW; 3444052 CN;
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Best Local S
Matches 22
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TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
TITLE OF INVENTION: RECEPTOR, NUCLEIC ACID MOLECULES ENC
TITLE OF INVENTION: PROTEIN, AND USES THEREOF
FILE REFERENCE: CL000178
CURRENT APPLICATION NUMBER: US/60/172,600
CURRENT FILING DATE: 1999-12-20
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 14
LENGTH: 877
TYPE: PRT
ORGANISM: UNKNOWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
OTHER INFORMATION: SEE GENEBANK REPORT
SEQUENCE 877 AA; 98119 MW; 4229727 CN;
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                                                                                                                                                                                                                                                                                                                                                                            NIHINETVDIIEKNTKVNVVVSFAKSSQM-KLLYEGLRSRNVPKNKVWVASDNWSTSKNI 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPTVLAVIGPDSTNRAATTAALLSPFLV-HISYAASSETLSVKRQYPSFLRTIPNDKYQV 132
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LCHLILFSLLGSFISVIFFVGEPSNESCRVRQVIFGLSFTLCVSCILVKSLKILLAFQMN
                               WAPEGSQTCFPRTYVFLALREHTSWVLLAANTLLLLLLLGTAGLFAWHLDTPVVRSAGGR
                                                                                             HGKNHQVPKSVCSSDCLEGH-QRVVTGFHHCCFECVPCGAGTFLNKSELYRCQPCGTEE- 479
                                                                                                                             SNIENVLSK--CSDSCQPGEYKKTAEGQHTCCYECLACAENQYSNHTDADTCSKCDTESL
                                                                                                                                                             VHFLLHKDTVAFN-DNRDPLS-SYNIIAWDWNGPKWTFTVLGSSTWSPVQLNINETKIQW 421
                                                                                                                                                                                                                             AFMAHTMPKIKAFSMSSAYNAYRAVYAVAHGIHQIIGCASEIC-SRGRVYPWQIIEQIHK
                                                                                                                                                                                                                                                         NAANAVQEQIKNTHLDMVFSVQMAVSAIAKAVVEL -- CVERQCKTPSAIQPWELLKQLRN 430
                                                                                                                                                                                                                                                                                                                        LKDVNLSDIGNILGFTF-KSG--NVTAFLQ-YLKDLKFGSEAKMNNSFLEEFLKL-PEIG
                                                                                                                                                                                                                                                                                                                                                         QCLMRH----LAQAGATV-VVV-FS-SRQLARVFFESVVLTNLT-GKVWVASEAWALSRHI
                                                              WSNANSSKCYPKFYEYFEWNSGFAIALLTLAALGILLLISMSALFFWQRNSLVVKAAGGP
                                                                                                                                                                                                                                                                                           TGVPGIQRIGMVLGVAIQKRAVPGLKAFEEAYARADKEAPRPCHKGSWCSSN-QLCRECQ
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Best Local :
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                                                         Local Similarity
                 60
                                                                                                                                                                                            TELEFAX: (202)639-6604
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: U.S.
ZIP: 20004-1008
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                TOPOLOGY: not relevant
MOLECULE TYPE: protein
HYPOTHETICAL: NO
JENCE 1059 AA; 118068 MW; 5859863 CN;
                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Sanzo, Michael A.
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: BETELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Quinn, Stephen J.
TITLE OF INVENTION: The Avia
TITLE OF INVENTION: Receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 1:1-
OTTY: Washington
 CIRYNFRGFRWLQAMIFAIEEINNSPNLLPNMTLGYRIFDTCNTVSKALEA--TLSFVAQ 117
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                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                      TELEPHONE:
                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                 LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
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                                            Conservative
                                                                                                                                                                                 1059 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bai, Mei
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Brown, Edward
                                                                                                                                                                                                                                                                                                                                                                             Patentin Release #1.0,
                                                                                                                                                                                                                                      (202)639-6585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vinson & Elkins L.L.P.
                                                         20.2%;
                                                                                                                                                       not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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                                                                                                                                                                                                                                                                                                                                                   US/09/134,513
                                            230;
                                        Score 1182; DB 16;
Pred. No. 1.27e-101;
230; Mismatches 252;
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                                                                     Length 1059;
                                           Indels
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                                         Gaps
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                                                                                             sequence 5, Applicati GENERAL INFORMATION:
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                                                                                                             Application US/08484719
 INVENTION:
                       Edward F. Nemeth, Edward M. Brown, Steven C. Hebert, Bradford C. Van Wagenen, Manuel F. Balandrin, Forrest H. Fuller, Eric G.
                                                                                                                                                                                                                       STANDARD;
Scott T. Moe
CALCIUM RECEPTOR-ACTIVE
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Best Local S
Matches 26
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116 ROYPSFLRTIPNDKYQVETMVLLLQKFGWTWISLVGSSDDYGQLGVQALENQALVRGICI
                             179 NQFKSFLRTIPNDEHQATAMADIIEYFRWNWVGTIAADDDYGRPGIEKFREEAEERDICI 238
                                                                                                                                              119 NKIDSLNLDEFCNCSEHIPSTIAVVGATGSGISTAVANLLGLFYIPQVSYASSSRLLSNK 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: PCT/U-, APPLICATION NUMBER: PCT/U-, APPLICATION NUMBER: U.S. 08/292,827 FILING DATE: 23 August, 1994 APPLICATION NUMBER: U.S. 08/141,248 APPLICATION NUMBER: U.S. 08/141,248 APPLICATION NUMBER: U.S. 08/141,248 APPLICATION NUMBER: U.S. 08/009,389
                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 5:
                                                                                               62 HHIE-LQ-GDLLHYS---PTVLAVIGPDSTNRAATTAALLSPELV-HISYAASSETLSVK 115
                                                                                                                                                                                                                                                      61 CIRYNFRGFRWLQAMIFAIEEINSSPALLPNMTLGYRIFDTCNTVSKALEA--TLSFVAQ 118
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FILING DATE: 12 February, 1993
APPLICATION NUMBER: U.S. 07/934,161
APPLICATION NUMBER: U.S. 07/834,161
APPLICATION NUMBER: U.S. 07/834,044
APPLICATION NUMBER: U.S. 07/834,044
APPLICATION NUMBER: U.S. 07/834,044
APPLICATE 25 FC...
                                                                                                                                                                                                 3 C-SFNEHGYHLFQAMRLGVEEINNSTALLPNITLGYQLYDVCSDSANVYATLRVLSLPGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 1085 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 38,179
REFERENCE/DOCKET NUMBER: 21.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 11 February, 1992
APPLICATION NUMBER: U.S. 07/749,451
FILING DATE: 23 AUGUST, 1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
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MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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NUMBER OF SEQUENCES:
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STREET: Suite 4700
STREET: 633 West Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 08/3 FILING DATE: 9 December,
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67-3510
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121170 MW; 6189757 CN;
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7 June, 1995
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08/353,784
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                                                                                                                                                                                                                                                           Sequence 2, Application US/08943452 GENERAL INFORMATION:
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COUNTRY: USA
ZIF: 02421
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                  TITLE OF INVENTION:
                                                                                                                                                                                               APPLICANT:
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                                                                                                                                    NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LLFSLLCCFSSSLF-FIGEPQDWTCRLRQPAFGISFVLCISCILVKTNRVLLVFE--AKI 711
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                                                                                    STREET: Two Mil CITY: Lexington
                                                                         STATE:
                                                                                                                        ADDRESSEE:
                                                                         MA
                                                                                                        Two Militia Drive
                                                                                                                                                                Nearing, Jacqueline
VENTION: Mammalian Polycation-Sensing Receptor
VENTION: and Methods of Use Thereof
                                                                                                                                                                                                             Hebert, Steven
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                                                                                                                                                                                                                                         Harris, H. William
                                                                                                                        Hamilton,
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                                                                                                                      Brook, Smith & Reynolds,
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655 LLFSLLCCFSSSLF-FIGEPQDWTCRLRQPAFGISFVLCISCILVKTNRVLLVFE--AKI 711
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 CIRYNFRGFRWLQAMIFAIEEINSSPALLPNMTLGYRIFDTCNTVSKALEA--TLSFVAQ 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 781-861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Hogle, Doreen
REGISTRATION NUMBER: 36,361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 27-MAR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/622,738
FILING DATE: 27-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 02-OCT-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 536 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                            EQVTFDECGDLAGNYSIINWHLSPEDGSIVFKEVGYYNVYAKKGERLFINDEKILWSGFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DFSE-L-ISQYSDEEKIQQVVEVIQNSTAKVIVVFSSGPDLEPLIKE-IVRRNITGRIWL 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RQYPSFLRTIPNDXYQVETMYLLLQKFGWTWISLVGSSDDYGQLGVQALENQALVRGICI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NQFKSFLRTIPNDEHQATAMADIIEYFRWNWVGTIAADDDYGRPGIEKFREEAEERDICI 238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C-SFNEHGYHLFQAMRLGVEEINNSTALLPNITLGYQLYDVCSDSANVYATLRVLSLPGQ 61
                                           SQTCFPRTVVFLALREHTSWVLLAANTLLLLLLG-TAGLFAWHLDTPVVRSAGGRLCFL
                                                                                    HTSCIAKEIEFLSWTEPFG-IALTLFAVLGIFLTAFVLGVFIKFRNTPIVKATNRELSYL 654
                                                                                                                                                                            REVPFSNCSRDCLAGTRKGIIEGEPTCCFECVECPDGEYSDETDASACDKCPDDFWSNEN 595
                                                                                                                                                                                                                       DTVAFNDNRDPLSSYNIIAWDWNGPK-WT-FTVLGS-STWSP-VQ-LNINETKIQWHGKN 425
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                                                                                                                                                                                                                                                                                                            SSAYNAYRAVYAVAHGLHQLLGC-AS-EL----CS-RGRVYPWQLLEQIHKVHFLLHK-
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TOPOLOGY: li
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FILING DATE: 27-MAR-1997
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in Release #1.0, Version #1.30
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Pred. No. 2.08e-100;
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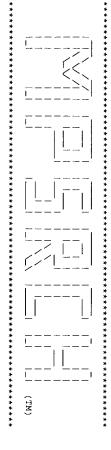
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                                                                                                              L-MALGELIGYTCLLAAICFFFAFKSRKLPENFNEAKFITFSMLIFFIVWISFIPAYAST
YDGKYLPAANMMAGLSSLSSGFGGY-FLPKCYVILCRPDLNSTE 761
                                    Y-GKFVSAVEVIAILAA-SFGLLACIFFNKVYIILFKPSRNTIE 871
                                                                                                                                                   PT-FYHAWVQNHGAGLFVMISSAAQLLICLTWLVVWTPLPAREYQRFPHLVMLECTETNS
                                                                                                                                                                                      PTSFHRKWWGLNLQFLLVFLCTFMQIVICAIWLNTAPPSSYRNHELEDEIIFITCHE-GS
                                                                         LGFILAFL-YNGLLSISAFACSYLGKDLPENYNEAKCVTFSLLFNFVSWIAFFTT-ASV
                                                                                                              829
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Search completed: Fri Mar 17 13:38:47 2000 Job time : 139 secs.

 $\begin{array}{c} \text{consons} \\ \text{consons}$



Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Mar 17 13:35:41 2000; MasPar time 13.42 Seconds 770.137 Million cell updates/sec

Tabular output not generated.

Title: >US-09-361-652-3 (1-777) from US09361652.pep 5838

Description: Perfect Score: Sequence: 1 RSCSFNEHGYHLFQAMRLGV.....NSTEHFQASIQDYTRRCGST 777

Scoring table: PAM 150 Gap 11

Searched: 134018 seqs, 13297625 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: a-issued 1:5A_COMB 2:5B_COMB 3:6_COMB 4:PCT9_COMB 5:backfiles1

Statistics: Mean 35.945; Variance 174.591; scale 0.206

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

22221111111111111111111111111111111111	Result
1170 1170 1170 1170 1160 1160 1160 1160	Score
20.00 20.00	% Query Match
1085 1085 1085 1085 1078 1078 1078 1078 1078 1079 1079 1079 1079 1088 1088 1088 1088 1088 1088	Length
14228221424282448224224	DB -
US-08-484 US-08-943 US-08-943 US-08-943 US-08-353 US-08-485 US-08-486	HD
Sequence 5, Sequence 5, Sequence 5, Sequence 7, Sequence 7, Sequence 7, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 6, Sequence 6, Sequence 6, Sequence 6, Sequence 6, Sequence 6, Sequence 5, Sequence 5, Sequence 5, Sequence 6, Sequence 1, Sequen	Description
Applicatio	
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ALIGNMENTS

661 770

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544 MLGSLAAG-SGSLYGFFGEPTRPACLLRQALFALGFTIFLSCLTVRSFQLIIIFKFSTKV
                     119 NKIDSLNLDEFCNCSEHIPSTIAVVGATGSGISTAVANLLGLFYIPQVSYASSSRLLSNK 178
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TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 CIRYNFRGFRWLQAMIFAIEEINSSPALLPNWTLGYRIFDTCNTVSKALEA--TLSFVAQ 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 1085 amino aci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                     REVPFSNCSRDCLAGTRKGIIEGEPTCCFECVECPDGEYSDETDASACDKCPDDFWSNEN 595
                                                                                                                                                                                                                                                            EQVTFDECGDLAGNYSIINWHLSPEDGSIVFKEVGYYNVYAKKGERLFINDEKILWSGFS
                                                                                                                                                                                                                                                                                                 SSAYNAYRAVYAVAHGLHQLLGC-AS-EL-----CS-RGRVYPWQLLEQIHKVHFLLHK- 370
                                                                                                                                                                                                                                                                                                                                    RISYNVYLAVYSIAHALQDIYTCIPGRGLFTNGSCADIKKVEAWQVLKHLRHLNFTSNMG
                                                                                                                                                                                                                                                                                                                                                                        AYA-R-AD--KEA-P----RPCHKG-SWCSSNQLC-RE-C--QAFMAHTMPKLKAFS-M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AFKDIMPFSAQVGDERMQCLMRHLAQAGATVVVVFSS-RQLARVFFESVVLTNLTGKVWV 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DFSE-L-ISQYSDEEKIQQVVEVIQNSTAKVIVVFSSGPDLEPLIKE-IVRRNITGRIWL 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NOFKSFLRTIPNDEHQATAMADIIEYFRWNWVGTIAADDDYGRPGIEKFREEAEERDICI 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HHIE-LQ-GDLLHYS---PTVLAVIGPDSTNRAATTAALLSPFLV-HISYAASSETLSVK 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C-SFNEHGYHLFQAMRLGVEEINNSTALLPNITLGYQLYDVCSDSANVYATLRVLSLPGQ 61
                                                                         SQTCFPRTVVFLALREHTSWVLLAANTLLLLLLLG-TAGLFAWHLDTPVVRSAGGRLCFL
                                                                                                            HTSCIAKEIEFLSWTEPFG-IALTLFAVLGIFLTAFVLGVFIKFRNTPIVKATNRELSYL 654
                                                                                                                                                HQVPKSVCSSDCLEGHQR-VVTGFHHCCFECVPCGAGTFLNKSELYRCQPCGTEEWAPEG
                                                                                                                                                                                                                          DTVAFNDNRDPLSSYNIIAWDWNGPK-WT-FTVLGS-STWSP-VQ-LNINETKIQWHGKN 425
                                                                                                                                                                                                                                                                                                                                                                                                             TFNCHLQEGAKGPLPVDTFLRGHEEGGARLSNSPTAFRPLCTGEENISSVETPYMDYTHL 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ASEAWA---L-SR----HITGVP-GIQ-RIGMVLGV-A-IQK---R-AVP-GL-KAF-EE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ASEAWASSSLIAMPEYFHVVGGTIGFGLKAGQIPGFREFLQKVHPRKSVHNGFAKEFWEE 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RQYPSFLRTIPNDKYQVETMVLLLQKFGWTWISLVGSSDDYGQLGVQALENQALVRGICI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 11 February, 19
APPLICATION NUMBER: U.S. 07/
FILING DATE: 23 August, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: U.S. 08/009,389
FILING DATE: 23 February, 1993
APPLICATION NUMBER: U.S. 08/017/127
FILING DATE: 12 February, 1993
APPLICATION NUMBER: U.S. 07/934,161
FILING DATE: 21 AUGUST, 1992
APPLICATION NUMBER: U.S. 07/834,044
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       h 20.0%; Sconsimilarity 31.9%; Pre-
263; Conservative 227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: protein
1085 AA; 121170 MW; 6189757 CN;
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pred. No. 3.80e-88;
227; Mismatches 256;
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                                                                                                                                                    APPLICATE: 9 JUNE PCT/US/3-,
APPLICATION NUMBER: PCT/US/3-,
APPLICATION NUMBER: 1994
APPLICATION NUMBER: U.S. 08/292,827
FILING DATE: 23 August, 1994
APPLICATION NUMBER: U.S. 08/14,248
APPLICATION NUMBER: U.S. 08/14,248
TILING DATE: 22 October, 1993
TILING DATE: 22 October, 1993
TILING DATE: 27 October, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 5, Application US/08485588
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: James E TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08
                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
FILING DATE:
ATTORNEY/AGENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Y-GKFVSAVEVIAILAA-SFGLLACIFFNKVYIILFKPSRNTIE 871
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     ADDRESSEE: Lyon & Lyon
STREET: First Interstate World
STREET: Suite 4700
STREET: 633 West Fifth Street
                                                                                                                   APPLIANG DATE: PILING DATE: 23 February, 1993
TIME DATE: 23 February, 1993
TIME DATE: 1993
TIME DATE: 1993
TIME DATE: 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: FASTSEQ
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CITY: Los Angeles
                                FILING DATE: 21 August, 1992
APPLICATION NUMBER: U.S. 07/834,044
FILING DATE: 11 February, 1992
APPLICATION NUMBER: U.S. 07/749,451
                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                            FILING DATE: 12 February, 1993
APPLICATION NUMBER: U.S. 07/934,161
                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 7 June,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
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VENTION: CALCIUM RECEPTOR-ACTIVE
VENTION: MOLECULES
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Steven C. Hebert
Forrest H. Fuller
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                                                                                                                                                                                                                                                                                                                                1: including application
1: described below: 9
08/353,784
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INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1085 amino acids
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEPAX: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
Y-GKFVSAVEVIAILAA-SFGLLACIFFNKVYIILFKPSRNTIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DTVAFNDNRDPLSSYNIIAWDWNGPK-WT-FTVLGS-STWSP-VQ-LNINETKIQWHGKN
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                                                                               LGFILAFL--YNGLLSISAFACSYLGKDLPENYNEAKCVTFSLLFNFVSWIAFFTT-ASV
                                                                                                                                   L-MALGFLIGYTCLLAAICFFFAFKSRKLPENFNEAKFITFSMLIFFIVWISFIPAYAST 829
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AYA-R-AD--KEA-P----RPCHKG-SWCSSNOLC-RE-C--QAFMAHTMPKLKAFS-M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TFNCHLQEGAKGPLPVDTFLRGHEEGGARLSNSPTAFRPLCTGEENISSVETPYMDYTHL 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ASEAWA---L-SR----HITGVP-GIQ-RIGMVLGV-A-IQK---R-AVP-GL-KAF-EE
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                                                                                                                                                                                       PT-FYHAWVQNHGAGLFVMISSAAQLLICLTWLVVWTPLPAREYQRFPHLVMLECTETNS
                                                                                                                                                                                                                                        PTSFHRKWWGLNLQFLLVFLCTFMQIVICAIWLNTAPPSSYRNHELEDEIIFITCHE-GS
                                                                                                                                                                                                                                                                                                                                                LLFSLLCCFSSSLF-FIGEPQDWTCRLRQPAFGISFVLCISCILVKTNRVLLVFE--AKI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HQVPKSVCSSDCLEGHQR-VVTGFHHCCFECVPCGAGTFLNKSELYRCQPCGTEEWAPEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SSAYNAYRAVYAVAHGLHQLLGC-AS-EL----CS-RGRVYPWQLLEQIHKVHFLLHK- 370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LE TYPE: protein
1085 AA; 121170 MW; 6189757 CN;
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GY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20.0%; Score 1170; DB 1; 1 larity 31.9%; Pred. No. 3.80e-88; Conservative 227; Mismatches 256;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA: including applic
PRIOR APPLICATION DATA: described below:
PRIOR APPLICATION NUMBER: 08/353,784

FILING DATE: 9 December, 1994
APPLICATION NUMBER: PCT/US/94/12117
FILING DATE: 21 October, 1994
APPLICATION NUMBER: U.S. 08/292,827
FILING DATE: 23 August, 1994
APPLICATION NUMBER: U.S. 08/141,248
APPLICATION NUMBER: U.S. 08/141,248
FILING DATE: 22 October, 1993
APPLICATION NUMBER: U.S. 08/09,389
                                                                                                                              APPLICATION NUMBER: U.S. 07/
FILING DATE: 23 August, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Heber, Sheldon O.
REGISTRATION NUMBER: 38,179
REFERENCE/DOCKET NUMBER: 213/
TELECOMMUNICATION INFORMATION:
                                       TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: PC-L
SOFTWARE: FASTSEQ
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: IBM PC compatible
COMPUTER: TOP TOP THE 
                                                                                                                                                                                                                                                APPLICANT: James E. Garrett, Jr.
TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
TITLE OF INVENTION: MOLECULES
NUMBER OF SEQUENCES: 20
SEQUENCE CHARACTERISTICS:
LENGTH: 1085 amino aci
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                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: U.S. 07/9
APPLICATION NUMBER: U.S. 07/9
FILING DATE: 21 August, 1992
APPLICATION NUMBER: U.S. 07/9
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ZIP: 900
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STREET: First Interstate World
STREET: Suite 4700
STREET: 633 West Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Los Angeles
STATE: California
                                                                                           TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
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Edward M. Brown
Steven C. Hebert
Forrest H. Fuller
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
                                                                                                                                                                                                                                                                                                                                                                                                                      23 February, 1993
UMBER: U.S. 08/017,127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    including application described below: 9 08/353,784
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1992
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                                                                                                                                                                                                                                                                                     /749,451
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SEQUENCE

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371 DTVAFNDNRDPLSSYNIIAWDWNGPK-WT-FTVLGS-STWSP-VQ-LNINETKIQWHGKN 425
                                                                                                                                                                                                                                                     830 Y-GKFVSAVEVIAILAA-SFGLLACIFFNKVYIILFKPSRNTIE 871
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                                                                                                                                                                                                     YDGKYLPAANMMAGLSSLSSGFGGY-FLPKCYVILCRPDLNSTE 761
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SQTCFPRTVVFLAUREHTSWVLLAANTLLLLLLLG-TAGLFAWHLDTPVVRSAGGRLCFL
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                                                                                                                                                                                                                                                                                                          LGFILAFL--YNGLLSISAFACSYLGKDLPENYNEAKCVTFSLLFNFVSWIAFFTT-ASV
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l Similarity 31.9%;
263; Conservative
                                                                                               STANDARD;
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Pred. No. 3.80e-88;
227; Mismatches 256;
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                                                                                                                                                                       Matches
                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                          SEQUENCE
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GENERAL INFORMATION:
61 CIRYNFRGFRWLQAMIFAIEEINSSPALLPNWTLGYRIFDTCNTVSKALEA--TLSFVAQ 118
                                                                                                                                                                                                                                                                                                                                                       NAME: Heber, Sheldon O.
REGISTRATION NUMBER: 38,179
REFERENCE/DOCKET NUMBER: 213,
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEEX: 67-3510
                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                          MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette,
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 1085 amino aci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: FASTSEQ
CURRENT APPLICATION DATA:
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APPLICANT: Steven C. Hebert
APPLICANT: James E. Garrett, Jr.
TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
TITLE OF INVENTION: MOLECULES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLIANG DATE: PILING DATE: 23 February, 1993
TIME DATE: 23 February, 1993
TIME DATE: 1993
TIME TO THE PILIP DATE: 1993
TIME TO THE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: Suite 4700
STREET: 633 West Fifth Street
                                                                                                                                                                                                                             TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: U.S. 07/
FILING DATE: 23 August, 1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: U.S. 08/141,248 FILING DATE: 22 October, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: PCT/US/94/12117
FILING DATE: 21 October, 1994
APPLICATION NUMBER: U.S. 08/292,827
FILING DATE: 23 August, 1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE: 03-OC
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                                                                                                                                                                     LE TYPE: protein
1085 AA; 121170 MW; 6189757
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: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MBER: 12 February, 1995
12 February, 1995
n.S. 07/934,161
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                                                                  Pred. No. 3.80e 227; Mismatches
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                                                                                             Score 1170;
Pred. No. 3
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                                                                                             ; DB 2;
3.80e-88;
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Sequence 5, Application US/08353784
                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Edward F. Nemeth, Edward M. APPLICANT: Brown, Steven C. Hebert, APPLICANT: Bradford C. Van Wagenen, Manuel APPLICANT: F. Balandrin, Forrest H. Fuller, APPLICANT: Eric G. DelMar, and Scott T. Moe TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE TITLE OF INVENTION: MOLECULES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MLGSLAAG-SGSLYGFFGEPTRPACLLRQALFALGFTIFLSCLTVRSFQLIIIFKFSTKV
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                                                                                                                                                                                                                                                                                                                                                                                                      YDGKYLPAANMMAGLSSLSSGFGGY-FLPKCYVILCRPDLNSTE
                                                                                                                                                                                                                                                                                                                                                                                                                                Y-GKFVSAVEVIAILAA-SFGLLACIFFNKVYIILFKPSRNTIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LGFILAFL--YNGLLSISAFACSYLGKDLPENYNEAKCVTFSLLFNFVSWIAFFTT-ASV 718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LLFSLLCCFSSSLF-FIGEPQDWTCRLRQPAFGISFVLCISCILVKTNRVLLVFE--AKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HTSCIAKEIEFLSWTEPFG-IALTLEAVLGIFLTAFVLGVFIKFRNTPIVKATNRELSYL 654
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AYA-R-AD--KEA-P----RPCHKG-SWCSSNQLC-RE-C--QAFMAHTMPKLKAFS-M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ASEAWA---L-SR----HITGVP-GIQ-RIGMVLGV-A-IQK---R-AVP-GL-KAF-EE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   L-MALGFLIGYTCLLAAICFFFAFKSRKLPENFNEAKFITFSMLIFFIVWISFIPAYAST
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                                                                                                                                                          5, Application o. 6011068
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Local Similarity 31.9%;
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PRIOR APPLICATION DATA: including applic
PRIOR APPLICATION DATA: described below
APPLICATION NUMBER: PCI/US/94/12117
FILING DATE: 21 October, 1994
APPLICATION NUMBER: U.S. 08/292,827
FILING DATE: 23 August, 1994
APPLICATION NUMBER: U.S. 08/141,248
APPLICATION NUMBER: U.S. 08/141,248
FILING DATE: 22 October, 1993
APPLICATION NUMBER: U.S. 08/009,389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: U.S. 07/83
FILING DATE: 11 February, 1992
APPLICATION NUMBER: U.S. 07/74
FILING DATE: 23 August, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Heber, Sheldon O.
REGISTRATION NUMBER: 38,179
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INFORMATION FOR SEQ ID NO:
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STREET: Suite 4700
STREET: Suite 4700
STREET: 633 West Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: 3.5" Di
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                                                                                                                                                      HHIE-LQ-GDLLHYS----PTVLAVIGPDSTNRAATTAALLSPFLV-HISYAASSETLSVK 115
                                                                                                                                                                                                                                                                   CIRYNFRGFRWLQAMIFAIEEINSSPALLPNMTLGYRIFDTCNTVSKALEA--TLSFVAQ 118
   AFKDIMPFSAQVGDERMQCLMRHLAQAGATVVVVFSS-RQLARVFFESVVLTNLTGKVWV
                                                                                                       NQFKSFLRTIPNDEHQATAMADIIEYFRWNWVGTIAADDDYGRPGIEKFREEAEERDICI
                                                                                                                                                                                          NKIDSLNLDEFCNCSEHIPSTIAVVGATGSGISTAVANILGLFYIPQVSYASSSRLLSNK 178
                                                                                                                                                                                                                               C-SFNEHGYHLFQAMRLGVEEINNSTALLPNITLGYQLYDVCSDSANVYATLRVLSLPGQ
                                     DFSE-L-ISQYSDEEKIQQVVEVIQNSTAKVIVVFSSGPDLEPLIKE-IVRRNITGRIWL
                                                                         RQYPSFLRTIPNDKYQVETMYLLLQKFGWIWISLVGSSDDYGQLGVQALENQALVRGICI 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FASTSEO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 12 February, 1993
APPLICATION NUMBER: U.S. 07/934,161
FILING DATE: 21 August, 1992
APPLICATION NUMBER: U.S. 07/834,044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 9 December, CLASSIFICATION: 514
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                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH:
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1085 AA; 121170 MW; 6189757 CN;
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Pred. No. 3.
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3.80e-88;
                                                                                                                                                                                                                                                                                                                                           Length 1085;
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Sequence 5 Patent No.

RESULT ID US

US-08-353-784-5

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Sequence 7, Application US/08943986
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ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Edward M. Brown
APPLICANT: Steven C. Hebbert
APPLICANT: James E. Garrett, Jr.
TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
TITLE OF INVENTION: MOLECULES
                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                           STREET: First Interstreet: Suite 4700 STREET: 633 West FCITY: Los Angeles
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                                                                                                                                                                          California
                                                                                                                                                                                                                          Suite 4700
633 West Fifth Street
                                                                                                                                                                                                                                                                            First Interstate World Center
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Best Local S
Matches 26
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INFORMATION FOR SEQ ID NO:
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APPLICATION NUMBER: PCI/UC/
FILING DATE: 21 October, 1994
APPLICATION NUMBER: U.S. 08/292,827
APPLICATION NUMBER: U.S. 08/141,248
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APPLICATION NUMBER: U.S. 07/
FILING DATE: 23 August, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Heber, Sheldon O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HHIE-LQ-GDLLHYS---PTVLAVIGPDSTNRAATTAALLSPFLV-HISYAASSETLSVK
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LENGTH: 1078 amino aci
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                          LRISYNVYLAVYSIAHALQDIYTCLPGRGLFTNGSCADIKKVEAWQVLKHLRHLNFTNNM 473
                                                                                                                                                                                                                    VASEAWA---L-S--R-HITGVP-GIQ-RIGMVLGV-A-IQK---R-AVP-GL-KAF-E
                                                                                                                                                                                                                                                                         LASEAWASSSLIAMPQYFHVVGGTIGFALKAGQIPGFREFLKKVHPRKSVHNGFAKEFWE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NQFKSFLRTIPNDEHQATAMADIIEYFRWNWVGTIAADDDYGRPGIEKFREEAEERDICI 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | :|::::|| ::::|| :::||| :::|| |:::| |::::| |::::| |::::| |:::| |::::| |::::| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |::|| |:::|| |::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |::
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        MSSAYNAYRAVYAVAHGLHQLLGC-AS-EL----CS-RGRVYPWQLLEQIHKVHFLLHK
                                                                                                                                                                     ETFNCHLQEGAKGPLPVDTFLRGHEESGDRFSNSSTAFRPLCTGDENISSVETPYIDYTH
                                                                                                                                                                                                                                                                                                                                 AFKDIMP-FSAQVGDERMQCLMRHLAQAGATVVVVFSS-RQLARVFFESVVLTNLTGKVW
                                                                                                               EAYA-R-ADKE-APRPCH---KGSWCSSNQLCRECQAF--M-A--HTMPKLKA----FS-
                                                                                                                                                                                                                                                                                                                                                                                 DFSELISQYSDE--EE-IQHVVEVIQNSTAKVIVVFSSGPDLEPLIKE-IVRRNITGKIW
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FILING DATE: 23 February, 1993
FILING TATON NUMBER: U.S. 08/017/127
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TITME DATE: 22 October, 1993
TITME DATE: 1993
TITMER: U.S. 08/009,389
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APPLICATION NUMBER: U.S. 07/934,161
1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Heber, Sheldon O. REGISTRATION NUMBER: 38,179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
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1078 AA; 120573 MW; 6153012 CN;
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67-3510
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Pred. No. 2.82e-87;
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ADDRESSEE:

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GENERAL INFORMATION:

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Sequence 7, Application
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   594
                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mt
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FASTSEQ
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/353,784
FILING DATE: 9 December, 1994
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                  Patent No. GENERAL I
                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 7, Application
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APPLICANT:
PRIOR APPLICATION DATA: includi
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PRIOR APPLICATION DATA: describ
APPLICATION NUMBER: PCT/US/94
FILING DATE: 21 October, 1994
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                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
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                                                                                                                                                                           ADDRESSEE:
STREET: Fi
STREET: 63
STREET: 63
CITY: Los
STATE: Cal
COUNTRY: U
ZIP: 90071
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                                                                                                                                                                                                                   Los Angeles
                                                                                                                                                                                                        California
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Suite 4700
633 West Fifth Street
                                                                                                                                                                                           USA
                                                                                                                                                                                                                                                                                                                                  Edward F. Nemeth, Edward M. Brown, Steven C. Hebert, Brown, Steven C. Habert, Bradford C. Van Wagenen, F. Balandrin, Forrest H. F. Eric G. DelMar, and Scott
                                                                                                                                                                                                                                                                     Lyon & Lyon
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          : including application
: described below: 8
PCT/US/94/12117
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652 483 593 424 370 473 413 274 353 233 293 175 237

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REFERENCE/DOCKET NUMBER: 209,
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1078 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               294 LASEAWASSSLIAMPQYFHVVGGTIGFALKAGQIPGFREFLKKVHPRKSVHNGFAKEFWE
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APPLICATION NUMBER: U.S. 08/009,389
FILING DATE: 23 February, 1993
APPLICATION NUMBER: U.S. 08/017,127
FILING DATE: 12 February, 1993
APPLICATION NUMBER: U.S. 07/934,161
FILING DATE: 21 AUGUST, 1992
APPLICATION NUMBER: U.S. 07/834,044
FILING DATE: 11 February, 1992
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NAME: Heber, Sheldon O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VASEAWA---L-S--R-HITGVP-GIQ-RIGMVLGV-A-IQK---R-AVP-GL-KAF-E
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GSQTCFPRTVVFLALREHTSWVLLAANTLLLLLLLG-TAGLFAWHLDTPVVRSAGGRLCF
                                                                                                                                 SREVPFSNCSRDCLAGTRKGIIEGEPTCCFECVECPDGEYSDETDASACNKC?DDFWSNE
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                                                                                                        NHQVPKSVCSSDCLEGHQR-VVTGFHHCCFECVPCGAGTFLNKSELYRCQPCGTEEWAPE
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                                               NHTSCIAKEIEFLSWTEPFG-IALTLFAVLGIFLTAFVLGVFIKFRNTPIVKATNRELSY
                                                                                                                                                                                                          -DTVAFNDNRDPLSSYNIIAWDWNGPK-WT-FTVLGS-STWSP-VQ-LNINETKIQWHGK
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APPLICATION NUMBER: U.S. 07/834,044
FILING DATE: 11 February, 1992
APPLICATION NUMBER: U.S. 07/749,451
FILING DATE: 23 August, 1991
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263; Conservative
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IMBER: U.S. 08/141,248
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pred. No. 2.82e-87;
232; Mismatches 250;
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RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Edward
                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: FASTSEQ CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: MOLECULES
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STREET:
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CITY: LC
STATE: CCUNTRY:
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                                           APPLIATION NUMBER: U.S. 1993
APPLICATION NUMBER: U.S. 08/017,127
TWARER: U.S. 08/017,127
                                                                                    APPLICATION NUMBER: U.S. 1993
TITING DATE: 22 October, 1993
TITING DATE: 22 October, 1993
TITING DATE: 1993
                                APPLICATION NUMBER: U.S. 08/017,127 FILING DATE: 12 February, 1993 APPLICATION NUMBER: U.S. 07/934,161
                                                                                                                                                         APPLICATION NUMBER: PCT/US/94/12117
FILING DATE: 21 October, 1994
APPLICATION NUMBER: U.S. 08/292,827
FILING DATE: 23 August, 1994
FILING DATE: 23 August, 1994
                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM:
SOFTWARE: FASTSEC
                                                                                                                                                                                                                                    APPLICATION NUMBER: 08/3: FILING DATE: 9 December,
                                                                                                                                                                                                                                                                                                                                             FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER:
     FILING DATE APPLICATION
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5.5688938
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                     DATE:
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Suite 4700
633 West Fifth Street
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Forrest H. Fuller
James E. Garrett, Jr.
VENTION: CALCIUM RECEPTOR-ACTIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Edward M. Brown
                                                                                                                                                                                                                                                                                                                                                                                                             IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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   NUMBER:
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 21 August, 1992
JMBER: U.S. 07/
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1: described below: 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 HHIE-IQ-GDLLHYS----PTVLAVIGPDSTNRAATTAALLSPELV-HISYAASSETLSVK 115
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APPLICATION NUMBER: U.S. 07/
FILING DATE: 23 August, 1991
ATTORNEY/ACENT INFORMATION:
NAME: Heber, Sheldon O.
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ENCE 1078 AA
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SL-MALGELIGYTCLLAAICEFFAFKSRKLPENFNEAKFITESMLIEFIVMISFIPAYAS
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                                                     VPT-FYHAWVQNHGAGLFVMISSAAQLLICLTWLVVWTPLPAREYQRFPHLVMLECTETN
                                                                                    IPTSFHRKWWGLNLQFLLVFLCTFMQIVICVIWLYTAPPSSYRNQELEDEIIFITCHE-G
                                                                                                                        LMLGSLAAG-SGSLYGFFGEPTRPACLLRQALFALGFTIFLSCLTVRSFQLIIIFKFSTK
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TOPOLOGY:
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TELEX: 67-3510
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REFERENCE/DOCKET NUMBER: 21:
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JMBER: U.S. 07/74
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                                                                                                                                                                                                                                     FILING DATE:

APPLICATION NUMBER: PCT/US/>*, --

FILING DATE: 21 October, 1994

APPLICATION NUMBER: U.S. 08/29,827

FILING DATE: 23 August, 1994

APPLICATION NUMBER: U.S. 08/141,248

FILING DATE: 22 October, 1993

APPLICATION NUMBER: U.S. 08/009,389

FILING DATE: 23 February, 1993

FILING DATE: 23 February, 1993

FILING DATE: 23 February, 1993

FILING DATE: 26 February, 1993

FILING DATE: 27 February, 1993

FILING DATE: 28 FEBRUARY, 1993

FILING DATE: 29 FEBRUARY, 1993

FILING DATE: 29 FEBRUARY, 1993

FILING DATE: 21 FEBRUARY, 1993

FILING DATE: 23 FEBRUARY, 1993

FILING DATE: 24 FEBRUARY, 1993

FILING DATE: 25 FEBRUARY, 1993
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                                                                                            FILING DATE: U.S. 08/01/,14/
APPLICATION NUMBER: U.S. 08/01/,14/
FILING DATE: 12 February, 1993
APPLICATION NUMBER: U.S. 07/934,161
FILING DATE: 21 August, 1992
APPLICATION NUMBER: U.S. 07/834,044
FILING DATE: 11 February, 1992
APPLICATION NUMBER: U.S. 07/749,451
FILING DATE: 23 August, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Heber, Sheldon O.
NAME: Heber, Sheldon O.
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TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
               NAME: Hober, Sheldon O.
REGISTRATION NUMBER: 38,179
REFERENCE/DOCKET NUMBER: 213/
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1500
TELEPAX: (213) 955-0440
TELEX: 67-3510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 7 June, 1
CLASSIFICATION: 435
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PRIOR APPLICATION DATA: inc
PRIOR APPLICATION DATA: des
APPLICATION NUMBER: 08/35
FILING DATE: 9 December.
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MEDIUM TYPE: 3.5" Diskette,
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Edward M. Brown
APPLICANT: Steven C. Hebbert
APPLICANT: James E. Garrett, Jr.
TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: MOLECULES NUMBER OF SEQUENCES: 20
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ZIP: 900
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STATE:
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California
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633 West Fifth Street
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described below: 9
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                                                                                                                                   TY-GKFVSAVEVIAILAA-SFGLLACIFFNKIYIILFKPSRNTIE
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                                                                                                                 VYDGKYLPAANMMAGLSSLSSGFGGY-FLPKCYVILCRPDLNSTE
                                                                                                                                                                                 SLGFILAFL--YNGLLSISAFACSYLGKDLPENYNEAKCYTFSLLFNFYSWIAFFTT-AS
                                                                                                                                                                                                                                                                                                                                                  LLLFSLLCCFSSSLF-FIGEPQDWTCRLRQPAFGISFVLCISCILVKTNRVLLVFE--AK
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                                                                                                                                                                                                                SL-MALGFLIGYTCLLAAICFFFAFKSRKLPENFNEAKFITFSMLIFFIVWISFIPAYAS
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Pred. No. 2.82e-87;
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Best Loc
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                    Query Match
                                         SEQUENCE
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Patent No
GENERAL
            Local Similarity
                                                                                                                                                                                                                                                      FILING DATE: 21 October, 1994
APPLICATION NUMBER: PCT/US/94/1211/
FILING DATE: 21 October, 1994
APPLICATION NUMBER: U.S. 08/292,827
FILING DATE: 23 August, 1994
APPLICATION NUMBER: U.S. 08/141,248
FILING DATE: 22 October, 1993
APPLICATION NUMBER: U.S. 08/009,389
FILING DATE: 23 February, 1993
APPLICATION NUMBER: U.S. 08/017,127
                                                                                                  TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                         APPLICATION NUMBER: U.S. 07,
FILING DATE: 23 August, 199,
ATTORNEY/AGENT INFORMATION:
NAME: Heber, Sheldon 0,
REGISTRATION NUMBER: 38,179
                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA: inc
PRIOR APPLICATION DATA: de:
APPLICATION NUMBER: 08/3:
FILING DATE: 9 December,
                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: FASTSEQ
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,751
FILING DATE: 7 June, 1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: James E. Garrett, Jr.
TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
TITLE OF INVENTION: MOLECULES
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
                                                                                                                              REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                   MOLECULE TYPE:
                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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                                                                                                                                                                               FILING DATE: APPLICATION NUMBER: U.S. APPLICATION NUMBER: U.S. 1992
FILING DATE: 11 February, 1992
FILING DATE: U.S. 07/749,451
                                                           TYPE: ami
TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET:
CITY: L
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APPLICATION NUMBER: U.S. 07/934,161
FILING DATE: 21 August, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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  263;
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o. 5858684
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                                       LE TYPE: protein
1078 AA; 120573 MW; 6153012 CN;
  19.9%; ilarity 31.9%; Conservative
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First Interstate World
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Edward M. Brown
Steven C. Hebert
Forrest H. Fuller
                                                                                                                      (213) 955-0440
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\: described below: 9
08/353,784
Score 1160; DB 2;
Pred. No. 2.82e-87;
232; Mismatches 250;
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                      TY-GKFVSAVEVIAILAA-SFGLLACIFFNKIYIILFKPSRNTIE
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VYDGKYLPAANMMAGLSSLSSGFGGY-FLPKCYVILCRPDLNSTE
                                                                                                                       SL-MALGELIGYTCLLAAICEFFAFKSRKLPENENEAKFITESMLIFFIVWISFIPAYAS 827
                                                                                                                                                                                          VPT-FYHAWVQNHGAGLFVMISSAAQLLICLTWLVVWTPLPAREYQRFPHLVMLECTETN
                                                                                                                                                                                                                                    IPTSFHRKWWGLNLQFLLVFLCTFMQIVICVIWLYTAPPSSYRNQELEDEIIFITCHE-G
                                                                                                                                                                                                                                                                                    LMLGSLAAG-SGSLYGFFGEPTRPACLLRQALFALGFTIFLSCLTVRSFQLIIIFKFSTK
                                                                                                                                                                                                                                                                                                               LLLFSLLCCFSSSLF-FIGEPQDWTCRLRQPAFGISFVLCISCILVKTNRVLLVFE--AK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SREVPFSNCSRDCLAGTRKGIIEGEPTCCFECVECPDGEYSDETDASACNKCPDDFWSNE
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                                                                                            SLGFILAFL--YNGLLSISAFACSYLGKDLPENYNEAKCVTFSLLFNFVSWIAFFTT-AS
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RESULT ID US XXXXXX US-08-484-565-8 Sequence 8, Application US/08484565 GENERAL INFORMATION:
APPLICANT: Edward
APPLICANT: Steven
APPLICANT: James E Sequence Patent No. 8, Application o. 5763569 Edward M. Brown Steven C. Hebert James E. Garrett, STANDARD; US/08484565 PRT; 1079 A

Jr.

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Query Match
Best Local S
Matches 26
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below: 9
APPLICATION NUMBER: 08,353,784
FILING DATE: 9 December, 1994
APPLICATION NUMBER: PCT/US/94/12117
FILING DATE: 21 October, 194
APPLICATION NUMBER: U.S. 08/292,827
FILING DATE: 23 August, 1994
APPLICATION NUMBER: U.S. 08/141,248
APPLICATION NUMBER: U.S. 08/141,248
FILING DATE: 20 October, 1993
FILING DATE: 20 October, 1993
FILING DATE: 20 October, 1993
                                                                                                                                                                                                                                                                                   SEQUENCE
     116
                                       178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Heber, Sheldon O
REGISTRAMION:
                                                                                                                                                                                                                                                                                                     MOLECULE
                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION: TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: FASTSEQ CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                   HHIE-LQ-GDLLHYS---PTVLAVIGPDSTNRAATTAALLSPFLV-HISYAASSETLSVK 115
                                                                                                                                      C-SFNEHGYHLFQAMRLGVEEINNSTALLPNITLGYQLYDVCSDSANVYATLRVLSLPGQ 61
                                                                                                                                                               CIRYNFRGFRWLQAMIFAIEEINSSPSLLPNMTLGYRIFDTCNTVSKALEA--TLSFVAQ 117
                                    NOYKSFLRTIPNDEHQATAMADIIEYFRWNWVGTIAADDDYGRPGIEKFREEAEERDICI
                                                                                            NKIDSLNLDEFCNCSEHIPSTIAVVGATGSGVSTAVANLLGLFYIPQVSYASSSRLLSNK 177
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STREET: Suite 4700
STREET: 633 West F
CITY: Los Angeles
     RQYPSFLRTIPNDKYQVETMVLLLQKFGWTWISLVGSSDDYGQLGVQALENQALVRGICI
                                                                                                                                                                                                                                                                                                                    TYPE: ami
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APPLICATION NUMBER: U.S. 07/834,044
FILING DATE: 11 February, 1992
APPLICATION NUMBER: U.S. 07/749,451
FILING DATE: 23 August, 1991
                                                                                                                                                                                                                                                                                                                                                      LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (213) 955-0440
TELEX: 67-3510
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: U.S. 08/009,389
FILING DATE: 23 February, 1993
APPLICATION NUMBER: U.S. 08/017,127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/484,565 FILING DATE: 7 June, 1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 12 February, 1993
APPLICATION NUMBER: U.S. 07/934,161
FILING DATE: 21 August, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                  262;
                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                   LE TYPE:
1079 AA;
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                                                                                                                                                                                                              19.8%; Score 1158; DB 1; larity 31.4%; Pred. No. 4.21e-87; Conservative 233; Mismatches 261;
                                                                                                                                                                                                                                                                                                                                    amino acid
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633 West Fifth Street
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120867 MW; 6054255 CN;
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                                                                                                                                                                        APPLICANT:
APPLICANT:
APPLICANT:
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                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                     TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
STREET: First Inte:
STREET: Suite 4700
STREET: 633 West F
CITY: Los Angeles
STATE: California
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                                                                                       ADDRESSEE:
                                                                                                                                                                                                                                                                                 No.
                                                                                                                                                                                                                                                                                                                                8, Application US/08480751
                                                                                                                                                                                                                                                                                   5858684
                                                                                                                                  I: Edward F. Nemeth
I: Edward M. Brown
I: Steven C. Hebert
I: Forrest H. Fuller
I: James E. Garrett, Jr.
INVENTION: CALCIUM RECEPTOR-ACTIVE
INVENTION: MOLECULES
                              First Interstate World
Suite 4700
633 West Fifth Street
                                                                                   Lyon & Lyon
                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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768 600 708 541

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Query Match 19.8%; Score 1158; DB 2; I Best Local Similarity 31.4%; Pred. No. 4.21e-87; Matches 262; Conservative 233; Mismatches 261;
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     354
                                                                                                                                                                                                                                                                                                                                                                                                                                       118 NKIDSLNLDEFCNCSEHIPSTIAVVGATGSGVSTAVANLLGLFYIPQVSYASSSRLLSNK 177
                                                                                                              294
                                                                                                                                                               176 AFKDIMP-FSAQVGDERMQCLMRHLAQAGATVVVVVFSS-RQLARVFFESVVLTNLTGKVW
                                                                                                                                                                                                                                                                           116 ROYPSFLRTIPNDKYQVETMVLLLQKFGWTWISLVGSSDDYGQLGVQALENQALVRGICI 175
                                                                                                                                                                                                                                                                                                                                 178 NQYKSFLRTIPNDEHQATAMADIIEYFRWNWVGTIAADDDYGRPGIEKFREEAEERDICI 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60 CIRYNFRGFRWLQAMIFAIEEINSSPSLLPNMTLGYRIFDTCNTVSKALEA--TLSFVAQ 117
                                                                                                                                                                                                                                                                                                                                                                                       62 HHIE-LQ-GDLLHYS---PTVLAVIGPDSTNRAATTAALLSPFLV-HISYAASSETLSVK
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NAME: Heber, Sheldon O.
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PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
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MEDIUM TYPE: 3.5" Di
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                                                                                                                                                                                                                     DFSELISQYSDE--EEIQQ-VVEVIQNSTAKVIVVFSSGPDLEPLIKE-IVRRNITGRIW 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C-SFNEHGYHLFQAMRLGVEEINNSTALLPNITLGYQLYDVCSDSANVYATLRVLSLPGQ 61
ETFNCHLQEGAKGPLPVDTFVRSHEEGGNRLLNSSTAFRPLCTGDENINSVETP-YMDYE
                                                     VASEAWA---L-SR----HITGVP-GIQ-RIGMVLGV-A-IQK---R-AVP-GL-KAF-E
                                                                                                         LASEAWASSSLIAMPEYFHVVGGTIGFGLKAGQIPGFREFLQKVHPRKSVHNGFAKEFWE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 21 AUGUST 17/85%, APPLICATION NUMBER: U.S. 07/85%, APPLICATION NUMBER: U.S. 07/749,451
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX:
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APPLICATION NUMBER: U.S. 07/
FILING DATE: 23 August, 1991
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FILING DATE: 21 October, 1994
APPLICATION NUMBER: U.S. 08/292,827
FILING DATE: 23 August, 1994
FILING DATE: 23 AUGUST, 1994
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1079 AA; 120867 MW; 6054255 CN;
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12 February, 1995
n.S. 07/934,161
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US-08-353-784-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION: APPLICANT: Edward
                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                          CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
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                                                                                                                                                                                                                                                         STREET: Fill 4700
STREET: Suite 4700
STREET: 633 West Fifth Street
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                                                                                                                                                                                                                                          CITY: Los Angeles
STATE: California
                      APPLICATION NUMBER:
                                                                   SOFTWARE:
                                                                                                                                                                                            ZIP: 90071
                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Lyon & Lyon
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                                                                                                                                                                                                                                                                                                                                       First Interstate World
                                                                                                                                                                                                                   USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                           F. Balandrin, Forrest H. Fuller, Eric G. DelMar, and Scott T. Moe VENTION: CALCIUM RECEPTOR-ACTIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Edward F. Nemeth, Edward M. Brown, Steven C. Hebert, Bradford C. Van Wagenen, Manuel
                                                                      FASTSEQ
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December,
                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULES
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                      US/08/353,784
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FILING DATE: 11 February, 1992
APPLICATION NUMBER: U.S. 077749,451
FILING DATE: 23 AUGUST. 1991
ATTORNEY/AGENT INFORMATION:
NAME: Heber, Sheldon O.
NAME: Heber, Sheldon O.
NAME: Heber, Sheldon O.
NAME: Heber, Sheldon O.
                                                                                                                                                                                                                                                                                                                                                                                                              178
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APPLICATION NUMBER: U.S. 08/292,827
FILING DATE: 23 August, 1994
APPLICATION NUMBER: U.S. 08/141,248
FILING DATE: 22 October, 1993
ADDITICATION NUMBER: U.S. 08/099,389
ADDITICATION NUMBER: U.S. 08/099,389
ADDITICATION NUMBER: U.S. 08/099,389
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEPHAX: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 514
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
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               FSREVPFSNCSRDCQAGTRKGIIEGEPTCCFECVECPDGEYSGETDASACDKCPDDFWSN
                                            K-DTVAFNDNRDPLSSYNIIAWDWNGPK-WT-FTVLGS-STWSP-VQ-LNINETKIQWHG
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FILING DATE: 12 Feb;
APPLICATION NUMBER:
FILING DATE: 21 Augu
                                                                            MGEQVTFDECGDLVGNYSIINWHLSPEDGSIVFKEVGYYNVYAKKGERLFINEEKILWSG
                                                                                                                                           HLRISYNVYLAVYSIAHALQDIYTCLPGRGLFTNGSCADIKKVEAWQVLKHLRHLNFTNN
                                                                                                                                                                            EAYA-R-AD--KEA-P----RPCHKGS-W---CSSN-Q-LCRECQAFMAHTMPKLKAFS
                                                                                                                                                                                                                                                                                                                                                                            ROYPSFLRTIPNDKYQVETMVLLLQKFGWTWISLVGSSDDYGQLGVQALENQALVRGICI
                                                                                                             -MSSAYNAYRAVYAVAHGLHQLLGC-AS-EL----CS-RGRVYPWQLLEQIHKVHFLLH
                                                                                                                                                                                                                                                                                                                                          DFSELISQYSDE--EEIQQ-VVEVIQNSTAKVIVVFSSGPDLEPLIKE-IVRRNITGRIW
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UMBER: U.S. 07/934,161
21 August, 1992
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JMBER: U.S. 08/017,127
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: described below: 8
PCT/US/94/12117
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Pred. No. 4.21e-87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1079;
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US-08-943-986-8
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APPLICATION NUMBER: PCT/US/94/1211,
APPLICATION NUMBER: PCT/US/94/1211,
APPLICATION NUMBER: U.S. 08/292,827
APPLICATION NUMBER: U.S. 08/292,827
APPLICATION NUMBER: U.S. 08/141,248
APPLICATION NUMBER: U.S. 08/141,248
FILING DATE: 22 October, 1993
*PDLICATION NUMBER: U.S. 08/09,389
*PDLICATION NUMBER: U.S. 08/09,389
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: James E. Garrett,
TITLE OF INVENTION: CALCIUM RI
TITLE OF INVENTION: MOLECULES
NUMBER OF SEQUENCES: 20
                                                                                                                                                                                                                                                                                  COMPUTER: Lbm. - POPERATING SYSTEM: POPERATING SYSTEM: POPERATE PASTSEQ
                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44
                                                                                                                                                                                                         CLASSIFICATION: 530 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Y-GKEVSAVEVIAILAA-SEGLLACIEENKVYIILEKPSRNTIEEVRSSTAAHA
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                                                                                                                                                                       APPLICATION NUMBER: 0
FILING DATE: 7-June-1
                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/943,986 FILING DATE: 03-OCT-1997
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California
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633 West Fifth
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Steven C.
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Best Local
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TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 1079 amino acids
TYPE: amino acid
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FILING DATE: 12 February, 1993
APPLICATION NUMBER: U.S. 07/934,161
FILING DATE: 21 August, 1992
APPLICATION NUMBER: U.S. 07/834,044
FILING DATE: 11 February, 1992
APPLICATION NUMBER: U.S. 07/749,451
FILING DATE: 23 August, 1991
ATTORNEY/ACENT INFORMATION:
NAME: USBOT OF STATE OF ST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60 CIRYNFRGFRWLQAMIFAIEEINSSPSLLPNMTLGYRIFDTCNTVSKALEA--TLSFVAQ 117
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Local Similarity 31.4%;
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                                                                                                                                                                                                                                                                                                           FSREVPFSNCSRDCQAGTRKGIIEGEPTCCFECVECPDGEYSGETDASACDKCPDDFWSN 592
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                                                                                                                                                                                                                                                                                                                                                                                                                MGEQVTFDECGDLVGNYSIINWHLSPEDGSIVFKEVGYYNVYAKKGERLFINEEKILWSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HLRISYNVYLAVYSIAHALQDIYTCLPGRGLFTNGSCADIKKVEAWQVLKHLRHLNFTNN 472
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                                                                                             YLLLESLLCCFSSSLF-FIGEPQDWTCRLRQPAFGISFVLCISCILVKTNRVLLVFE--A
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KIPTSFHRKWWGLNLQFLLVFLCTFMQILICIIWLYTAPPSSYRNHELEDEIIFITCHEG
                                                FLMLGSLAAG-SGSLYGFFGEPTRPACLLRQALFALGFTIFLSCLTVRSFQLIIIFKFST
                                                                                                                                                        EGSQTCFPRTVVFLALREHTSWVLLAANTLLLLLLLG-TAGLFAWHLDTPVVRSAGGRLC
                                                                                                                                                                                                           ENHTSCIAKEIEFLAWTEPFG-IALTLFAVLGIFLTAFVLGVFIKFRNTPIVKATNRELS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -MSSAYNAYRAVYAVAHGLHQLLGC-AS-EL----CS-RGRVYPWQLLEQIHKVHFLLH
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1079 AA; 120867 MW; 6054255 CN;
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OGY: linear
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Pred. No. 4.21e-87;
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Sequence 8, Application US/08485588
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PRIOR APPLICATION DATA: includi:
PRIOR APPLICATION DATA: describ
APPLICATION NUMBER: 08/353,78
FILING DATE: 9 December, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: FASTSEQ CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Edward K. Brown
APPLICANT: Steven C. Hebert
APPLICANT: Forrest H. Fuller
APPLICANT: James E. Garrett, Jr.
TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
TITLE OF INVENTION: MOLECULES
                  ATTORNEY/AGENT INFORMATION: NAME: Heber, Sheldon O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                      APPLICATION NUMBER: PCT/US/57, --
FILING DATE: 21 October, 1994
APPLICATION NUMBER: U.S. 08/292,827
FILING DATE: 23 August, 1994
FILING DATE: 23 August, 1994
FILING DATE: 1994
FILING DATE: 1994
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                                                                       FILING DATE: 21 Aug. 0//APPLICATION NUMBER: U.S. 0//APPLICATION THE 11 February, 19
                                                                                                                                                                               FILING LATE: U.S. 00/11.
APPLICATION NUMBER: U.S. 00/11.
FILING DATE: 22 October, 1993
FILING DATE: U.S. 08/009,389
                                                                                                                                                     APPLICATION NUMBER: U.S. 08/017,127
FILING DATE: 12 February, 1993
APPLICATION NUMBER: U.S. 07/934,161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 7 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC OPERATING SYSTEM:
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CITY: Los Angeles
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                                                     APPLICATION NUMBER: U.S. 07/
FILING DATE: 23 August, 1991
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REGISTRATION NUMBER:
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First Interstate World
Suite 4700
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                                                                                                      21 August, 1992
TMBER: U.S. 07/834,044
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08/353,784
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Best Local S
Matches 26
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEFAX: (7-3510
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 1079 amino acids
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                                  Y-GKFVSAVEVIAILAA-SFGLLACIFFNKVYIILFKPSRNTIEEVRSSTAAHA 880
                                                                                          FLMLGSLAAG-SGSLYGFFGEPTRPACLLRQALFALGFTIFLSCLTVRSFQLIIIFKFST
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YDGKYLPAANMMAGLSSLSSGFGGY-FLPKCYVILCRPDLNSTEHFQASIQDYT
                                                                      NSLGFILAFLYNGLLSISAFACSYLGKDLPENYNEAKCVTFSLLFNFVSWIAFFTT-ASV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EAYA-R-AD--KEA-P----RPCHKGS-W---CSSN-Q-LCRECQAFMAHTMPKLKAFS
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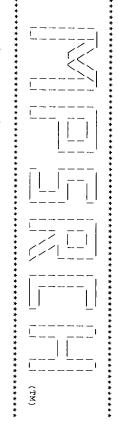
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Search completed: Fri Mar 17 13:36:11 Job time : 30 secs.

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp Run on: protein - protein database search, using Smith-Waterman algorithm Fri Mar 17 13:26:21 2000; MasPar time 39.48 Seconds 466.217 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: Title:

Sequence: >US-09-361-652-3 (1-777) from US09361652.pep 5838 1 RSCSFNEHGYHLFQAMRLGV.....NSTEHFQASIQDYTRRCGST 777

Scoring table: PAM 150 Gap 11

Searched: 188963 seqs, 23686106 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: a-geneseq36 1:geneseqp

Statistics: Mean 38.193; Variance 172.438; scale 0.221

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

2221165544321 2221065544321 3221065544321	Result
1170 1170 1160 1160 1160 1158 1158 1158 1158 1158 1159 1163 1063 1063 1063 1063 1063 1063 1063	Score
11344557330000 6775573300000000000000000000000000000000	% Query Match
1085 1085 1085 1078 1078 1078 1079 1079 1088 1088 1088 1088 1088 1088 1088 108	Length
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11.6	11.6	12.0	12.2	12.2	12.2	12.2	12.3	12.5	12.5	12.9	13.0	13.0	13.1	13.2	13.2	13.2	13.4	13.5	13.5	13.5	13.6
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R72093	W94925	W94918	R64252	R82657	W94919	W94917	W94903	W01099	W94920	W49928	W41568	R89580	R64255	R64254	R64253	W94901	R95052	R42199	W25765	R64250	R25080
a	Rat pheromone receptor	Rat pheromone receptor	Human mGluR3.	Human mGluR3.	Rat pheromone receptor	Rat pheromone receptor	Mouse pheromone recept	Metabotropic glutamate		Human metabotropic glu	opic	Metabotropic glutamate	Human mGluR5c.	Human mGluR5b.	Human mGluR5a.	Mouse pheromone recept	Human metabotropic glu	HSmGluR1.	Amino acid sequence of	Human mGluR1B.	GLU-G-R subtype la.
3.02e-48	2.45e-48	.27e-5	Ġ	.11e-5	.53e-5	.11e-5	Ġ	.24e-5	.24e-5	.13e-5	.14e	.92e-5		5.83e-57	. 20e	ģ		.59e-5	1.96e-58	.40e-	2.35e-59

ALIGNMENTS

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recombinant nucleic acid. The present sequence represents bowine parathyroid CR, designated a BoPCAR 1. The nucleic acid sequence of BoPCAR 1 can be used as part of the recombinant nucleic acid in the	ffect the one or more CR activities in a cell not compri-	compound to affect one or more activities of the calcium receptor; and	provided that the cell does not have functional CK expression from endogenous nucleic acid; (3) determining the ability of the test	recombinant cell comprises a recombinant nucleic acid expressing the CR,	tacting a recombinant cell with a test compound, where the	ctivities of a calcium receptor (CR) comprises: (A)	nound able to affec		acid encoding calcium receptor and determ	calcium	N-PSDB; V82483.	•	Hebert SC, Nemeth EF, Van Wagenen BC;	NE DESCRIPTION OF THE PROPERTY	(BGHM) BRIGHAM & WOMENS HOSPITAL.	US-353784.	21-OCT-1994; WO-U12117.	19-AUG-1994; US-292827.	22-OCT-1993; US-141248.	23-FEB-1993; US-009389.	12-FEB-1993; US-017127.	21-AUG-1992; US-934161.	11-FEB-1992; US-834044.	SU-	US-	48075	12-JAN-1999.	US5858684-A.			Huntington's disease; Parkinson's disease; dementia; muscle tension;	neonatal distress: neurodegenerative disease: Alzheimer's disease:	spinal cord injury: hypoxia-induced nerve cell damage: cardiac arrest:	original variations of the property of the pro	atctum receptor borcax I.	,	₩ ₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩	8956	7 1

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Query Match
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Matches 26
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719
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DTYAFNDNRDPLSSYNIIAWDWNGPK-WT-FTVLGS-STWSP-VQ-LNINETKIQWHGKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HHIE-LQ-GDLLHYS---PTVLAVIGPDSTNRAATTAALLSPELV-HISYAASSETLSVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NKIDSLNLDEFCNCSEHIPSTIAVVGATGSGISTAVANLLGLFYIPQVSYASSSRLLSNK 178
                                                         Y-GKFVSAVEVIAILAA-SFGLLACIFFNKVYIILFKPSRNTIE
                                                                                                                                                                                     L-MALGFLIGYTCLLAAICFFFAFKSRKLPENFNEAKFITFSMLIFFIVWISFIPAYAST
                                                                                                                                                                                                                                                         PT-FYHAWVQNHGAGLFVMISSAAQLLICLTWLVVWTPLPAREYQRFPHLVMLECTETNS
                                                                                                                                                                                                                                                                                                               PTSFHRKWWGLNLQFLLVFLCTFMQIVICAIWLNTAPPSSYRNHELEDEIIFITCHE-GS
                                                                                                                                                                                                                                                                                                                                                                                            MLGSLAAG-SGSLYGFFGEPTRPACLLRQALFALGFTIFLSCLTVRSFQLIIIFKFSTKV
                                                                                                                                                                                                                                                                                                                                                                                                                                 LLFSLLCCFSSSLF-FIGEPQDWTCRLRQPAFGISFVLCISCILVKTNRVLLVFE--AKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SQTCEPRIVYELALREHISWYLLAANTLLLLLLLG-TAGLFAWHLDTPVVRSAGGRLCFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HTSCIAKEIEFLSWTEPFG-IALTLFAVLGIFLTAFVLGVFIKFRNTPIVKATNRELSYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HQVPKSVCSSDCLEGHQR-VVTGFHHCCFECVPCGAGTFLNKSELYRCQPCGTEEWAPEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REVPFSNCSRDCLAGTRKGIIEGEPTCCFECVECPDGEYSDETDASACDKCPDDFWSNEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EQVTFDECGDLAGNYSIINWHLSPEDGSIVFKEVGYYNVYAKKGERLFINDEKILWSGFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SSAYNAYRAVYAVAHGLHQLLGC-AS-EL----CS-RGRVYPWQLLEQIHKVHFLLHK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RISYNVYLAVYSIAHALODIYTCIPGRGLFTNGSCADIKKVEAWQVLKHLRHLNFTSNMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AYA-R-AD--KEA-P----RPCHKG-SWCSSNQLC-RE-C--QAFMAHTMPKLKAFS-M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TFNCHLQEGAKGPLPVDTFLRGHEEGGARLSNSPTAFRPLCTGEENISSVETPYMDYTHL 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ASEAWA---L-SR----HITGVP-GIQ-RIGMVLGV-A-IQK---R-AVP-GL-KAF-EE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ASEAWASSSLIAMPEYFHVVGGTIGFGLKAGQIPGFREFLQKVHPRKSVHNGFAKEFWEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AFKDIMPFSAQVGDERMQCLMRHLAQAGATVVVVFSS-RQLARVFFESVVLTNLTGKVWV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DFSE-L-ISQYSDEEKIQQVVEVIQNSTAKVIVVFSSGPDLEPLIKE-IVRRNITGRIWL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RQYPSFLRTIPNDKYQVETMVLLLQKFGWTWISLVGSSDDYGQLGVQALENQALVRGICI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NQFKSFLRTIPNDEHQATAMADIIEYFRWNWVGTIAADDDYGRPGIEKFREEAEERDICI 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C-SFNEHGYHLFQAMRLGVEEINNSTALLPNITLGYQLYDVCSDSANVYATLRVLSLPGQ
YDGKYLPAANMMAGLSSLSSGFGGY-FLPKCYVILCRPDLNSTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20.08;
1 Similarity 31.98;
263; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1085 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         disease, dementia, muscle tension, depression, and anxiety
                                                                                                                            YNGLLSISAFACSYLGKDLPENYNEAKCYTFSLLFNFVSWIAFFTT-ASV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1170; DB 1; 1
Pred. No. 4.34e-94;
227; Mismatches 256;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1085;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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Best Local
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21-OCT-1994;
08-DEC-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-JUN-1995;
23-AUG-1991;
11-FEB-1992;
11-AUG-1992;
12-FEB-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                          antibody production claims and solve that can be used to treat diseases associated with the receptors in these tissues. They can be used to treat diseases associated with the receptors and receptors also be used to treat diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Calcium receptor poly:peptide(s) - useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (BGHM) BRIGHAM & WOMENS HOSPITAL.
(NPSP-) NPS PHARM INC.
Brown EM, Garrett JE, Hebert SC;
WPI; 98-347412/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bos sp.
US5763569-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bovine parathyroid calcium Calcium ion concentration;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        W54844 standard;
W54844;
01-SEP-1998 (fir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; V26962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (BGHM ) BRIGHAM (NPSP-) NPS PHAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-FEB-1993;
22-OCT-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                    to raise antibodies for use in detection assays.
Sequence 1085 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    kidney; calcium receptor;
                                                                                                                            296
                                                                                                                                                                                                           116
320
                         416
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                                                                                                                                                                                                                                                                                                                                CIRYNFRGFRWLQAMIFAIEEINSSPALLPNWTLGYRIFDTCNTVSKALEA--TLSFVAQ 118
                        RISYNVYLAVYSIAHALQDIYTCIPGRGLFTNGSCADIKKVEAWQVLKHLRHLNFTSNMG
                                                                                             ASEAWA---L-SR----HITGVP-GIQ-RIGMVLGV-A-IQK---R-AVP-GL-KAF-EE
                                                                                                                                                                                                                                                                           NKIDSLNLDEFCNCSEHIPSTIAVVGATGSGISTAVANLLGLFYIPQVSYASSSRLLSNK 178
                                                                                                                                                                                                                                                                                                                C-SFNEHGYHLFQAMRLGVEEINNSTALLPNITLGYQLYDVCSDSANVYATLRVLSLPGQ 61
SSAYNAYRAVYAVAHGLHQLLGC-AS-EL----
                                                                            TFNCHLQEGAKGPLPYDTFLRGHEEGGARLSNSPTAFRPLCTGEENISSVETPYMDYTHL 415
                                                                                                                              ASEAWASSSLIAMPEYFHVVGGTIGFGLKAGQIPGFREFLQKVHPRKSVHNGFAKEFWEE
                                                                                                                                                         AFKDIMPFSAQVGDERMQCLMRHLAQAGATVVVVFSS-RQLARVFFESVVLTNLTGKVWV
                                                                                                                                                                                 DFSE-L-ISQYSDEEKIQQVVEVIQNSTAKVIVVFSSGPDLEPLIKE-IVRRNITGRIWL
                                                                                                                                                                                                           RQYPSFLRTIPNDKYQVETMVLLLQKFGWTWISLVGSSDDYGQLGVQALENQALVRGICI
                                                                                                                                                                                                                                    NQFKSFLRTIPNDEHQATAMADIIEYFRWNWVGTIAADDDYGRPGIEKFREEAEERDICI 238
                                                                                                                                                                                                                                                               HHIE-LQ-GDLLHYS---PTVLAVIGPDSTNRAATTAALLSPFLV-HISYAASSETLSVK 115
                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33 484565.

US-749455.

US-749451.

US-934061.

US-934161.

US-9077127.

US-009389.

US-141248.

US-292827.

WO-U12117.
                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-353784.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein;
                                                                                                                                                                                                                                                                                                                                                                              20.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     detection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1085
                                                                                                                                                                                                                                                                                                                                                                Score 1170; DB 1; 1
Pred. No. 4.34e-94;
227; Mismatches 256;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              receptor 1 protein 5Kb parathyroid hormone; ho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B
-CS-RGRVYPWQLLEQIHKVHFLLHK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      drug
                                                                                                                                                                                                                                                                                                                                                                                          Length 1085;
                                                                                                                                                                                                                                                                                                                                                                  Indels 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       screening
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Query Match
Best Local S
Matches 26
                                                                                                                                                                                                                                             18-NOV-1997.

18-NOV-1997.

07-JUN-1995; US-485588.

07-JUN-1995; US-485588.

07-JUN-1995; US-834044.

11-FEB-1992; US-834044.

21-AUG-1992; US-834061.

12-FEB-1993; US-017127.

23-FEB-1993; US-019389.

23-FEB-1993; US-0141248.

19-AUG-1994; WS-292827.

21-OCT-1994; WS-292827.

21-OCT-1994; WO-U12117.

08-DEC-1994; US-353784.

(BGHM) BRIGHAM & WOMENS HOSPITAL.

(NPSP-) NPS PHARM INC.

(NPSP-) NPS PHARM INC.

(NPSP-) NPS PHARM INC.

BIOWN EM, Fuller FH, Garrett JE, He
WPI; 98-008040//01.
                                                                           receptor 1 (BoPCaR 1).

The specification includes details of molecules that can modulate one or more inorganic ion receptor activities, and antibodies and antibody fragments targetted to inorganic ion receptor proteins. The proteins, nucleic acids and antibodies may be used to treat disorders by modulating one or more inorganic ion receptor activities, preferably disorders of calcium homeostasis, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bovine parathyroid cell calcium receptor 1 (BoPCaR 1).
Bovine parathyroid cell calcium receptor 1; BoPCaR 1;
calcium homeostasis; hyperparathyroidism; osteoporosis
                                                     hyperparathyroidism Sequence 1085 AA;
                                                                                                                                                                             DNA encoding calcium receptor polypeptide(s) - useful for therapeutic purposes, e.g. hyperparathyroidism and osteoporosis Claim 4; Columns 107-116; 174pp; English.

The present sequence is bovine parathyroid cell calcium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bos sp.
US5688938-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W38272;
08-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T 3
W38272 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Y-GKFVSAVEVIAILAA-SFGLLACIFFNKVYIILFKPSRNTIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LGFILAFL--YNGLLSISAFACSYLGKDLPENYNEAKCVTFSLLFNEVSWIAFFTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HTSCIAKEIEFLSWTEPFG-IALTLFAVLGIFLTAFVLGVFIKFRNTPIVKATNRELSYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HQVPKSVCSSDCLEGHQR-VVTGFHHCCFECVPCGAGTFLNKSELYRCQPCGTEEWAPEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REVPFSNCSRDCLAGTRKGIIEGEPTCCFECVECPDGEYSDETDASACDKCPDDFWSNEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    L-MALGFLIGYTCLLAAICFFFAFKSRKLPENFNEAKFITFSMLIFFIVWISFIPAYAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SQTCFPRTVVFLALREHTSWVLLAANTLLLLLLG-TAGLFAWHLDTPVVRSAGGRLCFL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EQVTFDECGDLAGNYSIINWHLSPEDGSIVFKEVGYYNVYAKKGERLFINDEKILWSGFS
20.0%;
l Similarity 31.9%;
263; Conservative
                                                                                                                                                                                                                                       T95857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein;
                                                                    and osteoporosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entry)
                                                                                                                                                                                                                                                                                             HOSPITAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1085
Pred.
227;
        Score 1170; DB 1;
Pred. No. 4.34e-94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8
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Best Local S
Matches 26
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22-OCT-1993; US-141248.
19-AUG-1994; US-292827.
21-OCT-1994; WO-U12117.
08-DEC-1994; US-353784.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antibody production
Claim 7; Fig 49; 174pp; English.
The tissue from which the human parathyroid calcium receptor and receptors from bovine parathyroid and rat kidney are derived, respond to changes, and control changes, in calcium ion concentration, e.g. parathyroid hormone regulattes Ca2+ homeostasis in blood and extracellular fluid, and kidney function alters through changes in Ca2+ levels in juxtaglomerular and proximal tubule cells in the kidney. The purified receptors (produced recombinantly) can be used to screen for compounds that modulate calcium receptor activity, especially those that can be used to treat diseases associated with the receptors in these tissues. They can also be used to raise antibodies for use in detection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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N-PSDB; V26964.
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(NPSP-) NPS PHARM INC.
Brown EM, Garrett JE, Hebert SC:
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                                  LLLFSLLCCFSSSLF-FIGEPQDWTCRLRQPAFGISFVLCISCILVKTNRVLLVFE--AK
                                                                                                                                                                                                                                                   GEQVTFDECGDLVGNYSIINWHLSPEDGSIVFKEVGYYNVYAKKGERLFINEEKILWSGF
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   LMLGSLAAG
                                                                     GSQTCFPRTVVFLALREHTSWVLLAANTLLLLLLLG-TAGLFAWHLDTPVVRSAGGRLCF
                                                                                                       NHTSCIAKEIEFLSWTEPFG-IALTLFAVLGIFLTAFVLGVFIKFRNTPIVKATNRELSY
                                                                                                                                          NHQVPKSVCSSDCLEGHQR-VVTGFHHCCFECVPCGAGTFLNKSELYRCQPCGTEEWAPE
                                                                                                                                                                                                              -DTVAFNDNRDPLSSYNIIAWDWNGPK-WT-FTVLGS-STWSP-VQ-LNINETKIQWHGK
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·SGSLYGFFGEPTRPACLLRQALFALGFTIFLSCLTVRSFQLIIIFKFSTK
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Pred. No. 3.73e-93;
232; Mismatches 250
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                                                                                                                                                                                                                                                                                  -CS-RGRVYPWQLLEQIHKVHFLLHK
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                                           PT Screening for calcium receptor-active compounds - by recombinant PT Screening for calcium receptor and determining PT the effect of compounds on calcium receptor activity PS Claim; Fig. 49; 176pp; English.

CC A method has been developed of screening for a compound able to affect cone or more activities of a calcium receptor (CR) comprises: (A) CC contacting a recombinant cell with a test compound, where the cell comprises a recombinant nucleic acid expressing the CR, compound that the cell does not have functional CR expression from CC endogenous nucleic acid; (B) determining the ability of the test compound to affect one or more activities of the calcium receptor; and CC (C) comparing the ability with the ability of the test compound to affect the one or more CR activities in a cell not comprising the CR affect the one or more CR activities in a cell not comprising the CR affect the one or more CR activities in a cell not comprising the CR affect the one or more CR activities in a cell not comprising the CR affect the one will be present sequence represents human CC parathyroid CR, designated a pHuPCAR 4.0. The nucleic acid sequence of PHuPCAR 4.0 can be used as part of the recombinant nucleic acid in the CR disease or disorders characterised by abnormal calcium homeostasis, e.g. hyperparathyroidism, osteoporosis and other bone and mineral-related CC disorders associated with disrupted Ca2+ responses, e.g. seizures, cc stroke, spinal cord injury, hypoxia-induced nerve cell damage such as in CC cardiac arrest or meonatal distress, epilepsy, neurodegenerative and constructive disease and constructive disease and constructive disease. Huntinoton's disease and
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(NPSP) Nr_
Balandrin MF, P
Hebert SC, Nem
17; 99-11987
781; 99-24
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11-FEB-1992;
21-AUG-1992;
12-FEB-1993;
23-FEB-1993;
23-FEB-1993;
21-AUG-1994;
21-OCT-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human parathyroid calcium receptor pHuPCaR 4.0.

Parathyroid calcium receptor; inorganic ion receptor; osteoporosis;

calcium homeostasis; hyperparathyroidism; seizure; stroke; epilepsy

spinal cord injury; hypoxia-induced nerve cell damage; cardiac arre

neonatal distress; neurodegenerative disease; Alzheimer's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-OCT-1994;
08-DEC-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Huntington's disease; Parkinson's disease; dementia; muscle tension; depression; anxiety.
                   Parkinson's
                                    diseases such as Alzheimer's disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; V82485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-JUN-1995;
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12-JAN-1999.
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NPS PHARM INC.
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 disease,
1078 AA;
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US-749451.

US-834044.

US-934161.

US-017127.

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US-141248.

US-292827.

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                    dementia,
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                   tension,
                                      Huntington's disease
                    depression,
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                    and anxiety
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                                                   Parathyroid calcium receptor encoded by clone pHuPCaR4.0. Parathyroid calcium receptor; human parathyroid gland adenoma tumour; pBoPCaR1; primary hyperparathyroidism; Xenopus oocyte; alternative splicing; calcium-activated chloride current; agonist; NPS R-467; NPS R-568; variant; untranslated region; alternative polyadenylation; probe; alternative transcription initiation; pHuPCaR4.0;
Homo sapiens
W09612697-A2
                                                                                                                                                                                        W11889;
                                                                                                                                                                                                        W11889 standard;
                                   human CaR gene;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LLLFSLLCCFSSSLF-FIGEPQDWTCRLRQPAFGISFVLCISCILVKTNRVLLVFE--AK
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                                                                                                                                                                                                                                                                                    VYDGKYLPAANMMAGLSSLSSGFGGY-FLPKCYVILCRPDLNSTE
                                                                                                                                                                                                                                                                                                                       TY-GKFVSAVEVIAILAA-SFGLLACIFFNKIYIILFKPSRNTIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IPTSFHRKWWGLNLQFLLVFLCTFMQIVICVIWLYTAPPSSYRNQELEDEIIFITCHE-G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GSQTCFPRTVVFLALREHTSWVLLAANTLLLLLLG-TAGLFAWHLDTPVVRSAGGRLCF
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                                                                                                                                                                                                                                                                                                                                                                                               SL-MALGELIGYTCLLAAICFFFAFKSRKLPENFNEAKFITFSMLIFFIVWISFIPAYAS
                                                                                                                                                                                                                                                                                                                                                                                                                                       VPT-FYHAWVQNHGAGLFVMISSAAQLLICLTWLVVWTPLPAREYQRFPHLVMLECTETN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LMLGSLAAG-SGSLYGFFGEPTRPACLLRQALFALGFTIFLSCLTVRSFQLIIIFKFSTK
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263; Conse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CC The cDNAs encoding these sequences were isolated from human parathyroid consisted from a Jay pear old caucasian male diagnosed with primary isolated from any year old caucasian male diagnosed with primary consisted from the primary consists and the primary consists and the primary consists and two clones of approx. 5 and 4 kb were consisted from the presence of incitional calcium receptors. Both clone consists, consists, conspus cocytes which were consisted for the presence of functional calcium receptors. Both clone consists, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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Best Local .
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23-OCT-1995; U13704.
21-OCT-1994; WC-U12117.
08-DEC-1994; US-353784.
(NPSP-) NPS PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New di:arylalkyl amine cpds. useful for modulating inorganic ion receptor activities - esp. for modulating effect of extracellular calcium on cell surface calcium receptors, useful for treating e.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      missing from from the EPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The sequences given in W11888-89
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WPI; 96-230520/23.
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LRISYNVYLAVYSIAHALQDIYTCLPGRGLFTNGSCADIKKVEAWQVLKHLRHLNFTNNM
                                                                                                                                                                                            LASEAWASSSLIAMPQYFHVVGGTIGFALKAGQIPGFREFLKKVHPRKSVHNGFAKEFWE
                                                                                                                                                                                                                                         AFKDIMP-FSAQVGDERMQCLMRHLAQAGATVVVVFSS-RQLARVFFESVVLTNLTGKVW
                                                                                                                                                                                                                                                                     DFSELISQYSDE--EE-IQHYVEVIQNSTAKVIVVFSSGPDLEPLIKE-IVRRNITGKIW
                                                                                                                                                                                                                                                                                                                                       RQYPSFLRTIPNDKYQVETMVLLLQKFGWTWISLVGSSDDYGQLGVQALENQALVRGICI
                                                                                                                                                                                                                                                                                                                                                                       NQFKSFLRTIPNDEHQATAMADIIEYFRWNWVGTIAADDDYGRPGIEKFREEAEERDICI 237
                                                                                                                                                                                                                                                                                                                                                                                                                                    HHIE-LQ-GDLLHYS---PTVLAVIGPDSTNRAATTAALLSPELV-HISYAASSETLSVK 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NKIDSLNLDEFCNCSEHIPSTIAVVGATGSGVSTAVANLLGLFYIPQVSYASSSRLLSNK 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C-SFNEHGYHLFQAMRLGVEEINNSTALLPNITLGYQLYDVCSDSANVYATLRVLSLPGQ
                                             EAYA-R-ADKE-APRPCH---KGSWCSSNQLCRECQAF--M-A--HTMPKLKA----FS-
                                                                                          ETFNCHLQEGAKGPLPVDTFLRGHEESGDRFSNSSTAFRPLCTGDENISSVETPYIDYTH
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                                                                                                                                            ---L-S--R--HITGVP-GIQ-RIGMVLGV-A-IQK--
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31.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1160; DB 1;
Pred. No. 3.73e-93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ST,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         represent functional calcium receptors es were isolated from human parathyroid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1078;
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23-AUG-1991; US-749451.
11-FEB-1992; US-844044.
21-AUG-1992; US-934161.
12-FEB-1993; US-017127.
23-FEB-1993; US-017127.
23-FEB-1993; US-141248.
19-AUG-1994; US-92827.
21-OCT-1994; US-353784.
                   DNA encoding calcium receptor polypeptide(s) - useful for therapeutic purposes, e.g. hyperparathyroidism and osteoporosis Claim 20; Columns 125-134; 174pp; English.

The present sequence is human parathyroid cell calcium receptor 4.0 (HupCaR 4.0).

The specification includes details of molecules that can modulate one or more inorganic ion receptor activities, and antibodies and antibody fragments targetted to inorganic ion receptor proteins. The proteins, nucleic acids and antibodies may be used to treat disorders by modulating one or more inorganic ion receptor activities, preferably disorders of calcium homeostasis, e.g.
                                                                                                                                                                                                                                                                                                                                        18-NOV-1
07-JUN-1
                                                                                                                                                                                                                                                                                                                                                                                                                                    W38274 standard;
W38274;
                                                                                                                                                         N-PSDB; T95859
                                                                                                                                                                  Brown EM, Fuller F. WPI; 98-008040/01.
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                                                                                                                                                                             EM, Fuller FH,
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NPS PHARM INC.
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           osteoporosis.
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Query

Match

19

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Score

1160;

DВ $\ddot{};$

Length

1078;

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Best Local Similarity 31.9%; Matches 263; Conservative
reproduction; rodent; ins
Rattus sp.
W09900422-A1.
07-JAN-1999; U13680.
30-JUN-1998; U13680.
30-JUN-1997; US-051284.
(HARD) HARVARD COLLEGE.
                                                                                                                    04-MAY-1999 (first entry)
Rat kidney extracellular calcium/polyvalent cation-sensing
Pheromone receptor; signal transduction; fertility; behavio
                                                                                                                                                       W94928;
04-MAY-1999
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Matches 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                calcium/polyvalent cation-sensing receptor.
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HHIE-LQ-GDLLHYS---PTVLAVIGPDSTNRAATTAALLSPELV-HISYAASSETLSVK 115
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99-095684/08
                                                     KVPT-FYHAWVQNHGAGLFVMISSAAQLLICLTWLVVWTPLPAREYQRFPHLVMLECTET
                                                                                      KIPTSFHRKWWGLNLQFLLVFLCTFMQILICIIWLYTAPPSSYRNHELEDEIIFITCHEG
                                                                                                                        FLMLGSLAAG-SGSLYGFFGEPTRPACLLRQALFALGFTIFLSCLTVRSFQLIIIFKFST
                                                                                                                                                       YLLLFSLLCCFSSSLF-FIGEPQDWTCRLRQPAFGISFVLCISCILVKTNRVLLVFE--A
                                                                                                                                                                                          EGSQTCFPRTVVFLALREHTSWVLLAANTLLLLLLG-TAGLFAWHLDTPVVRSAGGRLC
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larity 31.4%;
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Pred. No. 5.73e-93;
233; Mismatches 261
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Best Local
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07-JUN-1995 WS-484565
23-AUG-1991 WS-749451
11-FEB-1992 WS-83404
21-AUG-1992 WS-934161
12-FEB-1993 WS-017127
23-FEB-1993 WS-017127
23-FEB-1993 WS-141248
19-AUG-1994 WS-141248
19-AUG-1994 WS-18127
21-OCT-1994 WS-35784
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Claim 8; Fig 50; 174pp; English.

The tissue from which the rat kidney calcium receptor and receptors from bovine parathyroid and rat kidney are derived, respond to changes, and control changes, in calcium ion concentration, e.g. parathyroid hormone regulates Ca2+ homeostasis in blood and extracellular fluid, and kidney function alters through changes in Ca2+ levels in juxtaglomerular and proximal tubule cells in the kidney. The purified receptors (produced receptor activity) can be used to screen for compounds that modulate calcium receptor activity, especially those that can be used to treat diseases associated with the receptors in these tissues. They can also be used to raise antibodies for use in detection assays.
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W54847
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07-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Calcium receptor poly:peptide(s) - useful for drug
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                                                       VASEAWA---L-SR----HITGVP-GIQ-RIGMVLGV-A-IQK---R-AVP-GL-KAF-E
                                                                                                                                                                          AFKDIMP-FSAQVGDERMQCLMRHLAQAGATVVVVFSS-RQLARVFFESVVLTNLTGKVW
                                                                                                                                                                                                            DFSELISQYSDE--EEIQQ-VVEVIQNSTAKVIVVFSSGPDLEPLIKE-IVRRNITGRIW
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ETFNCHLQEGAKGPLPVDTFVRSHEEGGNRLLNSSTAFRPLCTGDENINSVETP-YMDYE
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-) NPS PHARM INC.
EM, Garrett JE, Hebert
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Pred. No. 5.73e-93; 
233; Mismatches 261;
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07-JUN-1995; US-480751.
07-JUN-1995; US-480751.
17-FEB-1992; US-749451.
11-FEB-1992; US-934161.
12-FEB-1993; US-017127.
12-FEB-1993; US-017127.
12-FEB-1993; US-141248.
12-OCT-1993; US-141248.
19-AUG-1994; US-292827.
19-AUG-1994; US-292827.
19-BEC-1994; US-293784.
(BGHM) BRIGHAM & WOMENS HOSPITAL.
(NPSP-) NPS PHARM INC.
BALANDITA EG, GENERAL EG, GENER
screening for calcium receptor-active compounds -
expression of nucleic acid encoding calcium recept
the effect of compounds on calcium receptor activi
Claim 1, Fig 50; 176pp; English.
A method has been developed of screening for a com
one or more activities of a calcium receptor (CR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Parathyroid calcium receptor; inorganic ion receptor; osteoporosis; calcium homeostasis; hyperparathyroidism; seizure; stroke; epilepsy; spinal cord injury; hypoxia-induced nerve cell damage; cardiac arrest; neonatal distress; neurodegenerative disease; Alzheimer's disease; Huntington's disease; Parkinson's disease; dementia; muscle tension;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JT 10
W89566 standard;
                                                                                                                                                                        N-PSDB; V82486.
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parathyroid calcium receptor pRakCaR 3A.
                                                                                                                                                                                              rt SC, Nemeth EF, 99-119871/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Y-GKFVSAVEVIAILAA-SFGLLACIFFNKVYIILFKPSRNTIEEVRSSTAAHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     K-DTVAFNDNRDPLSSYNIIAWDWNGPK-WT-FTVLGS-STWSP-VQ-LNINETKIQWHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YDGKYLPAANMMAGLSSLSSGFGGY-FLPKCYVILCRPDLNSTEHFQASIQDYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NSLGFILAFLYNGLLSISAFACSYLGKDLPENYNEAKCVTFSLLFNFVSWIAFFTT-ASV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SLMALGSLIGYTCLLAAICFFFAFKSRKLPENFNEAKFITFSMLIFFIVWISFIPAYAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KIPTSFHRKWWGLNLQFLLVFLCTFMQILICIIWLYTAPPSSYRNHELEDEIIFITCHEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FLMLGSLAAG-SGSLYGFFGEPTRPACLLRQALFALGFTIFLSCLTVRSFQLIIIFKFST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YLLLFSLLCCFSSSLF-FIGEPQDWTCRLRQPAFGISFVLCISCILVKTNRVLLVFE--A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EGSQTCFPRTVVFLALREHTSWVLLAANTLLLLLLLC-TAGLFAWHLDTPVVRSAGGRLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KNHQVPKSVCSSDCLEGHQR-VVTGFHHCCFECVPCGAGTFLNKSELYRCQPCGTEEWAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KVPT-FYHAWVQNHGAGLFVMISSAAQLLICLTWLVVWTPLPAREYQRFPHLVMLECTET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENHTSCIAKEIEFLAWTEPFG-IALTLFAVLGIFLTAFVLGVFIKFRNTPIVKATNRELS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FSREVPFSNCSRDCQAGTRKGIIEGEPTCCFECVECPDGEYSGETDASACDKCPDDFWSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MGEQVTFDECGDLVGNYSIINWHLSPEDGSIVFKEVGYYNVYAKKGERLFINEEKILWSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HLRISYNVYLAVYSIAHALQDIYTCLPGRGLFTNGSCADIKKVEAWQVLKHLRHLNFTNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EAYA-R-AD--KEA-P----RPCHKGS-W---CSSN-Q-LCRECQAFMAHTMPKLKAFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -MSSAYNAYRAVYAVAHGLHQLLGC-AS-EL----CS-RGRVYPWQLLEQIHKVHFLLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein;
                                                                                                                                                                                                                       Van
                                                                                                                                                                                                                       Wagenen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1079
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                                                                                                                                                                                                                             BC;
                                                                                                                                                                                                                                                      Garrett
                                                                                  receptor activity
                                 compound able
        comprises:
                                                                                                                 and
                                                                                                                 determining
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provided that the cell does not have functional CR expression from cendogenous nucleic acid; (B) determining the ability of the test compound to affect one or more activities of the calcium receptor; and (C) comparing the ability with the ability of the test compound to affect the one or more CR activities in a cell not comprising the recombinant nucleic acid. The present sequence represents rat parathyroid CR, designated a pRakCaR 3A. The nucleic acid in the parathyroid CR, designated a practivities in a cell not comprising the parathyroid CR, designated a practice of the recombinant nucleic acid in the method described above. The compounds identified can be used to treat diseases or disorders characterised by abnormal calcium homeostasis, e.g. hyperparathyroidism, osteoporosis and other bone and mineral-related disorders. They can also be used for the treatment of diseases and cisorders associated with disrupted C21+ responses, e.g. seizures, stroke, spinal cord injury, hypoxia-induced nerve cell damage such as in cardiac arrest or neonatal distress, epilepsy, neurodegenerative diseases such as Alzhelmer's disease, Huntington's disease and any any approach to the compounds in the compounds described and any interest on any any approach as any any content of the compounds of t
Query Match
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Matches 26
                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  contacting a recombinant cell with a test compound, where the recombinant cell comprises a recombinant nucleic acid expressing
                                                                                                                                                                  1079
                                                                                                                                                                                                    disease, dementia,
                                                                                                                                                              AA;
                                     19.8%;
                                     Score
Pred.
                                                                                                                                                                                                        muscle tension,
                                 1158; DB 1;
No. 5.73e-93;
                                                                                                                                                                                               depression,
                                                                      Length 1079;
                                                                                                                                                                                                        and
                                                                                                                                                                                               anxiety
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the CR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   e.g.
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Similarity

Conservative

Mismatches

261;

Indels

78;

Gaps

밁 Š B Š Db Ş В Ω_γ В Š 밁 Ş 밁 Ş 밁 Š 멍 δÃ 밁 δÃ 뫄 483 593 424 370 473 319 413 275 354 234 176 116 294 238 178 118 62 60 ω DFSELISQYSDE--EEIQQ-VVEVIQNSTAKVIVVFSSGPDLEPLIKE-IVRRNITGRIW HHIE-LQ-GDLLHYS---PTVLAVIGPDSTNRAATTAALLSPFLV-HISYAASSETLSVK 115 CIRYNFRGFRWLQAMIFAIEEINSSPSLLPNMTLGYRIFDTCNTVSKALEA--TLSFVAQ 117 YLLLFSLLCCFSSSLF-FIGEPQDWTCRLRQPAFGISFVLCISCILVKTNRVLLVFE--A KNHQVPKSVCSSDCLEGHQR-VVTGFHHCCFECVPCGAGTFLNKSELYRCQPCGTEEWAP K-DTVAFNDNRDPLSSYNIIAWDWNGPK-WT-FTVLGS-STWSP-VQ-LNINETKIQWHG MGEQVTFDECGDLVGNYSIINWHLSPEDGSIVFKEVGYYNVYAKKGERLFINEEKILWSG HLRISYNVYLAVYSIAHALQDIYTCLPGRGLFTNGSCADIKKVEAWQVLKHLRHLNFTNN EAYA-R-AD--KEA-P----RPCHKGS-W---CSSN-Q-LCRECQAFMAHTMPKLKAFS VASEAWA---L-SR----HITGVP-GIQ-RIGMVLGV-A-IQK---R-AVP-GL-KAF-E LASEAWASSSLIAMPEYFHVVGGTIGFGLKAGQIPGFREFLQKVHPRKSVHNGFAKEFWE AFKDIMP-FSAQVGDERMQCLMRHLAQAGATVVVVFSS-RQLARVFFESVVLTNLTGKVW RQYPSFLRTIPNDKYQVETMVLLLQKFGWTWISLVGSSDDYGQLGVQALENQALVRGICI NQYKSFLRTIPNDEHQATAMADIIEYFRWNWVGTIAADDDYGRPGIEKFREEAEERDICI NKIDSLNLDEFCNCSEHIPSTIAVVGATGSGVSTAVANLLGLFYIPQVSYASSSRLLSNK 177 C-SFNEHGYHLFQAMRLGVEEINNSTALLPNITLGYQLYDVCSDSANVYATLRVLSLPGQ EGSQTCFPRTVVFLALREHTSWVLLAANTLLLLLLLG-TAGLFAWHLDTPVVRSAGGRLC ENHTSCIAKEIEFLAWTEPFG-IALTLFAVLGIFLTAFVLGVFIKFRNTPIVKATNRELS FSREVPFSNCSRDCQAGTRKGIIEGEPTCCFECVECPDGEYSGETDASACDKCPDDFWSN ETFNCHLQEGAKGPLPVDTFVRSHEEGGNRLLNSSTAFRPLCTGDENINSVETP-YMDYE -MSSAYNAYRAVYAVAHGLHQLLGC-AS-EL----CS-RGRYYPWQLLEQIHKVHELLH 651 532 472 412 61 541 482 274 233 369

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709

KIPTSFHRKWWGLNLQFLLVFLCTFMQILICIIWLYTAPPSSYRNHELEDEIIFITCHEG

-SGSLYGFFGEPTRPACLLRQALFALGFTIFLSCLTVRSFQLIIIFKFST

600

KVPT-FYHAWVQNHGAGLFVMISSAAQLLICLTWLVVWTPLPAREYQRFPHLVMLECTET

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Matches 26
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07-JUN-1995

07-JUN-1995; US-485588

07-JUN-1995; US-749451

11-FEB-1992; US-834044

21-AUG-1992; US-934161

12-FEB-1993; US-017127

12-FEB-1993; US-017127

23-FEB-1993; US-017127

23-FEB-1993; US-017127

21-OCT-1994; US-92897

21-OCT-1994; US-9353784
                                                                                                                                                                                                                                                                                                                                                             The specification includes details of molecules that can modulate one or more inorganic ion receptor activities, and antibodies and antibody fragments targetted to inorganic ion receptor proteins. The proteins action activities and antibodies may be used to treat disorders by modulating one or more inorganic ion receptor activities, preferably disorders of calcium homeostasis, e.g. hyperparathyroidism and osteoporosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      calcium
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                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          therapeutic purposes, e.g. hyperparathyroidism and osteoporosis Claim 20: Columns 133-142; 174pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Brown EM,
WPI; 98-00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is rat kidney cell calcium receptor 3A (RakCaR 3A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA encoding calcium receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; T95860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (BGHM ) BRIGHAM & WOMENS (NPSP-) NPS PHARM INC.
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   234
                              294
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                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                ω
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                                                                                                                                                                                                                                                    CIRYNFRGFRWLQAMIFAIEEINSSPSLLPNMTLGYRIFDTCNTVSKALEA--TLSFVAQ 117
                                                                                                                                                                       HHIE-LQ-GDLLHYS---PTVLAVIGPDSTNRAATTAALLSPELV-HISYAASSETLSVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98-008040/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Y-GKFVSAVEVIAILAA-SFGLLACIFFNKVYIILFKPSRNTIEEVRSSTAAHA
   VASEAWA---L-SR---
                           LASEAWASSSLIAMPEYFHVVGGTIGFGLKAGQIPGFREFLQKVHPRKSVHNGFAKEFWE
                                                                                  DFSELISQYSDE--EEIQQ-VVEVIQNSTAKVIVVFSSGPDLEPLIKE-IVRRNITGRIW
                                                                                                                                          NQYKSFLRTIPNDEHQATAMADIIEYFRWNWVGTIAADDDYGRPGIEKFREEAEERDICI 237
                                                                                                                                                                                                    NKIDSLNLDEFCNCSEHIPSTIAVVGATGSGVSTAVANLLGLFYIPQVSYASSSRLLSNK 177
                                                                                                                                                                                                                               C-SFNEHGYHLFQAMRLGVEEINNSTALLPNITLGYQLYDVCSDSANVYATLRVLSLPGQ
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                                                         AFKDIMP
                                                                                                               RQYPSFLRTIPNDKYQVETMVLLLQKFGWTWISLVGSSDDYGQLGVQALENQALVRGICI
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                                                                                                                                                                                                                                                                                        262;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   homeostasis; hyperparathyroidism; osteoporosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fuller FH, Garrett JE,
                                                                                                                                                                                                                                                                                                                                                   1079
                                                         -FSAQVGDERMQCLMRHLAQAGATVVVVFSS
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                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entry)
-HITGVP-GIQ-RIGMVLGV-A-IQK---R-AVP-GL-KAF-E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HOSPITAL.
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                                                                                                                                                                                                                                                                                                      Pred.
                                                                                                                                                                                                                                                                                                                     Score
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                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                    1158; DB 1;
No. 5.73e-93;
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                                                                                                                                                                                                                                                                                        261;
                                                       -RQLARVFFESVVLTNLTGKVW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          useful for
                                                                                                                                                                                                                                                                                                                  Length 1079;
                                                                                                                                                                                                                                                                                        Indels
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            New isolated Aquatic polyvalent cation-sensing receptor - used to develop products for increasing or decreasing the salinity tolerance of fish for use in aquaculture claim 9; Fig 5A-B; 57pp; English.

This protein comprises dogifish shark kidney calcium receptor related protein (SKCaR-RP), an aquatic polyvalent cation-sensing receptor (PVCR). Its amino acid sequence was deduced from a kidney cDNA clone (see T89290). It shows 74% homology to rat kidney PCVR and bovine parathyroid PVCR and possesses general features that are homologous to PVCR proteins, including a large extracellular domain, 7 transmembrane domains and a cytoplasmic acceptance of the contraction of the c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dogfish shark kidney calcium receptor related protein (SKCaR-RP). Calcium receptor related protein; CaR-RP; dogfish shark; SKCaR-RP polycation-sensing receptor; aquaculture; fish farming;
                                                                                                                                                                                                                                                                                           27-MAR-1996; US-622738.
(BGHM) BRIGHAM & WOMENS HO
Brown E, Harris HW, Hebert
WPI; 97-489640/45.
N-PSDB; T89290.
     C-terminal domain.
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27-MAR-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DFSE-M-ISQYYTQKQLEFIADVIQNSSAKVIVVFSNGPDLEPLI-QEIVRRNITDRIWL | : | : : : | |:| :: : : | |:| ::| : : : | |:| ::| : : : | |:| ::| : | |:| ::| : | |:| ::| : | |:| ::| : | |:| ::| : | |:| ::| : | |:| ::| : | |:| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::
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                                     VSTY-GKFVSAVEVIAILAS-SFGLLGCIYFNKCYIILFKP
                                                                                                             TNSLGFILAFL--YNGLLSISAFACSYLGKDLPENYNEAKCVTFSLLFNFVSWIAFFTT-
                                                                                                                                                                                                                                                                                                                                                                                                                               SYLLLFSLICCESSSLI-FIGEPRDWICRLRQPAFGISFVLCISCILVKTNRVLLVFE---
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   ASVYDGKYLPAANMMAGLSSLSSGFGGY-FLPKCYVILCRP
                                                                                                                                                            -GSL-MALGFLIGYTCLLAAICFFFAFKSRKLPENFNEAKFITFSMLIFFIVWISFIPAY 832
                                                                                                                                                                                                                                                            TKVPT-FYHAWVQNHGAGLFVMISSAÅQLLICLTWLVVWTPLPAREYQRFPHLVMLECTE
                                                                                                                                                                                                                                                                                                                         AKIPTSLHRKWVGLNLQFLLVFLCILVQIVTCIIWLYTAPPSSYRNHELEDEVIFITCDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMGEQVDFDDQGDLKGNYTIINWQLSAEDESVLFHEVGNYNAYAKPSDRLNINEKKILWS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1026 AA;
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Best Local S
Matches 26
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11-FEB-1992;
21-AUG-1992;
12-FEB-1993;
23-FEB-1993;
23-CCT-1993;
19-AUG-1994;
21-CCT-1994;
08-DEC-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
US5688938-A.
18-NOV-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA encoding calcium receptor polypeptide(s) - useful for therapeutic purposes, e.g. hyperparathyroidism and osteoporosis claim 20; columns 117-126; 174pp; English.

The present sequence is human parathyroid cell calcium receptor 5.2 (HuPCaR 5.2).

The specification includes details of molecules that can modulate one or more inorganic ion receptor activities, and antibodies and antibody fragments targetted to inorganic ion receptor proteins. The proteins, nucleic acids and antibodies may be used to treat disorders by modulating one or more inorganic ion receptor activities, preferably disorders of calcium homeostasis, e.g. sequence 1088 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Brown WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W38273 standard; Protein; W38273; 08-MAY-1998 (first entry)
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319
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                                                                                                                       VASEAWA---L-S--R--HITGVP-GIQ-RIGMVLGV-A-IQK---R-AVP-GL-KAF-
                                                                                                                                                     LASEAWASSSLIAMPQYFHVVGGTIGFALKAGQIPGFREFLKKVHPRKSVHNGFAKEFWE
                                                                                                                                                                                                         DFSELISQYSDE--EE-IQHVVEVIQNSTAKVIVVFSSGPDLEPLIKE-IVPRNITGKIW
                                                                                                                                                                                                                                                                               NQFKSFLRTIPNDEHQATAMADIIEYFRWNWVGTIAADDDYGRPGIEKFREEAEERDICI 237
                                                                                                                                                                                                                                                                                                                                              NKIDSLNLDEFCNCSEHIPSTIAVVGATGSGVSTAVANLLGLFYIPQVSYASSSRLLSNK 177
                                                                                                                                                                                                                                                                                                                                                                              C-SFNEHGYHLFQAMRLGVEEINNSTALLPNITLGYQLYDVCSDSANVYATLRVLSLPGQ 61
                                                                                                                                                                                                                                                                                                                                                                                                            CIRYNFRGFRWLQAMIFAIEEINSSPALLPNLTLGYRIFDTCNTVSKALEA -- TLSFVAQ
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MSSAYNAYRAVYAVAHGLHQLLGC-AS-EL-
                           LRISYNVYLAVYSIAHALQDIYTCLPGRGLFTNGSCADIKKVEAWQVLKHLRHLNFTNNM
                                                                                                                                                                                     AFKDIMP-FSAQVGDERMQCLMRHLAQAGATVVVVFSS-RQLARVFFESVVLTNLTGKVW
                                                                                                                                                                                                                                                    RQYPSFLRTIPNDKYQVETMVLLLQKFGWTWISLVGSSDDYGQLGVQALENQALVRGICI
                                                                                                                                                                                                                                                                                                                  HHIE-LQ-GDLLHYS---PTVLAVIGPDSTNRAATTAALLSPFLV-HISYAASSETLSVK
                                                                                          ETFNCHLQEGAKGPLPVDTFLRGHEESGDRFSNSSTAFRPLCTGDENISSVETPYIDYTH
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Similarity 31.6%;
264; Conservative
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US-749451

US-834041

US-934161

US-934161

US-017127

US-017127

US-002389

US-141248

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                                                            KGSWCSSNQLCRECQAF - - M - A - - HTMPKLKA - - -
                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1064; DB 1;
Pred. No. 3.37e-84;
231; Mismatches 250;
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Pred. No. 3.
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CS-RGRVYPWQLLEQIHKVHFLLHK
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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-JUN-1995; US-484565.
23-AUG-1991; US-740441.
11-FEB-1992; US-934161.
12-FEB-1993; US-017127.
23-FEB-1993; US-00389.
23-FEB-1993; US-00389.
23-FEB-1993; US-141248.
19-AUG-1994; US-292827.
21-OCT-1994; US-353784.
                                                                                                                                                                                                            antibody production
Claim 6; Fig 48; 174pp; English.
Claim 6; Fig 48; 174pp; English.
The tissue from which the human parathyroid calcium receptor and receptors from bovine parathyroid and rat kidney are derived, respond to changes, and control changes, in calcium ion concentration, e.g. parathyroid hormone regulates Ca2+ homeostasis in blood and extracellular fluid, and kidney function alters through changes in Ca2+ levels in juxtaglomerular and proximal tubble cells in the kidney. The purified receptors (produced recombinantly) can be used to screen for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Brown 9
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(NPSP-) NF
Brown EM,
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Calcium receptor poly:peptide(s) - useful
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01-SEP-1998
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W54845 standard;
                                                                               Sequence
                                                                                                                                     tissues.
                                                                                                                                                                                           compounds that
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                                                                                                                         pound to they
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     M) BRIGHAM & WOMENS HOSPITAL.
P-) NPS PHARM INC.
n EM, Garrett JE, Hebert SC;
98-347412/30.
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                                                                                                                                  modulate calcium receptor activity, especially those treat diseases associated with the receptors in these can also be used to raise antibodies for use in detection.
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1063; DB 1;
No. 4.17e-84;
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hormone; homeostasis; kidney;
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Homo sapiens.
US5858584-A.
12-JAN-1999.
                                                                                                               w89564;
19-MAR-1999 (first entry)
19-marathyroid calcium receptor pHuPCaR 5.2.
                                                        Parathyroid Calcium receptor; inorganic ion receptor; osteoporosis; calcium homeostasis; hyperparathyroidism; selizure; stroke; epilepsy; spinal cord injury; hypoxia induced nerve cell damage; cardiac arrest; neonatal distress; neurodegenerative disease; Alzheimer's disease; Huntington's disease; Parkinson's disease; dementia; muscle tension;
                                                Huntington's disease depression; anxiety
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W89564 standard;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    endogenous nucleic acid; (B) determining the ability of the test compound to affect one or more activities of the calcium receptor; and (C) comparing the ability with the ability of the test compound to affect the one or more CR activities in a cell not comprising the recombinant nucleic acid. The present sequence represents human parathyroid CR, designated a pHuPCAR 5.2. The nucleic acid sequence of PHuPCAR 5.2 can be used as part of the recombinant nucleic acid in the method described above. The compounds identified can be used to treat diseases or disorders characterised by abnormal calcium homeostasis, e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Screening for calcium receptor-active compounds - by recombinant expression of nucleic acid encoding calcium receptor and determining the effect of compounds on calcium receptor activity (laim 1; Fig 48; 176pp; English.

A method has been developed of screening for a compound able to affect one or more activities of a calcium receptor (CR) comprises: (A) contacting a recombinant cell with a test compound, where the recombinant cell comprises a recombinant nucleic acid expressing the provided that the cell does not have functional CR expression from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Balandrin MF, Brown El
Hebert SC, Nemeth EF,
WPI; 99-119871/10.
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08-DEC-1994;
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19-AUG-1994;
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                                                                            VASEAWA---L-S--R--HITGVP-GIQ-RIGMYLGV-A-IQK---R-AVP-GL-KAF-E 274
                                                                                                                                                                               DFSELISQYSDE--EE-IQHVVEVIQNSTAKVIVVFSSGPDLEPLIKE-IVRRNITGKIW 293
                                                                                                                                                                                                                                                                                                                                                      NKIDSLNLDEFCNCSEHIPSTIAVVGATGSGVSTAVANLLGLFYIPQVSYASSSRLLSNK 177
                                                                                                                    LASEAWASSSLIAMPQYFHVVGGTIGFALKAGQIPGFREFLKKVHPRKSVHNGFAKEFWE 353
                                                                                                                                                         AFKDIMP-FSAQVGDERMQCLMRHLAQAGATVVVVFSS-RQLARVFFESVVLTNLTGKVW
                                                                                                                                                                                                                                     RQYPSFLRTIPNDKYQVETMVLLLQKFGWTWISLVGSSDDYGQLGVQALENQALVRGICI
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                                                                                                                                                                                                                                                                                                                                                                                              C-SFNEHGYHLFQAMRLGVEEINNSTALLPNITLGYQLYDVCSDSANVYATLRVLSLPGQ 61
                                                                                                                                                                                                                                                                         NOFKSFLRTIPNDEHQATAMADIIEYFRWNWVGTIAADDDYGRPGIEKFREEAEERDICI 237
    EAYA-R-ADKE-APRPCH---KGSWCSSNQLCRECQAF--M-A--HTMPKLKA----FS-
                                      ETFNCHLQEGAKGPLPVDTFLRGHEESGDRFSNSSTAFRPLCTGDENISSVETPYIDYTH 413
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Similarity 31.6%;
264; Conservative
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Pred. No. 4.17e-84;
231; Mismatches 250;
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LRISYNVYLAVYSIAHALQDIYTCLPGRGLFTNGSCADIKKVEAWQVLKHLRHLNFTNNM 473

Ş 밁 δÃ 밁 ρ 맑 δÃ 밁 Š 맑 Š 밁 Š 828 651 770 592 533 474 594 424 371 474 319 709 712 WISFIPAYASTY-GKFVSAVEVIAILAA-SFGLLACIFINKIYIILFKPSRNTIE VRSAGGRICELMIGSLAAG-SGSLYGFFGEPTRPACLIRQALFALGFTIFLSCLTVRSFQ WIAFFTT-ASVYDGKYLPAANMMAGLSSLSSGFGGY-FLPKCYVILCRPDLNSTE 761 LVMLECTETNSLGFILAFL--YNGLLSISAFACSYLGKDLPENYNEAKCVTFSLLFNFVS IIFITCHE-GSL-MALGFLIGYTCLLAAICFFFAFKSRKLPENFNEAKFITFSMLIFFIV LIIIFKFSTKVPT-FYHAWVQNHGAGLFVMISSAAQLLICLTWLVVWTPLPAREYQRFPH VLLVFE---AKIPTSFHRKWWGLNLQFLLVFLCTFMQIVICVIWLYTAPPSSYRNQELEDE VKATNRELSYLLLESLLCCESSSLE-FIGEPQDWTCRLRQPAFGISFVLCISCILVKTNR KCPDDFWSNENHTSCIAKEIEFLSWTEPFG-IALTLFAVLGIFLTAFVLGVFIKFRNTPI 652 SREPLIFVLSVLQVPFSNCSRDCLAGTRKGIIEGEPTCCFECVECPDGEYSDETDASACN 593 GEQVTFDECGDLVGNYSIINWHLSPEDGSIVFKEVGYYNVYAKKGERLFINEEKILWSGF 533 PCGTEEWAPEGSQTCFPRTVVFLALREHTSWVLLAANTLLLLLLLG-TAGLFAWHLDTPV -DTVAFNDNRDPLSSYNIIAWDWNGPK-WT-FTVLGS-STWSP-VQ-LNINETKIQWHG- 423 -KNH-----QVPKSVCSSDCLEGHQR-VVTGFHHCCFECVPCGAGTFLNKSELYRCQ 370 473 650 708 769 591 711 532

Search completed: Fri Mar 17 13:27:57 2000 Job time: 96 secs.

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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

112 112 113 114 114 115 116 116 116 116 116 116 116 116 116	Result
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78.00 78.00	Query Match
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99988898755919 2222666337141122	B
PCT-US-9-16-552-4 PCT-US-9-361-652-5 PCT-US-9-361-652-6 US-09-361-652-6 US-09-361-631-3 US-09-361-631-3 US-09-361-631-3 US-09-361-631-3 US-09-361-631-3 US-60-178-308-1069 US-60-178-308-1069 US-60-169-841-23 US-60-169-841-23 US-60-169-842-23 US-09-489-036-32321 US-09-489-036-323241	
Sequence 4, Appli Sequence 5, Appli Sequence 5, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 7, Appli Sequence 7, Appli Sequence 8, Appli Sequence 9, Appli Sequence 1069, Appli Sequence 1069, Appli Sequence 23, Appli Sequence 23, Appl Sequence 2312, Appl Sequence 2312, Appl Sequence 23241, A	

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RESULT 1
PCT-US99-17099-4

Sequence 4, Application PC/TUS9917099
GENERAL INFORMATION:
APPLICANT: Zuker, Charles S.
APPLICANT: Zuker, Charles S.
APPLICANT: Hodemeier, Juergen
APPLICANT: Hoon, Mark
APPLICANT: Hoon, Mark
APPLICANT: Hoon, Mark
APPLICANT: The Regents of the University of California
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Nucleic Acids Encoding a G-Protein Coup
TITLE OF INVENTION: Involved in Sensory Transduction
FILE REFERENCE: 02307E-088610pC
CURRENT APPLICATION NUMBER: PCT/US99/17099
CURRENT FILING DATE: 1999-07-27

PARLIER APPLICATION NUMBER: US 60/094,465

EARLIER FILING DATE: 1998-07-28

NUMBER OF SEQ ID NOS: 8

NUMBER OF SEQ ID NOS: 8

SOTTWARE: Patentin Ver. 2.1

SEQ ID NO 4
LENGTH: 2771
TYPE: DNA
ORGANISM: Rattus sp.
                                                                                                                                                                                                              ; FEATURE:
; OTHER INFORMATION:
PCT-US99-17099-4
                                                                                                                                              Query Match
Best Local Similarity
Matches 2771; Conser
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Sequence 4, Application US/09361652

GENERAL INFORMATION:
APPLICANT: Zuker, Charles S.
APPLICANT: Adler, Jon Elliot
APPLICANT: Adler, Jon Elliot
APPLICANT: Hoon, Mark
APPLICANT: Hoo Hooked the University of California
TITLE OF INVENTION: Nucleic Acids Encoding a G-Protein Cou
TITLE OF INVENTION: Involved in Sensory Transduction
FILE REFERENCE: 02307E-088610US
CURRENT APPLICATION NUMBER: US/09/361,652
CURRENT APPLICATION NUMBER: US 60/094,465
EARLIER FILLING DATE: 1998-07-28
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.1
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TYPE: DNA
ORGANISM: Rattus sp
FEATURE:
OTHER INFORMATION: 1
15-09-361-652-4
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Best Local Similarity
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APPLICANT: Charles S.
APPLICANT: Lindemeier, Jon Elliot
APPLICANT: Lindemeier, Juergen
APPLICANT: Lindemeier, Juergen
APPLICANT: Hoon, Mark
APPLICANT: Hoon, Mark
APPLICANT: The Regents of the University of California
ITILE OF INVENTION: Nucleic Acids Encoding a G-Protein Courille OF INVENTION: Involved in Sensory Transduction
ITILE OF INVENTION NUMBER: PCT/US99/17099
CURRENT APPLICATION NUMBER: PCT/US99/17099
CURRENT FILING DATE: 1999-07-27
EARLIER APPLICATION NUMBER: US 60/094,465
EARLIER APPLICATION NUMBER: US 60/094,465
EARLIER FILING DATE: 1998-07-28
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 5
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Sequence 5 Application US/09361652

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GENERAL INFORMATION:
APPLICANT: Adler, Charles S.
APPLICANT: Lindemeier, Juergen
APPLICANT: Lindemeier, Juergen
APPLICANT: Hoon, Mark
APPLICANT: The Regents of the University of California
ITILE OF INVENTION: Nucleic Acids Encoding a G-Protein Cou
ITILE OF INVENTION: Involved in Sensory Transduction
FILE REFERENCE: 02307E-088610US
CURRENT APPLICATION NUMBER: US/09/361,652

CURRENT APPLICATION NUMBER: US/09/361,652

CURRENT APPLICATION NUMBER: US 60/094,465

EARLIER APPLICATION NUMBER: US 60/094,465

EARLIER FILING DATE: 1998-07-28

NUMBER OF SEQ ID NOS: 8

SOFTWARE: Patentin Ver: 2.1

SEQ ID NO 5
LENGTH: 2579
ITED: DNA
ORGANISM: Mus sp.
FEATURE:
OTHER INFORMATION: mouse G-protein coupled receptor B3 (G
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343 to	מס	1303 acccctggcagcttcttcagcagatctacaaggtgaattttcttctacatgagaatactg 1362
283	o da ,	43 cccacqqcctccaccagctcctgggatqtacttct
223 to	O D K	1183 cgcttggagccttctccatgagtgccgcctacagagtgtatgaggctgtgtacgccgtgtgg 1242
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APPLICANT: Zuker, Charles S.

APPLICANT: Adler, Jon Elliot
APPLICANT: Adler, Jon Elliot
APPLICANT: Lindemeier, Juergen
APPLICANT: Ryba, Nick
APPLICANT: Hoon, Mark
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Nucleic Acids Encoding a G-Protein Cou
TITLE OF INVENTION: Involved in Sensory Transduction
FILE REFERENCE: 02307E-088610PC
CURRENT APPLICATION NUMBER: PCT/US99/17099
CURRENT FILING DATE: 1999-07-27
EARLIER APPLICATION NUMBER: US 60/094,465
EARLIER APPLICATION NUMBER: US 60/094,465
EARLIER APPLICATION SERVER DATE: 1998-07-28
NUMBER OF SEQ. ID NOS: 8
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RESULT

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Sequence 6, Application U

GENERAL INFORMATION:
APPLICANT: Zuker, Charle
APPLICANT: Lindemeler, J

APPLICANT: Lindemeler, J

APPLICANT: Hoon, Mark
APPLICANT: The Regents o

ITILE OF INVENTION: Invo

FILE REFERENCE: 02307E-0

CURRENT FILING DATE: 199

EARLIER APPLICATION NUMB

CURRENT FILING DATE: 199

EARLIER APPLICATION NUMB

CURRENT FILING DATE: 199

EARLIER APPLICATION NUMB

SOFTWARE: Patentin Ver.

SEQ ID NO 6

LENGTH: 2333

TYPE: DNA

ORGANISM: Homo sapiens
          APPLICANT: Auker, Charles S.
APPLICANT: Auker, Charles S.
APPLICANT: Lindemeier, Juergen
APPLICANT: Lindemeier, Juergen
APPLICANT: Hono, Mark
APPLICANT: Hoon, Mark
APPLICANT: Hoon, Mark
APPLICANT: The Regents of the University of California
ITILE OF INVENTION: Nucleic Acids Encoding a G-Protein Cou;
ITILE OF INVENTION: Involved in Sensory Transduction
FILE REFERENCE: 02307E-088610US
CURRENT APPLICATION NUMBER: US/09/361/652
CURRENT APPLICATION NUMBER: US/09/361/652
CURRENT APPLICATION NUMBER: US/09/361/652
EARLIER APPLICATION NUMBER: US/09/361/652
EARLIER FILING DATE: 1999-07-27
EARLIER FILING DATE: 1998-07-28
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO
LENGTH: 2333
TYPE: DNA
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Matches 1869; Conservative
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GENERAL INFORMATION:

APPLICANT: Zuker, Charles S.

APPLICANT: Adler, Jon Elliot

APPLICANT: Lindemeler, Juergen

APPLICANT: The Regents of the University of California

TITLE OF INVENTION: Nucleic Acids Encoding a G-Protein (
TITLE OF INVENTION: Nucleic Acids Encoding a G-Protein (
TITLE OF INVENTION: Nucleic Acids Encoding a G-Protein (
TITLE OF INVENTION: Involved in Sensory Transduction FILE REFERENCE: 02307E-088720US

CURRENT APPLICATION NUMBER: US/09/361,631

CURRENT FILING DATE: 1998-07-27

EARLIER APPLICATION NUMBER: US 60/095,464

EARLIER APPLICATION NUMBER: US 60/112,747

EARLIER APPLICATION NUMBER: US 60/112,747

EARLIER APPLICATION NUMBER: US 50/112,747

EARLIER FILING DATE: 1998-12-17

NUMBER OF SEQ ID NOS: 10

SOFTWARE: Patentin Ver. 2.0

SOFTWARE: Patentin Ver. 2.0

TYPE: DIA

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; OTHER INFORMATION:
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Best Local Similarity
Matches 1266; Conserv
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1557	caggtgcctgtgtcagtgtgtaccacggactgtc	1498	γQ
1462	officeaaageafegeefectaffeeecaecageaagaggefaacefacaffaaca	1406	Db
1497	cctcactgtctccagttcatctggacataaataagacaa	4.	Qу
1405	aggggacatgccgatgctcttggacatcatccagtggcagtgggacctgagccagaatc	1346	Db
1437	ggacactctaggttactacgacatcatcgcctgggactggaatggacctgaatgga	1378	Q.
1345	gylydarttcacgotoctgggtaaccggctottctttgaccaac	1286	Dp 43
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31	gctcctgggatgtacttctgagatctgttccagagggcccagtctacccctlggcagcttc	2 2	P 69
1225	gtggtctacagcgtgtactcggcagtttacgcggtggcccatgccctcaca	1166	dg
1257	gagtgccgcctacagagtgtatgaggctgtgtacgctgtggcccacggcctccacc	1198	Qy
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1137	cagegettgeeeggagggteetggtgeageactaace	1078	Qy
1051	cgtcaccatccagagggtgtccatccctggcttcagtcag	992	DЬ
1077	cygtytyggcgtccaycayagacaagtccctyggctgaaggagtttgaggagtcttatg	1018	Qy
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837	cccgggtgggtgacccgaggatgcagagcatgatgcagc	796	Qy
751	gtotgaccaaaacgagcgacatotgcattgcottccaggaggttotgcccatac	692	Дb
795	ggagctggccgtgcccgggggcatctgcgtcgccttcaaggacatcgtgcctttct	736	Qy
691			ρb
735	tggatctcgctcattggcagctacggtgattacgggcagctgggtgtgcaggcgc	679	Οy
631	aggccatggtgcagctgatggttcacttccaatgga	572	Db
678	ccccagtgaccggcaccaggtggaggtcatggtgcagctgctgcagagttttgggtggg	619	Qy
571	agogocatotoogacaagotgogggacaagoggcaottoootagcatgotaogcacag	512	DЪ
618	.tgaggcaagcagcgtggtactcagtgccaagcgcaagttcccgtctttccttcgtaccg	559	Qγ
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CURRENT FILING DATE: 1999-07-27
EARLIER APPLICATION NUMBER: US 60/095,464
EARLIER APPLICATION NUMBER: US 60/112,747
EARLIER APPLICATION NUMBER: US 60/112,747
EARLIER FILING DATE: 1998-12-17
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PATENTIN Ver. 2.0
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LENGTH: 2532
TYPE: DNA
ORGANISM: MUS:
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Best Local Similarity 51.6%;
Matches 1265; Conservative
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APPLICANT: Adler, Jon Elliot
APPLICANT: Lindemeiar, Juergen
APPLICANT: Lindemeiar, Juergen
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Nucleic Acids Encoding a G-Protein
TITLE OF INVENTION: Involved in Sensory Transduction
FILE REFERENCE: 02307E-08872005
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Pred. No. 9.4e-102;
0; Mismatches 1145;
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Sequence 7046, Application US/09471275
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: Novel Contigs Obtained
TITLE OF INVENTION: From Various Libraries
FILE REFERENCE: 782
CURRENT APPLICATION NUMBER: US/09/471,275
CURRENT FILING DATE: 1999-12-23
EARLIER APPLICATION NUMBER: US 09/235,076
EARLIER FILING DATE: 1999-01-20
EARLIER FILING DATE: 1999-01-22
EARLIER APPLICATION NUMBER: US 09/234,611
EARLIER APPLICATION NUMBER: US 09/237,771
EARLIER APPLICATION NUMBER: US 09/240,371
EARLIER APPLICATION NUMBER: US 09/277,227
EARLIER APPLICATION NUMBER: US 09/277,227
EARLIER APPLICATION NUMBER: US 09/271,490
EARLIER FILING DATE: 1999-03-18
EARLIER FILING DATE: US 09/271,490
EARLIER FILING DATE: US 09/271,490
EARLIER FILING DATE: US 09/271,490
EARLIER FILING DATE: US 09/293,972
EARLIER FILING DATE: US 09/293,972
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EARLIER APPLICATION NUMBER: US 60/126,605
EARLIER FILING DATE: 1999-03-26
EARLIER APPLICATION NUMBER: US 09/306,350
EARLIER FILING DATE: 1999-05-07
EARLIER FILING DATE: 1999-09-27
EARLIER FILING DATE: 1999-09-21
EARLIER APPLICATION NUMBER: US 09/404,284
EARLIER APPLICATION NUMBER: US 09/404,284
EARLIER APPLICATION NUMBER:
EARLIER APPLICATION NUMBER:
EARLIER FILING DATE: 1999-09-21
EARLIER APPLICATION NUMBER:
EARLIER FILING DATE: 1999-12-16
NUMBER OF SEQ ID NOS: 10451
SEQ ID NO 7046
SEQ ID NO 7046
LENGTH: 1147
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; NAME/KEY: misc_feature
; LOCATION: (6)...(965)
; OTHER INFORMATION: similar to gi4337086 in the genepept database
; OTHER INFORMATION: Run with FASTXY 3.3t00, default parameters
US-09-471-275-7046
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FILING DATE: 1999-03-23
APPLICATION NUMBER: US 60/125,453
FILING DATE: 1999-03-19
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Pred. No. 2.5e-91;
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APPLICANT: Edwer, Charles S.
APPLICANT: Adler, Jon Elliot
APPLICANT: Edwer, Jon Elliot
APPLICANT: Lindemeler, Juergen
APPLICANT: Lindemeler, Juergen
APPLICANT: The Regents of the University of California
ITILE OF INVENTION: Nucleic Acids Encoding a G-Protein Coupled Rece
ITILE OF INVENTION: Involved in Sensory Transduction
ITLE REFERENCE: 02307E-088720US
CURRENT APPLICATION NUMBER: US/09/361.631
CURRENT FILING DATE: 1999-07-27
EARLIER APPLICATION NUMBER: US 60/095,464
EARLIER APPLICATION NUMBER: US 60/095,464
EARLIER APPLICATION NUMBER: US 60/112,747
EARLIER APPLICATION NUMBER: US 50/112,747
EARLIER FILING DATE: 1998-12-17
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 8
LENGTH: 2010
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US-09-361-631-8
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Best Local Similarity
Matches 1046; Conserv
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FEATURE:
OTHER INFORMATION: human G-protein coupled receptor
OTHER INFORMATION: nucleotide sequence
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Sequence 1, Application US/60172600
GENERAL INFORMATION:
APPLICANT: BONAZZI, VIVIEN
TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
TITLE OF INVENTION: RECEPTOR, NUCLEIC ACID MOLECULES ENC
TITLE OF INVENTION: PROTEIN, AND USES THEREOF
FILE REFERENCE: CL000178
CURRENT APPLICATION NUMBER: US/50/172,600
CURRENT FILING DATE: 1999-12-20
NUMBER OF SED ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 4.0
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; LENGTH: 2466
; TYPE: DNA
; TYPE: DNA
; ORGANISM: HUMAN
; ORGANISM: HUMAN
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Best Local Similarity
Matches 1154; Conserv
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                                    cacctgcccaggtgttacctgctcatgcggcagccagggctcaacacccccgagttcttc
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CURRENT APPLICATION NUMBER: US/60/178,308
CCURRENT FILING DATE: 2000-01-27
NUMBER OF SEQ ID NOS: 3344
SOFTWARE: FAStSEQ for Windows Version 4.0
SEQ ID NO 1069
LENGTH: 571
TYPE: DNA
ORGANISM: HUMAN
US-60-178-308-1069
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Sequence 1069, Application US/60178308
GENERAL INFORMATION:
APPLICANT: BONAZZI, VIVIEN
TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
TITLE OF INVENTION: PROTEINS, AND USES THEREOF
TITLE OF INVENTION: PROTEINS, AND USES THEREOF
US-60-160-202-36
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US-60-160-202-36
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GENERAL INFORMATION:
APPLICANT: BONAZZI, VIVIEN
TITLE OF INVENTION: ISOLATED HUMAN GPCR PROTEIN, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN GPCR PR
FILE REFERENCE: CLOO0114
FILE REFERENCE: CLOO0114
                                                                          CURRENT APPLICATION NUMBER: US/60/160,202
CURRENT FILING DATE: 1999-10-19
NUMBER OF SEQ ID NOS: 4392
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 36
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Best Local Similarity
Matches 313; Conserv
                    ORGANISM: HUMAN
                                     LENGTH: 558
TYPE: DNA
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Pred. No. 5.9e-59;
0; Mismatches 73;
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Sequence 23, Application US/60169841

GENERAL INFORMATION:

APPLICANT: BONAZZI, VIVIEN

ITILE OF INVENTION: ISOLATED HUMAN ION CHANNEL PROTEINS,

ITITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN I

ITITLE OF INVENTION: AND USES THEREOF

FILE REFERENCE: CLOOOL63

CURRENT APPLICATION NUMBER: US/60/169,841

CURRENT APPLICATION NUMBER: US/60/169,841

CURRENT FILING DATE: 1999-12-09

NUMBER OF SEQ ID NOS: 2910

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 23

LENGTH: 558

TYPE: DNA

ORGANISM: Human

US-60-169-841-23
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Best Local Similarity
Matches 309; Conserv
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Best Local Similarity
Matches 309; Conserv
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nilarity 76.5%;
Conservative (
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                                                                                                                                                                                                                  Score 252; DB 86;
Pred. No. 1.6e-54;
0; Mismatches 95;
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Pred. No. 1.6e-54;
0; Mismatches 95;
                                                                                                                                                                                                                                                                                                                                                                                                                                        ENCODING HUMAN ION CHANNEL PROTEINS
                                                                                                                                                                                                                                             Length 558;
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Sequence 23, Application US/60169842

GENERAL INFORMATION:
APPLICANT: Bonazzi, Vivien
TITLE OF INVENTION: ISOLATED HUMAN GPCR PROTEIN, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN GPCR PROTE
FILE REFERENCE: CLO00162
CURRENT APPLICATION NUMBER: US/60/169,842
CURRENT FILING DATE: 1999-12-09
NUMBER OF SEO ID NOS: 5232
SOFTMARE: FastSEQ for Windows Version 4.0
SEO ID NO 23
LENGTH: 558
TYPE: DNA
ORGANISM: Human
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US-60-169-842-23
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US-08-687-2898-2
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PCT-US-3-70-5
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US-08-485-588-3
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GENERAL INFORMA
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OPERATING SYSTEM: CONFIGURES
SOFTWARE: FASTSEQ
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,588
FILING DATE: 7 June, 1995
CLASSIFICATION ENTA: including applic prior APPLICATION DATA: including applic prior APPLICATION DATA: including applic prior APPLICATION DATA: including applic prior APPLICATION NUMBER: 08/353,784
FILING DATE: 21 October, 1994
APPLICATION NUMBER: U.S. 08/292,827
FILING DATE: 23 August, 1994
APPLICATION NUMBER: U.S. 08/141,248
FILING DATE: 22 October, 1993
APPLICATION NUMBER: U.S. 08/017,127
FILING DATE: 12 February, 1993
APPLICATION NUMBER: U.S. 08/017,127
FILING DATE: 12 February, 1993
APPLICATION NUMBER: U.S. 07/934,161
FILING DATE: 12 February, 1993
APPLICATION NUMBER: U.S. 07/834,044
FILING DATE: 11 February, 1992
APPLICATION NUMBER: U.S. 07/834,044
FILING DATE: 11 February, 1992
APPLICATION NUMBER: U.S. 07/834,044
FILING DATE: 11 February, 1992
APPLICATION NUMBER: U.S. 07/834,044
FILING DATE: 12 August, 1992
APPLICATION NUMBER: U.S. 07/749,451
FILING DATE: 13 August, 1991
APPLICATION NUMBER: U.S. 07/749,451
FILING DATE: 13 August, 1991
APPLICATION NUMBER: U.S. 07/749,451
FILING DATE: 13 August, 1991
APPLICATION NUMBER: U.S. 07/749,451
FILING DATE: SABIDON O.
REGISTRATION NUMBER: 38,179
REFERENCE/DOCKET NUMBER: 38,179
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ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Di
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APPLICANT: Steven C. Hebert
APPLICANT: Forrest H. Fuller
APPLICANT: James E. Garrett, Jr.
TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
TITLE OF INVENTION: MOLECULES
NUMBER OF SEQUENCES: 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: First Inter
STREET: Suite 4700
STREET: 633 West Fi
CITY: Los Angeles
STATE: California
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STREET: First Interstate World
STREET: Suite 4700
STREET: 633 West Fifth Street
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US-08-367-264-11
US-08-232-463-14
PCT-US91-09422-18
PCT-US91-09422-20
US-08-407-875-1
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Best Local Similarity 49.6%;
Matches 522; Conservative
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TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 3:
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LENGTH: 3809 base pairs
TYPE: nucleic acid
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LOCATION: 373..3606
OTHER INFORMATION:
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Pred. No. 3.6e-38;
0; Mismatches 524;
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RESULT 2
US-08-484-565-3
; Sequence 3, Application US/08484565
; Patent No. 5763569
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PRIOR APPLICATION DATA: including applic
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER: 08/353,784

FILING DATE: 9 December, 1994
APPLICATION NUMBER: PCT/VS/94/12117
FILING DATE: 21 October, 1994
APPLICATION NUMBER: U.S. 08/292,827
FILING DATE: 23 August, 1994
APPLICATION NUMBER: U.S. 08/11,248
FILING DATE: 23 August, 1994
APPLICATION NUMBER: U.S. 08/11,248
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                                                                           APPLICATION NUMBER: U.S. 08/009,389
FILING DATE: 23 February, 1993
APPLICATION NUMBER: U.S. 08/017,127
FILING DATE: 12 February, 1993
APPLICATION NUMBER: U.S. 07/934,161
FILING DATE: 21 August, 1992
APPLICATION NUMBER: U.S. 07/834,044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compation operating system: PC-DC SOFTWARE: FASTSEQ CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Edward M. Brown
APPLICANT: Steven C. Hebbert
APPLICANT: James E. Garrett, Jr.
TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
TITLE OF INVENTION: MOLECULES
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      ATTORNEY/AGENT
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APPLICATION NUMBER: U.S. 07/834,044
FILING DATE: 11 February, 1992
APPLICATION NUMBER: U.S. 07/749,451
FILING DATE: 23 AUGUST, 1991
FITORNEY/AGENT INFORMATION:
                                                                                                                                                                          FILING DATE: U.S. APPLICATION NUMBER: U.S. 1993
TITING DATE: 22 October, 1993
TITING DATE: WITHBER: U.S. 08/009,389
                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: UFILING DATE: 7 June, CLASSIFICATION: 435
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SYSTEM: PC-DOS/MS-DOS
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Heber,

, Sheldon O. 38,179

213/005

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; NAME/KEY: CDS
; LOCATION: 373..36
; OTHER INFORMATION:
US-08-484-565-3
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REFERENCE/DOCKET NUMBER: 213
TELECOMMUNICATION INCORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity
Matches 522; Conserv
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 2590
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STRANDEDNESS: single
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GTGATCTGGCTCTACACCGCGCCCCCCTCAAGCTACCGCAACCAGGAGCTGGAGGATGAG
                            ctcacatggcttgtaatgtggaccccacgacccaccagggaataccagcgcttcccccat 2195
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Pred. No. 3.6e-38;
0; Mismatches 524;
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RESULT 3
US-08-480-751-3
; Sequence 3, Application Us
; Patent No. 5858684
; GENERAL INFORMATION:
APPLICANT: Edward F.
APPLICANT: Edward M.
APPLICANT: Steven C
APPLICANT: Forrest
APPLICANT: James E
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: FASTSEQ
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,751
FILING DATE: 7 June, 1995
CLASSIFICATION: 435
            APPLICATION NUMBER: 08/353,784
FILING DATE: 9 December, 1994
APPLICATION NUMBER: PCT/US/94/12117
FILING DATE: 21 October, 1994
APPLICATION NUMBER: U.S. 08/292,827
FILING DATE: 23 AUGUSE, 1994
APPLICATION NUMBER: U.S. 08/141,248
FILING DATE: 22 October, 1993
APPLICATION NUMBER: U.S. 08/009,389
FILING DATE: 23 February, 1993
APPLICATION NUMBER: U.S. 08/017,127
FILING DATE: 12 February, 1993
APPLICATION NUMBER: U.S. 08/017,127
FILING DATE: 12 February, 1993
APPLICATION NUMBER: U.S. 08/017,127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: James E. Garrett, Jr.
TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
TITLE OF INVENTION: MOLECULES
NUMBER OF SEQUENCES: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: 3.5" Diskette,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
ZIP: 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: First Interstate World
STREET: Suite 4700
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
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  DATE
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Edward M. Brown
Steven C. Hebert
Forrest H. Fuller
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NUMBER: U.S
: 21 August,
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\: described below: 9
08/353,784
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US-08-480-751-3
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FILING DATE: 11 February, 1992
APPLICATION NUMBER: U.S. 07/749,451
FILING DATE: 23 AUGUST, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Heber, Sheldon O.
REGISTRATION NUMBER: 38,179
REFERENCE/DOCKET NUMBER: 213/004
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (213) 489-1600
TELEFAX: (213) 955-0440
TELEFAX: 67-3510
INFORMATION FOR SEO ID NO: 3:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity
Matches 522; Conserv
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LOCATION: 373..36
OTHER INFORMATION:
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TOPOLOGY: lin
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Pred. No. 3.6e-38;
0; Mismatches 524;
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RESULT 4
US-08-943-986-3
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Patent No. 5963314
GENERAL INFORMATION:
APPLICANT: Edward M. Brown
APPLICANT: Steven C. Hebert
APPLICANT: James E. Garrett, Jr.
TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
TITLE OF INVENTION: MOLECULES
FILING DATE: 7-June-1995
APPLICATION NUMBER: 08/353,784
FILING DATE: 9 December: 1994
APPLICATION NUMBER: PCT/US/94/12117
FILING DATE: 21 October: 1994
APPLICATION NUMBER: U.S. 08/292,827
FILING DATE: 23 August, 1994
APPLICATION NUMBER: U.S. 08/141,248
APPLICATION NUMBER: U.S. 08/141,248
APPLICATION NUMBER: U.S. 08/09,389
FILING DATE: 23 FEBRUARY, 1993
APPLICATION NUMBER: U.S. 08/009,389
FILING DATE: 23 FEBRUARY, 1993
APPLICATION NUMBER: U.S. 08/0017,127
                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PC DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FASTSEQ
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/943,986
FILING DATE: 03-0CT-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/484,565
FILING DATE: 7-June-1995
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: First Interstate World
STREET: Suite 4700
STREET: S03 West Fifth Street
CITY: Los Angeles
STATE: California
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Best Local Similarity
Matches 522; Conserv
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APPLICATION NUMBER: U.S. 07/934,161
FILING DATE: 21 AUGUSt, 1992
APPLICATION NUMBER: U.S. 07/834,044
FILING DATE: 11 February, 1992
APPLICATION NUMBER: U.S. 07/749,451
FILING DATE: 23 AUGUST, 1991
ATTORNEY/AGENT INFORMATION:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
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LENGTH: 3809 base pairs
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MOLECULE TYPE:
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LOCATION: 373..3606
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
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                                                            caactggtcatcatcttcaagttttctaccaaggtgcccacattctaccgtacctgggcc
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Pred. No. 3.6e-38;
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RESULT 5
US-08-353-784-3
; Sequence 3, Application US/08353784
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SOFTWARE: FASTERO
CURRENT APPLICATION NUMBER: US/08/353,784
FILING DATE: 9 December, 1994
CLASSIFICATION DATA: 1994
FRIOR APPLICATION DATA: including application PRIOR APPLICATION DATA: described below: 8 APPLICATION NUMBER: PCT/US/94/12117
FILING DATE: 21 October, 1994
APPLICATION NUMBER: U.S. 08/292,827
FILING DATE: 23 AUGUST, 1994
APPLICATION NUMBER: U.S. 08/292,827
FILING DATE: 23 AUGUST, 1994
APPLICATION NUMBER: U.S. 08/292,827
FILING DATE: 23 AUGUST, 1994
APPLICATION NUMBER: U.S. 08/141,248
FILING DATE: 22 October, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Lyon & Lyon
STREET: First Interstate World Co
STREET: Suite 4700
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: USA
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APPLICANT: Brown, Steven C. Hebert,
APPLICANT: Bradford C. Van Wagenen, Manuel
APPLICANT: F. Balandrin, Forrest H. Fuller,
APPLICANT: Eric G. DelMar, and Scott T. Moe
TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
TITLE OF INVENTION: MOLECULES
                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDING TYPE: 3.5" Diskette, 1.44
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
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TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity
Matches 522; Conserv
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APPLICATION NUMBER: U.S. 07/749,451
FILING DATE: 23 August, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Heber, Sheldon O.
REGISTRATION NUMBER: 38,179
REFERENCE/DOCKET NUMBER: 209/069
                                                                                                                                                                                                                                                                                                                                                           2173 AAGGAGATCGAGTTTCTGTCGTGGACGGAGCCCTTTGGGATCGCACTCACCCTCTTTGCC
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LOCATION: 373..36
OTHER INFORMATION:
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TOPOLOGY: lin
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TYPE: nucleic acid
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FILING DATE: 23 February, 1993
APPLICATION NUMBER: U.S. 08/017,127
FILING DATE: 11 February, 1993
APPLICATION NUMBER: U.S. 07/934,161
FILING DATE: 21 AUGUST, 1992
APPLICATION NUMBER: U.S. 07/834,044
APPLICATION NUMBER: U.S. 07/834,044
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caactggtcatcatcttcaagttttctaccaaggtgcccacattctaccgtacctgggcc
                                      CAGCCGGCCTTTGGCATCAGCTTCGTGCTCTCCATCTCATGCATCCTGGTGAAAACCAAC
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Pred. No. 3.6e-38;
0; Mismatches 524;
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RESULT 6
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                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,588
FILING DATE: 7 June, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA: including at PRIOR APPLICATION DATA: described by APPLICATION NUMBER: 08353,784
APPLICATION NUMBER: 08353,784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Edward
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MEDIUM TYPE: 3.5" Diskette, 1.44
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Edward M. Brown
APPLICANT: Steven C. Hebbert
APPLICANT: Forrest H. Fuller
APPLICANT: James E. Garrett, Jr.
TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
TITLE OF INVENTION: MOLECULES
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STREET: Suite 4700
STREET: 633 West Fifth Street
                                                                                                                                                                                                                                                                                                                                                                    CITY: Los Angeles
STATE: California
  APPLICATION NUMBER: PCT/US/94 FILING DATE: 21 October, 1994
                                       APPLICATION NUMBER: 08/3 FILING DATE: 9 December,
                                                                                                                                                                                                                         SOFTWARE:
                                                                                                                                                                                                                                                                                                                                ZIP: 90071
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FILING DATE:
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; LOCATION: 515..37;
; OTHER INFORMATION:
US-08-485-588-1
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Best Local S
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LENGTH: 5275 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
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APPLICATION NUMBER: U.S. 07/749,451
FILING DATE: 23 August, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Heber, Sheldon O.
REGISTRATION NUMBER: 38,179
                                                                                                                                                                                                                                                                            1716
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 12 February, 1993
APPLICATION NUMBER: U.S. 07/934,161
FILING DATE: 21 August, 1992
APPLICATION NUMBER: U.S. 07/834,044
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TWN DATE: 23 February, 1993
TWN DATE: "WARER: U.S. 08/017,127
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FILING DATE: 23 August, 1994
APPLICATION NUMBER: U.S. 08/141,248
FILING DATE: 22 October, 1993
APPLICATION NUMBER: U.S. 08/009,389
                                                          atotgccagccttgtggaacagaagaatgggcacccaaggagagcactacttgcttccca
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Pred. No. 1e-36;
0; Mismatches 546;
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RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                               COMPUTER: IBM PC compa-
OPERATING SYSTEM: PC-DA
SOFTWARE: FASTSEQ
CURRENT APPLICATION DATA:
                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3035
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TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
TITLE OF INVENTION: MOLECULES
NUMBER OF SEQUENCES: 20
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STREET: Suite 4700
STREET: 633 West Fifth Street
                                                                                                                                                                                          STATE:
APPLICATION NUMBER: US/08/484,565 FILING DATE: 7 June, 1995 CLASSIFICATION: 435
                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                ADDRESSEE: Lyon & Lyon
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                                                                                                                                                                                          Los Angeles 
California
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Steven C. Hebert
                                                                                 IBM PC compatible SYSTEM: PC-DOS/MS-DOS
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Best Local Similarity
Matches 530; Conserv
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FILING DATE: 22 October, 1993
APPLICATION NUMBER: U.S. 08/009,389
FILING DATE: 23 February, 1993
APPLICATION NUMBER: U.S. 08/017,127
FILING DATE: 12 February, 1993
APPLICATION NUMBER: U.S. 07/934,161
FILING DATE: 21 August, 1992
APPLICATION NUMBER: U.S. 07/934,044
FILING DATE: 11 February, 1992
APPLICATION NUMBER: U.S. 07/49,451
FILING DATE: 11 February, 1992
APPLICATION NUMBER: U.S. 07/749,451
FILING DATE: 23 August, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Heber: Sheldon O.
REGISTRATION NUMBER: 38,179
REFERENCE/DOCKET NUMBER: 213/006
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 5275 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEPAN: (213) 955-0440
TELEX: (273) 955-0440
1836 cctgtagtgaggtcaggctggggttaggcttcctcatgctgggttccctggttggcc
                                                                                                                                                                                                                                                                            2078 CTCTTCATCAATGATGAAAAAATTCTGTGGAGTGGATTCTCAAGGGAGGTGCCTTTCTCC
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NAME/KEY: CDS
LOCATION: 515..3769
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LENGTH: 5275 base pair
                                                   2378 GTGCTGGGCATTTTCCTCACAGCCTTCGTGCTGGGCGTCTTCATCAAGTTCCGCAACACG
                                                                                                                                                                                                                                                                                                                               2138 AACTGCAGTCGAGACTGCCTGGCAGGGACCAGGAAAGGAATCATTGAGGGGGGAGCCCACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 23 Au
APPLICATION NUMBER:
FILING DATE: 22 Oc
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                                                                                   acyctattyctyctyctygttygyactyctygcctytttycctyycattttcacaca 1835
                                                                                                                                        cgcacggtggagttcttggcttggcatgaacccatctctttggtgctaatagcagctaac
                                                                                                                                                                                        GCCTGTGATAAGTGCCCTGATGACTTCTGGTCCAATGAGAACCACACTTCCTGCATCGCC
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                                                                                                                     AAGGAGATCGAGTTTCTGTCGTGGACCGAGCCCTTCGGGATCGCACTCACGCTCTTTGCT
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ilarity 49.0%;
Conservative
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A: described below: 9
08/353,784
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Pred. No. 1e-36;
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APPLICANT: Edward
APPLICANT: Edward
APPLICANT: Steven
APPLICANT: Forrest
APPLICANT: James E
                                                                                                                                                     APPLICANT: Edward F. Nemeth
APPLICANT: Edward M. Brown
APPLICANT: Steven C. Hebert
APPLICANT: Forrest H. Fuller
APPLICANT: James E. Garrett, Jr.
APPLICANT: James E. Garrett, Jr.
TITLE OF INVENTION: MOLECULES
NUMBER OF SEQUENCES: 20
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                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   2556 ac
                                                                 ADDRESSEE: Lyon & Lyon
STREET: First Interstate World
STREET: Suite 4700
STREET: 633 West Fifth Street
                 COUNTRY:
                                 STATE: California
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Sequence 1, Application US/08480751 Patent No. 5858684
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Best Local Similarity
Matches 530; Conserv
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ATTORNEY/AGENT INFORMATION:
NAME: Heber, Sheldon O.
REGISTRATION NUMBER: 38,179
REFERENCE/DOCKET NUMBER: 213/0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
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FILING DATE: 22 October, 1993
APPLICATION NUMBER: U.S. 08/009,389
FILING DATE: 23 February, 1993
APPLICATION NUMBER: U.S. 08/017,127
FILING DATE: 12 February, 1993
APPLICATION NUMBER: U.S. 07/934,161
FILING DATE: 11 February, 1992
APPLICATION NUMBER: U.S. 07/934,044
FILING DATE: 11 February, 1992
APPLICATION NUMBER: U.S. 07/749,451
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PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
    1716
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FILING DATE: 9 December, 1994
APPLICATION NUMBER: PCT/US/94/12117
FILING DATE: 21 October, 1994
APPLICATION NUMBER: U.S. 08/292,827
FILING DATE: 23 AUGUST, 1994
APPLICATION NUMBER: U.S. 08/11 246
APPLICATION NUMBER: U.S. 08/11 246
APPLICATION NUMBER: U.S. 08/11 246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
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cgcacggtggagttcttggcttggcatgaacccatctctttggtgctaatagcagctaac
                                                                       atctgccagccttgtggaacagaagaatgggcacccaaggagagcactacttgcttccca
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                                      GCCTGTGATAAGTGCCCTGATGACTTCTGGTCCAATGAGAACCACACTTCCTGCATCGCC
                                                                                                                    TGCTGCTTTGAGTGTGTAATGTCCTGATGGGGAGTACAGCGACGAGACAGATGCAAGT
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US-08-943-986-1
Sequence 1, Application US/08943986
Patent No. 5962314
GENERAL INFORMATION:
APPLICANT: Edward M. Brown
APPLICANT: Steven C. Hebert
APPLICANT: Steven C. Hebert
APPLICANT: James E. Garrett, Jr.
TITLE OF INVENTION: CALCIDY RECEPTOR-ACTIVE
TITLE OF INVENTION: MOLECULES
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                                                                                                                                                                                     Query Match 6.4%;
Best Local Similarity 49.0%;
Matches 530; Conservative
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FILING DATE: 21 August, 1992
APPLICATION NUMBER: U.S. 07/83
FILING DATE: 11 February, 1992
APPLICATION NUMBER: U.S. 07/74
FILING DATE: 23 August, 1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5275 base pairs
TYPE: nucleic acid
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STREET: 633 West rrangeles
CITY: Los Angeles
CTTATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 08/484,565
FILING DATE: 7-June-1995
APPLICATION NUMBER: 08/353,784
FILING DATE: 9 December, 1994
APPLICATION NUMBER: PCT/US/94/12117
FILING DATE: 21 October, 1994
APPLICATION NUMBER: U.S. 08/292,827
FILING DATE: 23 August, 1994
APPLICATION NUMBER: U.S. 08/141,248
FILING DATE: 22 October, 1993
APPLICATION NUMBER: U.S. 08/09,389
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OPERATING SYSTEM: PC-D
SOFTWARE: FASTSEQ
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                     1479 ctggacataaataagacaaaaatccagtggcacgggaagaacaatcaggtgcctgtgtca 1538
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                     1596
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LOCATION: 515..3769
OTHER INFORMATION:
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TELEX: 67-3510
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Heber, Sheldon O. REGISTRATION NUMBER: 38,179
AACTGCAGTCGAGACTGCCTGGCAGGGACCAGGAAAGGAATCATTGAGGGGGAGCCCACC
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SYSTEM: PC-DOS/MS-DOS
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JMBER: U.S. 07
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1992
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RESULT 10
US-08-353-784-1
; Sequence 1, Application U
; Patent No. 6011068
; Patent INFORMATION:

US/08353784

APPLICANT:

Edward F. Nemeth,

Edward M.

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                                                                                                                                                                                                                               NAME/KEY: CDS
LOCATION: 515..37
OTHER INFORMATION:
US-08-353-784-1
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MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage COMPUTER IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: FASTSEO CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/353,784
FILING DATE: 9 December: 1994
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: PCT/US/94/12117
FILING DATE: 21 October: 1994
APPLICATION NUMBER: US. 08/292,827
FILING DATE: 23 August, 1994
APPLICATION NUMBER: US. 08/293,89
FILING DATE: 25 Cotober: 1993
APPLICATION NUMBER: US. 08/01,127
FILING DATE: 12 February, 1993
APPLICATION NUMBER: US. 08/01,127
FILING DATE: 12 February, 1993
APPLICATION NUMBER: US. 07/934,161
FILING DATE: 21 August, 1992
APPLICATION NUMBER: US. 07/934,044
FILING DATE: 12 February, 1993
APPLICATION NUMBER: US. 07/934,044
FILING DATE: 11 February, 1992
APPLICATION NUMBER: US. 07/934,044
FILING DATE: 23 August, 1992
APPLICATION NUMBER: US. 07/934,044
FILING DATE: 23 August, 1992
APPLICATION SUMBER: US. 07/934,044
FILING DATE: 23 August, 1992
APPLICATION SUMBER: US. 07/934,044
FILING DATE: 23 August, 1992
APPLICATION SUMBER: US. 07/934,044
FILING DATE: 23 August, 1992
APPLICATION SUMBER: US. 07/934,044
FILING DATE: 23 August, 1992
APPLICATION SUMBER: US. 07/934,044
FILING DATE: 23 August, 1991
ATTORNEY/ACENT INFORMATION:
NAME: Heber US. 07/49,451
FILING DATE: Shelfon O.
                                                                                               Query Match
Best Local Similarity
Matches 530; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
                                               1479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEPAX: (213) 955-0440
TELEXX: 67-3510
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APPLICANT: Bradford C. Van Wagenen, Manuel
APPLICANT: F. Balandrin, Forrest H. Fuller,
APPLICANT: Eric G. DelMar, and Scott T. Moe
TITLE OF INVENTION: CALCTUM RECEPTOR-ACTIVE
TITLE OF INVENTION: MOLECULES
NUMBER OF SEQUENCES: 20
  2078
                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 5275 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: 1i
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STREET: Suite 4700
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
  CTCTTCATCAATGATGAAAAAAATTCTGTGGAGTGGATTCTCAAGGGAGGTGCCTTTCTCC 2137
                          Heber, Sheldon O.
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                                                                                               Score 176.4; DB Pred. No. 1e-36; 0; Mismatches 54
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                                                                     attetetgeegteeagaacteaacaatacagaacacttteaggeeteeateeaggaetae
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                                                                                                         GCCATCCTGGCGGCCAGCTTTGGCTTGCTGGCCTGTATCTTCTTCAACAAGGTCTACATC
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                                                     ATCCTCTTCAAGCCTTCCCGGAACACCATCGAGGAGGTGCGCTGCAGCACCGCGGCACAC
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RESULT 11 US-08-485-588-2

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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,588
FILING DATE: 7 June, 1995
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
EXAMPLICATION DATA:
PRIOR APPLICATION DATA: including application prior APPLICATION DATA: described below: 9
APPLICATION NUMBER: 08/353,784
FILING DATE: 9 December, 1994
APPLICATION NUMBER: PCT/US/94/12117
FILING DATE: 21 October, 1994
APPLICATION NUMBER: U.S. 08/292,827
FILING DATE: 22 AUGUST, 1993
APPLICATION NUMBER: U.S. 08/141,248
FILING DATE: 22 PEDICATION NUMBER: U.S. 08/09),389
FILING DATE: 23 FEBRUARY, 1993
APPLICATION NUMBER: U.S. 08/09),389
FILING DATE: 12 FEBRUARY, 1993
APPLICATION NUMBER: U.S. 08/01/1,127
FILING DATE: 12 FEBRUARY, 1993
APPLICATION NUMBER: U.S. 07/934,161
FILING DATE: 12 FEBRUARY, 1993
APPLICATION NUMBER: U.S. 07/934,044
FILING DATE: 13 FEBRUARY, 1992
APPLICATION NUMBER: U.S. 07/934,044
FILING DATE: 12 FEBRUARY, 1992
APPLICATION NUMBER: U.S. 07/749,451
FILING DATE: 23 AUGUST, 1991
APPLICATION NUMBER: U.S. 07/749,451
FILING DATE: 12 FEBRUARY, 1992
APPLICATION NUMBER: U.S. 07/749,451
FILING DATE: 13 AUGUST, 1991
APPLICATION NUMBER: U.S. 07/749,451
FILING DATE: 23 AUGUST, 1991
APPLICATION NUMBER: U.S. 07/749,451
FILING DATE: 23 AUGUST, 1991
APPLICATION NUMBER: 213/005
FEBRUARY/AGENT INFORMATION:
TELEPHONE: (213) 489-1600
TELEX: 67-3510
INFORMATION FOR SEQ IN NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 5006 base pairs
US-08-485-588-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FASTSEQ
                                                                                                              MOLECULE TYPE: cDNA to mRNA FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Lyon & Lyon
STREET: First Interstate World
STREET: Suite 4700
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Edward M. Brown
APPLICANT: Steven C. Hebert
APPLICANT: Forrest H. Fuller
APPLICANT: James E. Garrett, Jr.
TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
TITLE OF INVENTION: MOLECULES
NUMBER OF SEQUENCES: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                     NAME/KEY: CDS
LOCATION: 436..3699
OTHER INFORMATION:
                                                                                                                                                                                        LENGTH: 5006 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 90071
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First Interstate World Center
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US-08-484-55-2

US-08-484-55-2

Patent No. 756556

Patent No. 756566

Patent No. 756666

Patent No. 756666
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ACATCATTCTCTTCAAGCCATCCCGCAACACCATC
gtgctatgtgattctctgccgtccagaactcaa
CGTAGAGGTGATTGCCATCCTGGCAGCCAGCTTTGCCTGGCGTGCATCTTCTT
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AAGCTGCCGGAGAACTTCAATGAAGCCAAGTTCATCACCTTCAGCATGCTCATCTT
actgccagagaactataatgaagccaaatgtgtcaccttcagcctgctcct
Db 2788 TICCTGATCGGCTACACCTGCCTGCTGGCTGCCATCTGCTTCTTTGCCTTCAAGTCC 2847
acccacaacattctcctccatcagtaccttcgtctgcagcta
TGCCACGA
Qy 2181 cagogottocococatotggtgattotogagtgcacagaggtcaactotgtaggottoctg 2240
GTGATCTGGCTCTACACCGCGCCCCCCTC
atttgctcatctgtctcacatggcttgtaatgtggaccccacgacccaccagggaat
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ptgtagtgaggtcagctgggggtaggctgtgcttcctcatgc
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CCTCCTGCATTGCCAAGGAGATCGAGT
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Qy 1641 atgagtgagetteaeatetgeeageettgtggaaeagaagaatgggeaeeeaaggagge 1700
GGGGAGCCCACCTGCTGTGAGTGTGGGAGTGTCCTGATGG
tgggttoccaccactgctgctttgagtgtgtgccctgcgaagctgggacctttotca
TICTCCAACTGCAGCCGAGACTGCCTGGCAGGACCAGGAAAGGGA
aggtgcctgtgtcagtgtgtaccacggactgtctggcagggcaccacagggtgg
Query Match 6.1%; Score 170.2; DB 2; Length 5006; Best Local Similarity 49.5%; Pred. No. 4.1e-35; Matches 498; Conservative 0; Mismatches 503; Indels 6; Gaps

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COUNTRY: USA
ZIP: 90071

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 Diskette, 1.44 Mb storage
MEDIUM TYPE: 3.5 Diskette, 1.44 Mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FASTSED
CURRENT APPLICATION NOMER: US/08/480,751
FILING DATE: 7 June, 1995
CLASSIFICATION DATA:
APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below: 9
APPLICATION NUMBER: 08/353,784
FILING DATE: 9 December, 1994
APPLICATION NUMBER: PCT/US/94/12117
FILING DATE: 21 October, 1994
APPLICATION NUMBER: US. 08/292,827
FTLING DATE: 23 August, 1994
; NAME/KEY: CDS; LOCATION: 436..3699; OTHER INFORMATION: US-08-480-751-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-480-751-2
                                                                                                                                                                                                                                                       APPLICATION NUMBER: U.S. 07/834,044
FILING DATE: 11 February, 1992
APPLICATION NUMBER: U.S. 07/749,451
FILING DATE: 23 AUGUST, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Heber, Sheldon O.
REGISTRATION NUMBER: 38,179
REFERENCE/DOCKET NUMBER: 213/004
TELECOMMUNICATION INFORMATION:
TELECHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application Patent No. 5858684
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Edward F. Nemeth
APPLICANT: Edward M. Brown
APPLICANT: Steven C. Hebert
APPLICANT: Forrest H. Fuller
APPLICANT: James E. Garrett, Jr.
TITLE OF INVENTION: CACITUM RECEPTOR-ACTIVE
TITLE OF INVENTION: MOLECULES
                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 5006 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                               FEATURE:
                                                                                                                   TOPOLOGY: 1i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NOWMER: U.S. 08/017,127
APPLICATION NUMBER: U.S. 08/017,127
FILING DATE: 12 February, 1993
APPLICATION NUMBER: U.S. 07/934,161
FILING DATE: 21 August, 1992
APPLICATION NUMBER: U.S. 07/834,044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 23 August, 193
APPLICATION NUMBER: U.S. 08/141,248
FILING DATE: 22 October, 1993
FILING DATE: U.S. 08/009,389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Lyon & Lyon
STREET: First Interstate World Center
STREET: Suite 4700
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
                                                                                                                                                             STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 22 OC APPLICATION NUMBER: FILING DATE: 23 Fe
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5. 5858684
                                                                                                                                                                                     nucleic acid
                                                                                                                   linear
E: cDNA to
                                                                                                                     mRNA
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NAME/KEY: CDS:
LOCATION: 436..3699
COTHER INFORMATION:
US-08-943-986-2
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                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/943/986
FILING DATE: 03-OCT-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/484,565
FILING DATE: 7-June-1995
APPLICATION NUMBER: 08/353,784
FILING DATE: 9 December: 1994
APPLICATION NUMBER: PCT/US/94/12117
FILING DATE: 21 October: 1994
APPLICATION NUMBER: U.S. 08/292,827
FILING DATE: 22 October: 1994
APPLICATION NUMBER: U.S. 08/141,248
FILING DATE: 22 October: 1993
APPLICATION NUMBER: U.S. 08/09,389
FILING DATE: 12 February: 1993
APPLICATION NUMBER: U.S. 08/01,127
FILING DATE: 12 February: 1993
APPLICATION NUMBER: U.S. 07/934,161
FILING DATE: 12 February: 1993
APPLICATION NUMBER: U.S. 07/834,044
FILING DATE: 13 August. 1992
APPLICATION NUMBER: U.S. 07/834,044
FILING DATE: 13 August. 1991
ATTORNEY/AGENT INFORMATION:
NAME: Heber: Sheldon 0.
REGISTRATION NUMBER: 38.179
REFERENCE/DOCKET NUMBER: 213/006
TELEX: 67.3510
TELEPAX: (213) 489-1600
TELEX: 67.3510
TELEPAX: 67.3510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                               TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 5006 base pair:
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FASTSEO
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: James E. Garrett, Jr.
TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
TITLE OF INVENTION: MOLECULES
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
                                                                                             MOLECULE TYPE: cDNA to mRNA FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Edward M. Brown APPLICANT: Steven C. Hebert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Lyon & Lyon
STREET: First Interstate World Center
STREET: Suite 4700
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
                                                                                                                                                 LENGTH: 5006 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
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Qy 2481 cccaagtgctatgtgattctctgccgtccagaactcaacaatacaga 2527
Oy 2421 geggtcaatgtgctggcagggctgaccacactgagcggcggcttcagcggttacttcctc 2480
Cy 2351 ttogtatcotggatogocttottoaccatggcoagcatttaccagggcagctacctgcct 2420
Qy 2301 aaggaactgccagagaactataatgaagccaaatgtgtcaccttcagcctgctcctcaac 2360
Qy 2241 ttggctttcacccacaacattctcctctccatcagtaccttcgtctgcagctacctgggt 2300
Qy 2181 cagogottococcatotggtgattotogagtgcacagaggtcaactotgtaggottoctg 2240
Qy 2121 catttgctcatctgtctcacatggcttgtaatgtggacccacgacccacgaggaatac 2180
Qy 2061 taccgtacctgggcccaaaaccatggtgcaggtctattcgtcattgtcagctccacggtc 2120
Qy 2001 acaatcogctccttccaactggtcatcatcttcaagttttctaccaaggtgcccacattc 2060
41 gegtgettgetgegteageecetetttetetetgggtttgeseatetteeteteetgeetg 20
Qy 1881 ggttccctggtggccggaagttgcagcttctatagcttcttcggggaagcccacggtgccc 1940
QY 1821 tggcattttcacacacctgtagtgaggtcagctggggtaggctgtgcttcctcatgctg 1880
Qy 1761 ctaatagcagctaacacgctattgctgctgctgctggttgggactgctggtgctgtttgcc 1820
Qy 1701 actacttgottccoacgcacggtggagttcttggcttggc
Qy 1641 atgagtgagcttcacatctgccagccttgtggaacagaagaatgggcacccaaggagagc 1700
Qy 1581 gtgggttcccaccactgctgctttgagtgtgtgccctgcgaagctgggacctttctcaac 1640
Qy 1524 caggtgcctgtgtcagtgtgtaccacggactgtctggcagggcaccacagggtggtt 1580
Query Match 6.1%; Score 170.2; DB 4; Length 5006; Best Local Similarity 49.5%; Pred. No. 4.1e-35; Matches 498; Conservative 0; Mismatches 503; Indels 6; Gaps

RESULT 15 US-08-353-784-2

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; NAME/KEY: CDS
; LOCATION: 436..3699
; OTHER INFORMATION:
US-08-353-784-2
                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: U.S. 08/009,389
FILING DATE: 23 February, 1993
APPLICATION NUMBER: U.S. 08/017,127
FILING DATE: 23 February, 1993
APPLICATION NUMBER: U.S. 08/017,127
FILING DATE: 12 February, 1993
APPLICATION NUMBER: U.S. 07/934,161
FILING DATE: 21 August, 1992
APPLICATION NUMBER: U.S. 07/834,044
FILING DATE: 11 February, 1992
APPLICATION NUMBER: U.S. 07/749,451
FILING DATE: 13 August, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Heber, Sheldon O.
REGISTRATION NUMBER: 38,179
REGISTRATION NUMBER: 209/069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application Patent No. 6011068 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA: including applic
PRIOR APPLICATION DATA: described below:
APPLICATION UNUMBER: PCT/US/94/12117
FILING DATE: 21 October, 1994
APPLICATION NUMBER: U.S. 08/292,827
FILING DATE: 23 August, 1994
APPLICATION NUMBER: U.S. 08/141,248
APPLICATION NUMBER: U.S. 08/141,248
APPLICATION NUMBER: U.S. 08/009,389
FILING DATE: 22 October, 1993
APPLICATION NUMBER: U.S. 08/009,389
                                                                                                                                                                                                                                                                           TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER TEADABLE FORM:

COMPUTER: 3.5" Diskette, 1.44

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Edward F. Nemeth, Edward M.
APPLICANT: Brown, Steven C. Hebert,
APPLICANT: Bradford C. Van Wagenen, Manuel
APPLICANT: F. Balandrin, Forrest H. Fuller,
APPLICANT: Eric G. DelMar, and Scott T. Moe
TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
TITLE OF INVENTION: MOLECULES
                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEPAX: (213) 955-0440
                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 5006 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: FASTSEQ CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                     FEATURE:
                                                                                                                         MOLECULE TYPE: cDNA to mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/353,784 FILING DATE: 9 December, 1994 CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 633 West
CITY: Los Angeles
STATE: California
                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: First Interstate World STREET: Suite 4700
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                                                                                                                                                                                                                         5006 base pairs
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A: described below: 8
PCT/US/94/12117
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               2481 cccaagtgctatgtgattctctgccgtccagaactcaacaatacaga
3028 AACAAGATCTACATCATTCTCTTCAAGCCATCCCGCAACACCATCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2608 CACCGCAAGTGGTGGGGGCTCAACCTGCAGTTCCTGCTGGTTTTTCCTCTGCACCTTCATG 2667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2061 taccgtacctgggcccaaaaccatggtgcaggtctattcgtcattgtcagctccacggtc
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                                                                             gcagggctgaccacactgagcggcttcagcggttacttcctccccaagtgctatgtg
                                                                                                                                    TCCTTCATTCCAGCCTATGCCAGCACCTATGGCAAGTTTGTCTCTGCCGTAGAGGTGATT
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Pred. No. 4.1e-35;
0; Mismatches 524;
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Matches 522;
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23-AUG-1991;
11-FEB-1992;
11-AUG-1992;
12-FEB-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA encoding calcium receptor polypeptide(s) - useful for therapeutic purposes, e.g. hyperparathyroidism and osteoporosis Claim 15; Columns 125-134; 174pp; English.

The present sequence encodes human parathyroid cell calcium receptor 4.0 (HuPCaR 4.0).

The specification includes details of molecules that can modulate one or more inorganic ion receptor activities, and antibodies and antibody fragments targetted to inorganic ton receptor proteins. I
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21-OCT-1994;
08-DEC-1994;
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18-NOV-1997.
07-JUN-1995;
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                           1716
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Sequence 3809 BP; 910 A; 1071 C; 979 G; 849 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human parathyroid cell calcium receptor 4.0 (HuPCaR 4.0) Human parathyroid cell calcium receptor 4.0; HuPCaR 4.0, calcium homeostasis; hyperparathyroidism; osteoporosis;
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T95859;
08-MAY-1998 (first entry)
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22-OCT-1993;
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cgcacggtggagttcttggcttggcatgaacccatctcttttggtgctaatagcagctaac
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US-485588.

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09-JUN-1998.
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V26964;
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Human parathyroid calcium receptor 4.0 gene
ss; calcium ion concentration; parathyroid kidney; calcium receptor; detection.
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484565.
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Principle 27; Fig 49; 174pp; English.

Protein. The tissue from which the receptor and receptors from bovine protein. The tissue from which the receptor and receptors from bovine parathyroid and rat kidney are derived, respond to changes, and control control control and rat concentration, e.g. parathyroid hormone regulates changes, in calcium ion concentration, e.g. parathyroid hormone regulates calters through changes in Ca2+ levels in juxtaglomerular and proximal cubule cells in the kidney. The purified receptors (produced recombinantly) can be used to screen for compounds that modulate calcium receptor activity, especially those that can be used to treat diseases associated with the receptors in these tissues. They can also be used to raise antibodies for use in detection assays.

So Sequence 3809 BP; 910 A; 1071 C; 979 G; 849 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Sin
Matches 522;
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21-AUG-1992; US-934161.
12-FEB-1993; US-0017127.
23-FEB-1993; US-009389.
22-OCT-1993; US-141248.
19-AUG-1994; US-292827.
21-OCT-1994; WO-U12117.
08-DEC-1994; US-353784.
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(NPSP-) NPS PHARM INC.
Brown EM, Garrett JE, Hebert
WPI; 98-347412/30.
P-PSDB; W54846.
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22; Conservative
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Pred. No. 4.1e-35;
0; Mismatches 524;
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12-FEB-1993.
12-FEB-1993.
12-AUG-1993.
12-AUG-1993.
12-AUG-1993.
                                                                                                                                                                                                                                                                                                                                                                          Human parathyroid calcium receptor pHuPCaR 4.0 encoding cDNA.

Parathyroid calcium receptor; inorganic ion receptor; osteoporosis; calcium homeostasis; hyperparathyroidism; seizure; stroke; epilepsy; spinal cord injury; hypoxia-induced nerve cell damage; cardiac arrest; neonatal distress; neurodegenerative disease; Alzheimer's disease; Huntington's disease; Parkinson's disease; dementia; muscle tension;
expression of nucleic acid encoding calcium recept
the effect of compounds on calcium recept claim 1; Fig 49: 176pp; English.
                                                                 Balandrin MF, Brown EN
Hebert SC, Nemeth EF,
WPI; 99-119871/10.
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V82485;
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                                                                                                                                    21-OCT-1994;
08-DEC-1994;
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                                                                                            BRIGHAM & WOMENS HOSPITAL.

NPS PHARM INC.

in MF, Brown EM, Del Mar EG,
                                                                                                                                   US-834044

US-934161

US-971127

US-007127

US-00938

US-141248

US-922827

WO-U12117

US-353784
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US-480751.
US-749451.
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AAGGAGATCGAGTTTCTGTCGTGGACGGAGCCCTTTGGGATCGCACTCACCCTCTTTGCC

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S 밁 δÃ 밁 Š 밁 Ş В Qy compound to affect one or more activities of the ballity of the test
compound to affect one or more activities of the calcium receptor; and
c(C) comparing the ability with the ability of the test compound to
affect the one or more CR activities in a cell not comprising the
recombinant nucleic acid. The present sequence encodes human
parathyroid CR, designated a phupCaR 4.0. The nucleic acid in the
chipCaR 4.0 can be used as part of the recombinant nucleic acid in the
method described above. The compounds identified can be used to treat
chipcarathyroidism, osteoporosis and other bone and mineral-related
disorders. They can also be used for the treatment of diseases and
clisorders associated with disrupted Ca2+ responses, e.g. seizures,
stroke, spinal cord injury, hypoxia-induced nerve cell damage such as in
cardiac arrest or neonatal distress, epilepsy, neurodegenerative
cliseases such as Alzheimer's disease, Huntington's disease and
cliseases dementia, muscle tension, depression, and anxiety.
Sequence 3809 BP; 910 A; 1071 C; 979 G; 849 T; Matches Query Match Best Local 1596 1993 1479 ctggacataaataagacaaaatccagtggcacgggaagaacaatcaggtgcctgtgtca 1538 one or more activities of a calcium receptor (CR) comprises: (A) contacting a recombinant cell with a test compound, where the recombinant cell comprises a recombinant nucleic acid expressing 2113 1656 2053 provided that the cell does not have functional CR expression A method has been developed of screening for gtgtgtaccacggactgtctggcagggcac---cacagggtggttgttgtgggttcccaccac 1595 cgcacggtggagttcttggcttggcatgaacccatctctttggtgctaatagcagctaac GCCTGTAACAAGTGCCCAGATGACTTCTGGTCCAATGAGAACCACACCTCCTGCATTGCC atotgccagcottgtggaacagaagaatgggcacccaaggagagcactacttgcttccca TGCTGCTTTGAGTGTGGGGGTGTCCTGATGGGGAGTATAGTGATGAGACAGATGCCAGT AACTGCAGCCGAGACTGCCTGGCAGGGACCAGGGAAAGGGGATCATTGAGGGGGGAGCCCACC CTCTTCATCAACGAGGAGAAAATCCTGTGGAGTGGGTTCTCCAGGGAGGTGCCCTTCTCC 1992 522; Similarity Conservative 49.6%; Score 181.6; Pred. No. 4.1e 0; Mismatches 0; 181.6; DB 1; No. 4.1e-35; 524; compound able CR) comprises: Indels Length σ. ç from Gaps affect the 1715 1775 2172 the e.g. CR, ä Ŋ

Query Match
Best Local Sim
Matches 530;

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(NPSP-) NPS PHARM INC
Brown EM, Fuller FH, (
WPI; 98-008040/01.
P-PSDB; W38272.
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18-NOV-1997;
07-UN-1995;
07-UN-1995;
07-UN-1995;
11-FEB-1992;
11-FEB-1992;
12-FEB-1993;
12-FEB-1993;
12-FEB-1993;
12-FEB-1993;
12-FEB-1994;
108-DEC-1994;
108-DEC-1994;
                                                The specification includes details of molecules that can modulate one or more inorganic ion receptor activities, and antibodies and antibody fragments targetted to inorganic ion receptor proteins. proteins, nucleic acids and antibodies may be used to treat proteins.
                                                                                                             DNA encoding calcium receptor polypeptide(s) - useful for therapeutic purposes, e.g. hyperparathyroidism and osteoporos Claim 1: Columns 107-116; 174pp; English.

The present sequence encodes bovine parathyroid cell calcium
                          disorders by modulating one or more inorganic activities, preferably disorders of calcium ho
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Key
CDS
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Bovine parathyroid cell calcium
Bovine parathyroid cell calcium
calcium homeostasis; hyperparath
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    hyperparathyroidism 
Sequence 5275 BP;
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(BoPCaR 1).
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PHARM INC.
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US-834044.
US-834044.
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ell calcium receptor 1; BoPCaR 1;
hyperparathyroidism; osteoporosi
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1277 A; 147
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                                                                                                                                                                                                                                        PT Calcium receptor poly:peptide(s) - useful for drug screening or PT antibody production
PS Example 25; Fig 47; 174pp; English.

CC The bovine parathyroid calcium receptor gene encodes a 1085 amino acid protein. The tissue from which this receptor and receptors from human CC parathyroid and rat kidney are derived, respond to changes, and control CC changes, in calcium ion concentration, e.g. parathyroid hormone regulates CC charges, in calcium ion concentration, e.g. parathyroid hormone regulates CC clark homeostasis in blood and extracellular fluid, and kidney function CC alters through changes in Ca2+ levels in juxtaglomerular and proximal CC tubule cells in the kidney. The purified receptors (produced CC recombinantly) can be used to screen for compounds that modulate calcium CC receptors activity, especially those that can be used to treat diseases CC associated with the receptors in these tissues. They can also be used CC to raise antibodies for use in detection assays.

SQ Sequence 5275 BP; 1277 A; 1475 C; 1316 G; 1207 T;
                                                                                                                                                                      Query Match 6.4%;
Best Local Similarity 49.0%;
Matches 530; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (BGHM ) BRIGHAM & WOMEI
(NPSP-) NPS PHARM INC.
Brown EM, Garrett JE, 1
WPI: 98-347412/30.
P-PSDB; W54844.
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21-OCT-1994;
08-DEC-1994;
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21-AUG-1992;
12-FEB-1993;
23-FEB-1993;
22-OCT-1993;
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07-JUN-1995;
23-AUG-1991;
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kidney;
Bos sp.
Key
CDS
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Bovine parathyroid calcium receptor
ss; calcium ion concentration; parat
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V26962;
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TGCTGCTTTGAGTGTGTGGAATGTCCTGATGGGGAGTACAGCGACGAGACAGATGCAAGT
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US-934161.

US-934189.

US-009389.

US-141248.

US-292827.

WO-U12117.

WO-U12117.
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US-484565.
US-749451.
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                                                                                                                                                                      Score 176.4; DB 1;
Pred. No. 8.9e-34;
0; Mismatches 546;
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RESULT
V82483
ID V8
AC V8
DT 11
DE B6
KW P8
KW C3

V82483

V82483

standard;

CDNA ç

19-MAR-1999 (first entry)
Bovine parathyroid calcium receptor; boPCaR 1 encoding cDNA.
Parathyroid calcium receptor; inorganic ion receptor; osteoporosis;
calcium homeostasis; hyperparathyroidism; seizure; stroke; epilepsy

stroke; epilepsy;

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PT Screening for calcium receptor-active compounds - by recombinant PT expression of nucleic acid encoding calcium receptor and determining PT the effect of compounds on calcium receptor activity
PS Claim 1; Fig 47; 176pp; English
CC A method has been developed of screening for a compound able to affect
CC one or more activities of a calcium receptor (CR) comprises: (A)
CC contacting a recombinant cell with a test compound, where the
CC recombinant cell comprises a recombinant nucleic acid expressing the CR,
CC provided that the cell does not have functional CR expression from
CC endogenous nucleic acid; (B) determining the ability of the test
CC compound to affect one or more activities of the calcium receptor; and
CC affect the one or more CR activities in a cell not comprising the
CC comparing the ability with the ability of the test compound to
CC affect the one or more CR activities in a cell not comprising the
CC parathyroid CR, designated a BoPCaR 1. The nucleic acid sequence of
CC becard a care as a part of the recombinant nucleic acid in the
CC diseases or disorders characterised by abnormal calcium homeostasis, e.g.
CC hyperparathyroidism, osteoporosis and other bone and mineral-related
CC disorders associated with disrupted Ca2+ responses, e.g. setzures,
CC cardiac arrest or neonatal distress, epilepsy, neurodegenerative
CC diseases such as Alzheimer's disease, Huntington's disease and
CC carkinson's disease, dementia, muscle tension, depression, and anxiety.
Sequence 5275 BP; 1277 A; 1475 C; 1316 G; 1207 T;
                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 49.0
Matches 530; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            spinal cord injury; hypoxia-induced nerve cell damage; cardiac arrest; neonatal distress; neurodegenerative disease; Alzheimer's disease; Huntington's disease; Parkinson's disease; dementia; muscle to Bos sp.

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12-JAN-1995 480751.
07-JUN-1995 US-480751.
07-JUN-1995 US-480751.
11-FEB-1992 US-934161.
11-FEB-1992 US-934161.
12-FEB-1992 US-934161.
12-FEB-1993 US-017127.
23-FEB-1993 US-009389.
22-OCT-1994 US-292827.
21-OCT-1994 US-292827.
21-OCT-1994 US-353784.
(BGHM ) BRIGHAM & WOMENS (NPSP-) NPS PHARM INC.
Balandrin MF, Brown EM, DHEBERT SC, Nemeth EF, Van MPI: 99-119871/10.
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             T61381 standard; cDNA to mRNA; 5006 BP.
T61381;
22-APR-1997 (first entry)
Parathyroid calcium receptor coding sequence clone pHuPCaR5.
Calcium receptor; human parathyroid gland adenoma tumour; pB
primary hyperparathyroidism; Xenopus cocyte; alternative spl
calcium-activated chloride current; agonist; NPS R-467; NPS
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02-MAY 1996.
23-OCT-1995; U13704.
21-OCT-1994; W0-U12117.
08-DEC-1994; US-353784.
4 (NPSP-) NPS PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 498;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    These sequences were isolated from human parathyroid gland adenoma tumour using pBoPCaR1 as a hybridisation probe. mRNA was isolated from a 39 year old caucasian male diagnosed with primary hyperparathyroidism and two clones of approx. 5 and 4 kb were identified. These cDNA's were injected into xenopus occytes which were assayed for the presence of functional calcium receptors. Both clone types gave rise to functional calcium receptors. Both clone types gave rise to functional calcium receptors as assessed by the stimulation of calcium-activated chloride currents upon addition of appropriate calcium receptor agonists, e.g. NPS R-67 and NPS R-568. Sequence analysis of the two cDNA clones indicated the existence of at least two sequence variants differing in the 3' untranslated region and which may result from alternative polyadenylation. Sequence variation also exists in the 5' end of the inserts. These sequence differences may have arisen due to alternative translated regions and which may result from alternative constraints in the sequence constraints and the sequence of the constraints of the constraints and the sequence and the constraints of the constraints and the sequence constraints and the sequence of the constraints and the sequence of the constraints and the sequence constraints and the sequence of the constraints and the sequence constraints and 
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pharmacologically distinct.
Sequence 5006 BP; 1228
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Example 1; Page 85-93; 231pp; English.
The sequences given in T61381-82 encode functional calcium receptors.
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WPI; 96-230520/23.
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human CaR gene; isoform; ss.
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ctaatagcagctaacacgctattgctgctgctgctggttgggactgctggtctgtttgcc
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US5688938-A.
18-NOV-1997.
07-JUN-1995.
07-JUN-1995.
23-AUG-1991.
11-FEB-1992.
21-AUG-1993.
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08-MAY-1998
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US-485588.
US-485588.
US-749451.
US-834044.
US-934161.
US-017127.
US-009389.
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osteoporosis; ss.
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19-AUG-1994; US-292827.
21-OCT-1994; WO-U12117.
08-DEC-1994; US-353784.
(BGHM ) BRIGHAM & WOMENS H
(NPSP-) NPS PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence encodes human parathyroid cell calcium receptor 5.2 (HuPCaR 5.2).

The specification includes details of molecules that can modulate one or more inorganic ion receptor activities, and antibodies an antibody fragments targetted to inorganic ion receptor proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  proteins, nucleic acids and antibodies may be used to treat disorders by modulating one or more inorganic ion receptor activities, preferably disorders of calcium homeostasis, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA encoding calcium receptor polypeptide(s) - therapeutic purposes, e.g. hyperparathyroidism Claim 15; Columns 117-126; 174pp; English.
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Sequence 5006 BP; 1227 A; 1378
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cagcgcttcccccatctggtgattctcgagtgcacagaggtcaactctgtaggcttcctg
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                                   catttgctcatctgtctcacatggcttgtaatgtggaccccacgacccaccagggaatac
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23-AUG-1991; US-749451.
11-FEB-1992; US-934161.
12-FEB-1992; US-017127.
12-FEB-1993; US-017127.
23-FEB-1993; US-0171248.
19-AUG-1994; US-141248.
19-AUG-1994; US-352847.
21-OCT-1994; US-352847.
21-OCT-1994; US-352847.
antibody production

Example 27; Fig 48; 174pp; English.

The Human parathyroid calcium receptor gene encodes a 1088 amino acid protein. The tissue from which this receptor and receptors from bovine parathyroid and rat kidney are derived, respond to changes, and control changes, in calcium ion concentration, e.g. parathyroid hormone regulates ca2+ homeostasis in blood and extracellular fluid, and kidney function alters through changes in Ca2+ levels in juxtaglomerular and proximal tubule cells in the kidney. The purified receptors (produced recombinantly) can be used to screen for compounds that modulate calcium receptor activity, especially those that can be used to treat diseases associated with the receptors in these tissues. They can also be used to raise antibodies for use in detection assays.

Sequence 5006 Bp; 1228 A; 1376 C; 1220 G; 1182 T;
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P-) NPS PHARM INC.
n EM, Garrett JE, Hebert SC;
98-347412/30.
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GAGGGGGAGCCCACCTGCTTTGAGTGTGTGGAGTGTCCTGATGGGGAGTATAGTGAT 2190

CAGGTGCCCTTCTCCAACTGCAGCCGAGACTGCCTGGCAGGGACCAGGAAAGGGATCATT 2130

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PT Screening for calcium receptor-active compounds - by recombinant PT Screening for calcium receptor and determining PT the effect of compounds on calcium receptor activity

PS Claim 1; Fig 48; 176pp; English.

CC A method has been developed of screening for a compound able to affect CC one or more activities of a calcium receptor (CR) compounds on calcium receptor (CR) compound able to affect CC recombinant cell comprises a recombinant nucleic acid expressing the CR, CC provided that the cell does not have functional CR expression from CC endogenous nucleic acid; (B) determining the ability of the test compound to affect one or more activities of the calcium receptor; and CC compound to affect one or more cativities of the calcium receptor; and CC affect the one or more CR activities in a cell not comprising the ability with the ability of the test compound to affect the present sequence encodes human CC parathyroid CR, designated a pHuPCaR 5.2. The nucleic acid in the present sequence encodes human CC purpose or disorders characterised by abnormal calcium homeostasis, e.g. the preparathyroidism, osteoporosis and other bone and mineral-related CC disorders. They can also be used for the treatment of diseases and CC ation as plant of the responses, e.g. selzures, cc ation as alzabelmer's disease, Huntington's disease and CC diseases such as Alzabelmer's disease, Huntington's disease and anxiety.

Sequence 5006 BP; 1228 A; 1376 C; 1220 G; 1182 T;
                                                                      Query Match
Best Local
                                                     Matches 498;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-JUN-1995; 480751.
07-JUN-1995; US-480751.
23-AUG-1991; US-749451.
11-FEB-1992; US-834064.
21-AUG-1992; US-934161.
12-FEB-1993; US-017127.
23-FEB-1993; US-017127.
23-FEB-1993; US-0171248.
19-AUG-1994; US-292827.
21-OCT-1994; WG-212117.
08-DEC-1994; US-35784.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-MAR-1999 (first entry)
Human parathyroid calcium receptor; phupcar 5.2 encoding cDNA.
Parathyroid calcium receptor; inorganic ion receptor; osteoporosis;
calcium homeostasis; hyperparathyroidism; seizure; stroke; epilepsy;
spinal cord injury; hypoxia-induced nerve celi damage; cardiac arrest;
neonatal distress; neurodegenerative disease; Alzheimer's disease;
Huntington's disease; Parkinson's disease; dementia; muscle tension;
depression; anxiety; ss.
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Hebert SC, Nemeth EF, Van Wagenen B
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19-MAR-1999
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                                                                    Local Similarity
BRIGHAM & WOMENS HOSPITAL.

NPS PHARM INC.
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                                                   Conservative
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                                                                6.1%;
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                                                 Score 170.2; DB:
Pred. No. 2.9e-32
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                                                                                        T95860 standard;
                                  MAY-1998 (first entry)
kidney cell calcium receptor
kidney cell calcium receptor
cium homeostasis; hyperparathy
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Location/Qualifiers 574. .3813
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                                  hyperparathyro
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                                                                                         mRNA;
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                                            3A;
                                            (RakCaR
                                   Ldism;
                                                                                         ВP
                                  osteoporosis;
                                            3A)
3A;
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18-NOV-1997.
07-JUN-1995; US-485588.
07-JUN-1995; US-485588.
07-JUN-1995; US-834044.
21-AUG-1992; US-934161.
11-FEB-1992; US-934161.
12-FEB-1993; US-017127.
23-FEB-1993; US-017127.
23-FEB-1993; US-017127.
23-FEB-1993; US-017127.
23-FEB-1993; US-017127.
23-FEB-1994; US-292827.
21-OCT-1994; US-292827.
21-OCT-1994; US-353784.
(BGHX) BRIGHAM & WOMENS H (NPSP-) NPS PHARM INC.
BIOWN EM, FULLER FH, GAITE WPI; 98-008040/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA encoding calcium receptor polypeptide(s) - therapeutic purposes, e.g. hyperparathyroidism claim 15; Columns 133-142; 174pp; English. The present sequence encodes rat kidney cell careceptor 3A (RakCaR 3A).

The specification includes details of molecules
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The specification includes details of molecules that can modulate one or more inorganic ion receptor activities, and antibodies and antibody fragments targetted to inorganic ion receptor proteins nucleic acids and antibodies may be used to treat disorders by modulating one or more inorganic ion receptor whiles, preferably disorders of calcium homeostasis, e.g. sequence 4131 BP; 987 A; 1170 C; 1053 G; 921 T;
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cagococtottttctctcgggtttgccatcttcctcctgcctgacaatccgctccttc
                                                                                                                                                            GTGCTGGGCATTTTCCTGACCGCCTTTGTGCTGGGTGTCTTCATCAAGTTCCGAAACACA
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                                                             cctgtagtgaggtcagctgggggtaggctgtgcttcctcatgctggtgtgccctgtagtgtgtccttggtgcttcctcatgctggtgtgcct
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                                                                                                                                                                                                                                         cgcacggtggagttcttggcttggcatgaaccccatctctttggtgctaatagcagctaac
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                                                                                                    CCTATCGTCAAGGCCACCAACCGAGAACTGTCCTACCTCCTGCTCTTCTCCCTACTCTGC
                                                                                                                                                                                                                       AAGGAGATTGAGTTTCTGGCGTGGACCGAGCCCTTTGGAATCGCTCTCACTCTCTTTGCG
                                            TGCTTCTCCAGCTCCTTGTTCTTCATTGGGGAGCCCCAGGACTGGACGTGCCGCCTGCGA
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Pred. No. 6e-30;
0; Mismatches 5
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R 07-JUN-1995; US-484565.

R 23-AUG-1991; US-934044.

R 21-AUG-1992; US-934161.

R 21-FEB-1992; US-934161.

R 21-FEB-1993; US-017127.

R 21-FEB-1993; US-017127.

R 22-CCT-1994; US-292827.

R 19-AUG-1994; US-292827.

R 19-AUG-1994; WG-112117.

R 08-DEC-1994; WG-353784.

(BGHM ) BRIGHAM & WOMENS HOSPITAL.

(NPSP-) NPS PHARM INC.

(NPSP-) NPS 
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07-JUN-1995;
07-JUN-1995;
07-JUN-1995;
23-AUG-1992;
11-FEB-1992;
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Key
CDS
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Rat kidney calcium receptor 3A gene 4Kb frass; calcium ion concentration; parathyroid kidney; calcium receptor; detection.
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Matches 516; Conservative
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PT screening for calcium receptor-active compounds - by recombinant procession of nucleic acid encoding calcium receptor and determining the effect of compounds on calcium receptor activity the effect of compounds on calcium receptor activity the effect of compounds on calcium receptor activity of the effect of compound able to affect one or more activities of a calcium receptor (CR) comprises: (A) contacting a recombinant cell with a test compound, where the contacting a recombinant cell with a test compound, where the contacting a recombinant nucleic acid; (B) determining the ability of the test provided that the cell does not have functional CR expression from the compound to affect one or more activities of the calcium receptor; and compound to affect one or more activities of the test compound to affect one or more activities of the calcium receptor; and compound to affect one or more activities of the comprising the creombinant nucleic acid. The present sequence encodes rat recombinant nucleic acid. The present sequence encodes rat parathyroid CR, designated a pRakCaR 3A. The nucleic acid in the method described above. The compounds identified can be used to treat diseases or disorders characterised by abnormal calcium homeostasis, e.g. hyperparathyroidism, osteoporosis and other bone and mineral-related cold diseases and other bone and mineral-related cold diseases and calcium homeostasis and cold diseases and cold diseas
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12-FEB-1993
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19-AUG-1994
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Parathyroid calcium receptor; inorganic ion receptor; osteoporosis; calcium homeostasis; hyperparathyroidism; seizure; stroke; epilepsy; spinal cord injury; hypoxia-induced nerve cell damage; cardiac arrest; neonatal distress; neurodegenerative disease; Alzheimer's disease; Huntington's disease; Parkinson's disease; dementia; muscle tension;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Balandrin MF, Brown EN Hebert SC, Nemeth EF, WPI; 99-119871/10.
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GTGCTGGGCATTTTCCTGACCGCCTTTGTSCTGGGTGTCTTCATCAAGTTCCGAAACACA
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                                     aactataatgaagccaaatgtgtcaccttcagcctgctcctcaacttcgtatcctggatc
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                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This cDNA clone codes for dogfish shark kidney calcium receptor crelated protein (SKCaR-RP, see W32059), an aquatic polyvalent cation-sensing receptor (PVCR). It was isolated from a shark kidney cDNA library using a rat kidney calcium receptor cDNA as probe. Also claimed are: a probe comprising the 4131 bp SKCaR-RP sequence; an isolated PVCR present in the plasma membranes of sequence; an isolated PVCR present in the plasma membranes of cells of elasmobranch fish, particularly from cells found in the cells of elasmobranch fish, particularly from cells found in the collecting duct or late distal tubule in the kidney, intestine, gill, rectal gland, gonad or brain; an antibody that specifically binds to a PVCR; and a method of screening for aquatic PVCR aguatic PVCR activates or inhibits aquatic PVCR mediated ion aquatic PVCR activates or inhibits aquatic PVCR mediated ion
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      transport and endocrine changes that permit fish to adapt to free or salt water. The method facilitates the aquaculture of marine fish and can provide for the development of marine fish that are easily adaptable to fresh water aquaculture.

Sequence 4131 BP; 1028 A; 1161 C; 1019 G; 923 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (BGHM ) BRIGHAM & WOMENS HOSPITAL
Brown E, Harris HW, Hebert S;
WPI; 97-489640/45.
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27-MAR-1996;
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27-MAR-1998
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Search completed: March 18, 2000, 18:57:59 Job time: 2882 sec

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SUMMARIES

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ALIGNMENTS

REFERENCE		ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	LOCUS	AF127389	RESULT 1
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. 1 (bases 1 to 2520)	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;	Rattus norvegicus	Norway rat.		AF127389.1 GI:4337085	AF127389	Rattus norvegicus putative taste receptor TR1 mRNA, partial cds.	AF127389 2520 bp mrNA ROD 04-MAR-1999		

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Putative mammalian taste receptors: a class of ta with distinct topographic selectivity
Cell 96 (4), 541-551 (1999)
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FLMPLVSYEASSVYULSAKRKPFSFLRTYPSDRHQDVENVYGLLQSIGTYLGVAVQQQVPGLK
YQQLGVQALEELAVPRGICVAFKDIVPFSARVGDPRMQSMMQHLAQARTTVVVVFSNR
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YAVAHGLHQLLGCTSEICSRGPYYPWQLLQQIYKNTFLHENTVAFDDNGDTLGYIDI
IAWMWGPEWTFEIIGSASLSPYHLDINKTKIQWHGKNNQVPVSVCTTDCLAGHHRVV
VGSHHCCFECVPCEAGTFLNMSELHICDPCGTEEWAPKESTTCFPRTVEFLAWHEPIS
LVLIAANTLLLLLLVGTAGLFAHHFHFPVVRSAGGRLFUNGSSTYSFFGE
PTVPACLLRQPLFSLGAIFLSCLTIRSFQLVIIFKFSTKVPTFYRWAQNHGAGLFV
IVSSTYHLLICLTWLYMWTPRPTREYQRFDLVIIFKFSTKVPTFYRWAQNHGAGLFV
IVSSTYHLLICLTWLYMWTPRPTREYQRFDLNTIEHTSVSVLAFFHNILLSIS
TFVCSTYGKELPENYNEAKCYTTSSLLAWFUNGVGSYLPAVNVLAGUTT
LSGGFSGYFLPKCYVILCRPELNNTEHFQASIQDYTRRCGTT"
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/strain="Wistar"
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                                       GTAGCTCCCTGCTACCCGGCGTGCTGCTCGGCTACGAGATGGTGGATGTCTGTTACCTCT
                                                               cctcggccctgcttcccaacatcaccctggggtatgagctgtacgacgtgtgctcagaat
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                                                                                                                 AGGTGTTGGGCTACAACCTCATGCAGGCCATGCGTTTCGCTGTGGAGGAGATCAACAACT
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AF127390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (10-FEB-1999) Taste and Drive MSC 1188, Bethesda, MD 2089;
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Hoon, M.A., Adler, E.,
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Rattus norvegicus
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LIPQITYSAISDKLRDKRHFPSNLRTVPSATHHIEAMVOLMVHFQMWHIVLVSDDDY
GRENSHLLSORLTKTSDICIAFDEVLLF IPESQVMRSESQRQLDNILDKLRRTSARVV
VVFSPELSLYSSFHEVLRWNFFGFVWIASESWALDPVLHKTIELHTGTFIGVTIQRV
SIPGFSQFRVRRDKPGYPVPNTNLRTTCNQDCDACLNTTKSFNNILLIGGERVVYSV
YSAVYAVAHALHRLLGCNRVCTKQKVVPWQLLREIWHVNFTLLGNRLFFDQQGDMPM
LDDIIQWQWDLSQNEPQSIASYSPTSKRLTYINNVSWYTPNNTVEVSMCSKSCQPGQM
KKSVGLHPCCFECLDCMPGTYLNRSADEFNCLSCPGSMWSYKNDITCFQRRPTFLEWH
EVPTIVVALIAALGFTSTLAILFITWRHFQTPMVRSAGGMCFLMLVPLLLAFGMWPV
YVGPPTVTSCTCZQAPFTVCFSICLSCTTTNSFQIVCVFKMARRLPSAYSFWMRYHGP
YVFVAFITAIXVALVGNMLATTINFICRTDDDDNIMILSCHPWYRNGLLFNTSMDL
LLSVLGFSSAYMGKELPTNYNBEKFITLSMTFSFTSSISLCTTEMSYHDGVLVTIMDLL
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826 c 623 g 583 t
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/translation="MGFQARTLCLLSJLHVLPKPGKLVENSDFHLAGDYLLGGYENV
HANVKSISHLSYLQVPKCNEFTMKVLGYNLMQAMRFAVEEINNCSSLLPGVLLGYEMV
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/strain="Wistar"
/db_xref="taxon:10116"
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Pred. No. 1.4e-93;
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Qy Db

			tc 1317 2AC 1273	1cc 1257 1CA 1213	ct 1197	1cc 1137						ct 795 PAC 739	ogc 735	999 678 GA 619	cg 618 AG 559	JCt 558	1ca 498 	1 CA 379
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ОУ	Qy Db	Db Qy	Оy	dp oy	Дb	Оy	Оy	Ор	ру	Qу	Ор	рb	Оy	Дb	Дb	Оy	문	g B
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1138 1318 1214 1274 1094 1040 1078 1018 980 958 008 740 796 089 620 560 619 500 559 440 499 380 toggtgtggccgtccagcagagacaagtccctgggctgaaggagtttgaggagtcttat atctggctcaggccaggaccaccgtggttgtggttcttctctaaccggcacctggctaga **AAGGGGACATGCCGATGCTCTTGGACATCATCCAGTGGCAGTGGGAACCTGAGCCAGAA** agctcctgggatgtacttctgagatctgttccagaggcccagtctacccctggcagcti ccatgagtgccgcctacagagtgtatgaggctgtgtacgctgtgggcccacgggcctccac agctgtgccgggagtgccacacgttcacgactcgtaacatgcccacgcttgggagcctto tcagggctgtaacagctgctcccaggcgcttgcccggaggggtcctggtgcagcaactaac actgggccatctccacgtacatcaccagcgtgactgggatccaaggcattgggacggts GCTTCTTTCACGAGGTGCTCCGCTGGAACTTCACGGGTTTTGTGTGGATCGCCTCTGAC tgttcttcaggtccgtggtgctggccaacctgactggcaaagtgtgggtcgcctcagas ct-----gcccgggtgggtgacccgagga------tgcagagcatgatgcac tggaggagctggccgtgccccggggcatctgcgtcgccttcaaggacatcgtgcctttc acggggacactctaggttactacgacatcatcgcctgggactggaatggacctgaatg GACTCCTCGGCTGTAACCGGGTCCGCTGCACCAAGCAAAAGGTCTACCCGTGGCAGCT1 GGGAGCGCGTGGTCTACAGCGTGTACTCGGCAGTTTACGCGGTGGCCCATGCCCTCCA AGGACTGTGACGCCTGCTTGAACACCACCAAGTCCTTCAACAACATCCTTATACTTTC ACAAGCCAGGGTATCCCGTGCCTAACACGACCAACCTGCGACGACCTGC-----AAC CCTGGGCTATCGACCCAGTTCTGCATAACCTCACGGAGCTGCGCCACACGGGTACTTT CTGAGTCCAGCCAGGTCATGAGGTCCGAGGAGCAGAGACAACTGGACAACATCCTGGA GCCAGCGTCTGACCAAAACGAGCGACATCTGCATTGCCTTCCAGGAGGTTCTGCCCAT ACTGGATTGTGGTGCTGGTGAGCGACGACGATTACGGCCGCGAGAACAGCCACCTGTT tgtggatctcgctcattggcagctacggtgattacgggc---agctgggtgtgcaggcg atgaggcaagcagcgtggtactcagtgccaagcgcaagttcccgtctttccttcgtac CTGAGTCCGCCATTACCGTGTCCAACATTCTCTCTCATTTCCTCATCCCACAGATCAC ctgaccacgctgtcactaccgctgccttgctgggtccttttcctgatgcccctggtcagc tacagaaagaccttcgcaaccactcctccaaggtggtggccttcatcgggcctgacaac CCAACAATATCCACCTGGGCTCTACTTCCTGGCACAGGACG---ACGACCTCCTGCCC TCCTCAAAGACTACAGCCAGTACATGCCCCACGTGGTGGCTGTCATTGGCCCCGACAA

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Best Local Similarity
Matches 217; Conserv
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1 (bases 1 to 270)
Murray, J., Sheffield, V. Weber, J.L., Duyk, G. and Buetow, K.H.

Copperative Human Linkage Center
Unpublished (1995)
Synonyms: GCT15G02, CHLC.GCT15G02.T16713
Contact: Dr. Jeffrey C. Murray
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STS sequence; primer; sequence tagged site.
human vector-pJCPl host-E.coli dut+ung+ (DH10B) Marker Selected genomic DNA prepared from XY individual of French nationality.
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Primer B: TGGTGTTTTTGGCTTTGC
STS size: 124
PCR Profile:
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Department of Pediatrics, Iowa City,
Tel: (319) 356-3508
Fax: (319) 356-3347
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Sequence 3 f
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Brown, E.M., Hebert, S.C. and Garrett, J.E.
Calcium receptor-active molecules
Patent: US 5763569-A 3 09-JUN-1998;
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Sequence 3 :
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Nemeth, E.F., Brown, E.M., Hebert, S.C., Garrett, J.E. Jr Wagenen, B.C., Balandrin, M.F. and Del Mar, E.G. Method of screening calcium receptor-active molecules Patent: US 5858684-A 3 12-JAN-1999; Location/Qualifiers
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 3361)
Aida,K., Koishi,S., Tawata,M. and Onaya,T.
Molecular cloning of a putative Ca(2+)-sensing receptor
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Homo sapiens kidney cDNA
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                                        /product="Ca-sensing receptor"
/product="Ca-sensing receptor"
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/db_xref="G1:904210"
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rakdddlksrpesyecirynprerewidentarii lavygargsgystavanlldlf
yipywsassstlsnknofksflridenedeldaramadiieyrewnwyctiaaddy
grpgterfredaedenolcidfselisoysdeedidhyvvrygatigfalkagolpgfreefl
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/db_xref="taxon:9
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Submitted (07-FEB-1995) James E. Garrett, Molecular Biology, NPS Pharmaceuticals, Inc., 420 Chipeta Way, Salt Lake City, UT 84108
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Garrett, J.E., Capuano, I.V., Hammerland, L.G., Hung, B. Hebert, S.C., Nemeth, E.F. and Fuller, F. Molecular cloning and functional expression of human molecular cloning and functional expression of human molecular cloning and functional expression.
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PLCTGDENISSYETPYIDYTHLRISYNYYLAVSIAHALQDITYCLPGRGLETNSSCA
DIKKYEAMOVLKHLRHLHETNNMGEQUTFDEGGDLYGNYSINMHLSPEDGSIVEKEY
GYYNVYAKKGERLFINEEKILWGGFSREVPFSNCSRDCLAGTRKGIIEGEPTCCFECV
ECPDGEYSDETDASACNKCPDDFWSNENHTSCIAKEIEFLSWFEPFGIALTLFAVLGI
FLTAFVLGVFIKFNTPIVKATNRELSYLLFSLLCCFESSLEFIGEPQDWTCRLRQP
AFGISFVLCISGILVKRUNVLLVFEAKIPTSFHKKWGLNLQFLLVFLCFMQIVLCY
IWLYTAPPSSYRNQELEDEIIFITCHEGSLMALGFLIGYTCLLAAICFFFAFKSRKLP
                                                                                                                            ENFNEAKFITFSMLIFFIVWISFIPAYASTYGKFVSAVEVIAILAASFGLLACIFFNK
IYILLEKPSRWTIEEVWGSTAAHAFKYAARATLERSNVSRKESSSLGGSTGSTESSSI
SSKSNSEDEPPQPERGKQOQPLALTOQEQQOQPLTLPQOQPRGQOPRCKQVIFGSGT
VTFSLSFDEPQKNAWAHGNSTHONSLEAQKSSDTLTRHOPLLPLQCGETDLDLTVQET
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YIPQVSYASSSRLLSNKNQFKSFLRTIPNDEHQATAMADIIEYERWNWYGTIAADDDY
GRFGIEKFREEAEEBDICIDFSELISQYSDEBIGHVVEVIQNGTAKVIVYFSSGDBU
EPLIKEIVRRNITGKIWLASEAWASSSLIAMPQYFHVVGGTIGFALKAGQIPGFREFL
                                                                               GLQGPVGGDQRPEVEDPEELSPALVVSSSQSFVISGGGSTVTENVVNS
3607. .3783
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/function="seven transmembrane domain G protein-coupled
/function="seven transmembrane domain G protein-coupled
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/protein_id="AAA86503.1"
/db_xref="GI:683745"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   translation="MAFYSCCWVLLALTWHTSAYGPDQRAQKKGDIILGGLFPIHFGV/
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/clone_lib="lambdaZ-hPG2ss"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                           aactataatgaagccaaatgtgtcaccttcagcctgctcctcaacttcgtatcctggatc
                                                                                                                                                                                                                                                                                                                                                                                           ctggtgattctcgagtgcacagaggtcaactctgtaggcttcctgttggctttcacccac
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attctctgccgtccagaactcaacaatacaga
                                     GCCATCCTGGCAGCCAGCTTTGGCTTGCTGGCGTGCATCTTCTTCAACAAGATCTACATC
                                                                        gcagggctgaccacactgagcggcggcttcagcggttacttcctccccaagtgctatgtg
                                                                                                                  TCCTTCATTCCAGCCTATGCCAGCACCTATGGCAAGTTTGTCTCTGCCGTAGAGGTGATT
                                                                                                                                                                                               AACTTCAATGAAGCCAAGTTCATCACCTTCAGCATGCTCATCTTCATCGTCTGGATC
                                                                                                                                                                                                                                                                               ACCTGCCTGCTGCCATCTGCTTCTTTTTTCCCTTCAAGTCCCGGAAGCTGCCGGAG
                                                                                                                                                                                                                                                                                                     aacattctccttccatcagtaccttcgtctgcagctacctgggtaaggaactgccagag
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Pred. No. 6.4e-32;
0; Mismatches 524;
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S83176.1 GI:1836093
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Expression of a calcium-sensing thyroid carcinoma cell line and
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This sequence comes from Fi
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1 (bases 1 to 3234)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  under gibbsq 179653} from the original journal article. sequence comes from Fig. 6.
        AAKDQDLKSRPESVECIRYNERGFRWLQAMIFALEEINSSFALLPNITIGYRIEDTCN
TVSKALEATLGEVAQNKIDSIAKLBEFCNCSEHIPSTIAVVGATGSGVSTAVANLLGLF
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TILLFKPSKNTIEEVFGCSTAAHAFKVAARATLARSNVERKSSLGGSTGSSTESSSI
EXTRESPENCACHTAL
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/note="longer
/codon_start=1
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/protein_id="ABB46873.1"
/db_xref="G1:1836094"
/translation="MAFYSCCWVLLALTWHTSAYGPDQRAQXKGDIILGGLFPIHFGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="calcium-sensing
/protein_id="AAB46874.1"
/db_xref="GI:1836095"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="CaSR"
/note="calcium-sensing receptor isoform
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/db_xref="taxon:9606"
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                                                                                                                                                                     aacattctcctccatcagtaccttcgtctgcagctacctgggtaaggaactgccagag
                                                                                                                                                                                                                      ATCATCTTCATCACGTGCCACGAGGGCTCCCTCATGGCCCTGGGCTTCCTGATCGGCTAC
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                                                                                                                                                                                                                                                                                          GTGATCTGGCTCTACACCGCGCCCCCCCCCAAGCTACCGCAACCAGGAGCTGGAGGATGAG
                                                                                                                                                                                                                                                                                                                    ctcacatggcttgtaatgtggaccccacgacccaccagggaataccagcgcttcccccat
                                                                                                                                                                                                                                                                                                                                                                 GGGCTCAACCTGCAGTTCCTGCTGGTTTTCCTCTGCACCTTCATGCAGATTGTCATCTGT
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 TCCTTCATTCCAGCCTATGCCAGCACCTATGGCAAGTTTGTCTCTGCCGTAGAGGTGATT
                                 TGCTGCTTTGAGTGTGGGAGTGTCCTGATGGGGAGTATAGTGATGAGACAGATGCCAGT
                                                                         AACTTCAATGAAGCCAAGTTCATCACCTTCAGCATGCTCATCTTCTTCATCGTCTGGATC
                                                                                                                                              ACCTGCCTGCCTGCCATCTGCTTCTTTGCCTTCAAGTCCCGGAAGCTGCCGGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (16-AUG-1994) S.H.S. Group, Collier Bldg, Royal Posrevised by [3] MAT 2 (bases 1 to 3234) Pearce, S.H.S. and Thakker, R.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (05-DEC-1994) S.H.S. Pearce, MRC Molecular Medicine Group, Collier Bldg, Royal Postgrad Med School, London W12 ON On Dec 7, 1994 this sequence version replaced gi:556648.

Location/Qualifiers
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Pearce, S.H.S.
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1 (bases 1 to 3234)
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                                                    YIPQVSYASSELLSNKNQFKSFLRTIPNDEHQATAMADIIEYFRWNWVGTIAADDDY
GRPGIEKFREDAEERDICIDESELISQYSDEEEIQHVVEVIQNSTAKVIVVFSSGPDL
EPLIKEIVRRNITGKIWLASSEAWASSELIAMPDYFHVVGGTIGPATKAGQIPGFREFL
KKVHPRKSVHNGFAKEFWEETFNCHLQBEAKGPLPVDTFLRGHEESGDRFENSSTAFR
PLCTGDENISSVETPYIDYTHLRISYNVYLAVYSIAHALDDIYTCLPGRGLFTNGSCA
DIKKVEAMQVLKHLRHLNFTNNMGEOVFFDEGGDLVGNYSIINWHLSPEDGSIVFKEV
GYYNVYAKKGERLFINBEKILMSGFSREVPFSNCSRDCLAGTRKGIIEGEPTCCFECV
ECPDGEYSDETDASACNKCPDDFWSNEMHTSCLAKEIEFLSWTEPFGIALTLFAVLGI
FLTAFVLGVEIKFRNTPIVKATNRELSYILLFSLLCCFSSSLFEIGEPDDWTCRLRQP
AFGISFVLCISGILKKNNRVLLVFEAKIPTSFHAKWWGLNLQFLLVFLCTTEMQIVICV
IWLYTAPPSSYRNQELEDEIIFITCHBGSLAALGFLICZTCLLAAICFFFAFKSRKLP
ENFNEAKFITFSMLIFFIVMISFIPANASTYGKFVSAVEVIALIAASFGLLACIFFNK
IYIILFKPSRNTIEEVRCSTAAHAFKVAARATLRRSNVSRKRSSSLGGSTGSTPSSSSI
SKSNSEDEPPOPEROKOQOPLALTQOEOOOOPLTLPQQQRSQQOPRCKQKVIFGSGT
VTFSLSFDEPQKNAMAHRNSTHQNSLEAQKSSDTLTRHQPLLPLQCGETDLDLTVQETGLQGPVGGDQRPEVEDPEELSPALVVSSSQSFVISGGGSTVTENVVNS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="SWISS-PROT:P41180"
/translation="MARYSCGWVLLALIWHTSAYGPDQRAQKKGDIILGGLFPIHFGV/translation="MARYSCGWVLLALIWHTSAYGPDQRAQKKGDIILGGLFPIHFGVAAKODDLKSFPESYECIRVNFROFRHJQAMIFAIEEINSSPALLPHLTLGYRIFDTCN
TYSKALEATLSFYAQNKIDSLNLDEFCNCSEHIPSTIAVYGATGSGYSTAVANLLGLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="Calcium-sensing
/protein_id="CAA56990.1"
/db_xref="GI:599820"
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/map="q21-25"
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/chromosome="3"
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                                                                       ACCTTCAATGAAGCCAAGTTCATCACCTTCAGCATGCTCATCTTCTTCATCGTCTGGATC
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1539 gtgtgtaccacggactgtctggcagggcac---cacagggtggttgtgggttcccaccac 1595
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                                                 CTCTTCATCAATGATGAAAAAATTCTGTGGAGTGGATTCTCAAGGGAAGGTGCCTTTCTCC 2137
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Brown, E.M., Gamba, G., Riccardi, D., Lombardi, M., Butters, R., Kifor, O., Sun, A., Hediger, M.A., Lytton, J. and Hebert, S.C. Cloning and characterization of an extracellular Ca(2+)-sense receptor from bovine parathyroid Nature 366 (6455), 575-580 (1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entry [NCBI gibbsq 140593] from the This sequence comes from Fig. 2.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GenBank staff at the National library of Medicine created entry [NCBI gibbsq 140593] from the original journal artic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bos taurus
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                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                          /translation-"MALUSCCWILLAFSTWCTSAYGPDORAQKKGDIILGGLFPIHFG
VAVKDODLKSRRESVEGIRYNRRGFTW-QAMIFALEENSSPALLFNWTIGGYREDTC
NTVSKALEATLSFVAQNX IDSLINDEFCNCSEHIPSTIAVVGATGSGISTAVANLIGL
FYIPGVSYASSRLENSKNOFKSELFILFNDEHQATAMADIIFER WANWGTIADDD
YGRPGIEKFREEAEERDICIDFSELISOYSDEEKIQOVVEVIQNSTAKVIVVFSSGPD
LEPLIKBIVRRNITGR.WHLASEAMASSSLIAMPBYFHVVGGTIGGTLKAQDIPGFREF
LOKVHPRKSVHNGFAKEFWEETTSNCHLOEGAKGPLPUTFTLRGHEEGGARLSNSPTAF
RPLCTGEENISSVETPYMDYTHLRISYNVYLAVVSIAHALQDIVYCIPGRGLFTNOSC
ADIKKVEAMQVLKHLRHLNFTSNMGEOVTFDEOGDLAGNYSIINWHLSEEDFTCCFEC
VGYYNVYAKKGERLFINDEKILMSGFSREVFSCORSEDLAGTRKGIIEGEPTCCFEC
VECPOGEYSDETDASACOKCPDDFWSNENHTSCIAKELEFLSWTEPFGIALTLFAVLG
IFLTAFVLGVFIKFNNTPIVKATNRELSYLLLFSLLCGFSSLFFIGEPODWTCRLRQ
PAFGISFVLCISCILVKTNRVLLVFEAKIFTSHRKWAGILLOFTLVFLCTFMOIVG
AIMLNTAPSSSKYNHELEDBIIFITGTSHRSSKALFTIGYTCLLAALGTFFAKSTKL
PENFNEAKFITTSMLIFTIVMISFIPAKASTYGKFVSAVEVIAILAASFGILACIFFN
KVYILLFKPSRNTIEEVRCSTAAHAFKVAARATLRRSNYRGRSSSLGGGTGSTPSSS
ISSKSNSEDPFOQQPKROKOPOPLALSPHAAOOPOPRPPSTPOPOPOSOOPPRCKOK
VIFGSGTVTFSLSEDEPOKTAVAHRNSTHOTSLEAGKNNDALLFUNGCGFTDS
ELTSQETGLOGPVGEDHQLEMEDPEEMSPALVVSNSRSFVISGGGSTVTENMLRS"

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/db_xref="taxon:9913"
515. .3772
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/protein_id="AAB29171.1"
/db_xref="GI:453109"
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/note="This sequence comes from
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Brown,E.M., Hebert,S.C. and Garrett Calcium receptor-active molecules
Patent: US 5763569-A 1 09-JUN-1998;
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1 (bases 1 to 5275)

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Nemeth, E.F., Brown, E.M., Hebert, S.C., Garrett, J.E. Jr. Nemeth, B.C., Balandrin, M.F. and Del Mar, E.G. Magenen, B.C., Balandrin, Counting Calcium receptor active molecules Method of screening calcium receptor active molecules Patent: US 5838684-A 1 12-JAN-1999;

Location/Qualifiers
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Pred. No. 1e-30;
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175051
175051.1
1 (bases 1 to 5275)
Brown, E.M., Fuller, F.H., Hebert, S.C
Calcium receptor-active molecules
Patent: US 5688938-A 1 18-NOV-1997;
Location/Qualifiers
                                                                Unknown
                                                      Unclassified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oda,Y., Tu,C.-L., Mauro,T. and Bikle,D.
The calcium-sensing receptor and its alternatively-spliced murine epidermal differentiation
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oda,Y., Tu,C.-L.,
Direct Submission
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                                                                                                 KATNRELSYLLLESLLCCESSSLEFIGEPQDWTCRLRQPAFGISFVLCISCILVKTNR
VLLVEEAKIPTSEHRKWWGLMLQFLLVTLCTEWQIVICIIMLYRAPSSSYRNHELEDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="G protein-coupled membrane receptor; inactive
splice variant lacking exon 5; expression correlated
calcium-stimulated differentiation in keratinocytes"
                                                           QPLALTQQEQQQQPLTLQPQQQQQPQQPRCKQKVIFGSGTVTFSLSFDEPQKNAMAHR
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/protein_id="AAD28372.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=:
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/strain="C57BL/6"
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keratinocytes"
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	gccgggagtgccacacgttcacgactcgtaacatgcccacgcttggagccttctccat 1201	1142 gt 1598 CC	da S
	Ctgtaacagctgctcccagcgcttgcccggaggggtcctggtgcagcactaaccagct 1141	1082 gg 1538 TC	Оу
	tggccgtccagcagagacaagtccctgggctgaaggagttttgaggagtcttatgtcag 1081	1022 tg 1481 GT	Дb
	ccatctccacgtacatcaccagcgtgactgggatccaaggcattgggacggtgctcgg 1021	962 gg 1421 gg	Db
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	acatagagatacagaaagaccttcgcaaccactcctccaaggtggtggccttcatcgg 487	428 cc 887 TT	Оy
	clcagaatctgccaatgtgtatgccaccctgagggtgcttgccctgcaagggccccg 427	371 - 827 T	Дb
	acaactecteggeeetgetteeeaacateaceetggggtatgagetgtaegaegtgtg 370 	311 aaa !!! 767 AAA	дь 0 _У
	gcttcaacggccatggctaccacctcttccaagccatgcggttcactgttgaggagat 310 	251 ca 707 CA	ОУ
9	h 6.2%; Score 172.4; DB 12; Length 4319; Similarity 45.8%; Pred. No. 8.7e-30; 55; Conservative 0; Mismatches 1146; Indels 105; Gaps	uery Matc est Local atches 10	Qu Be

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2357 CGTGCTTTGTATCTCGTGCATCTTGGTGAAGACCAATCGAGTCCTCCTGGTATTTGAG 241	
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2237 AGAGCTGTCCTACCTCCTGCTCTCTCACTCCTCTGCTGCTTCTCCAGCTCCCTGTTCTT 229	
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2177 CTTTGTGCTGGGCGTCTTCATCAAGITCCGAAACACGCCCATTGTCAAGGCCAACCG 223	
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Number of hits that pass the 1: em_est1:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query Match Length DB	Length	BB	ID	
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c 2	294.8	11.4	298	48	AI562167	AI552167 vw73d10.x
ი ა	279.2	10.8	562	51	AI742401	AI742401 wg40e02.x
c 4	270.2	10.5	421	46	AI415100	AI415100 mb98d01.x
	204.4	7.9	496	39	AA853967	AA853967 aj51e10.s
Q	192.2	7.5	247	26	W18663	W18663 mb98d01.rl
c 7	80.4	3.1	464	40	AA937218	AA937218 ok13f08.s

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ACCESSION
VERSION
KEYWORDS
SOURCE
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AUTHORS
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AI390993
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                                                                                          TITLE
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52
51
                                                                                                            Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mus. 1 (bases 1 to 525)

1 (bases 1 to 525)

Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
                                               Unpublished (1999)
On Jan 17, 1998 this sequence version replaced gi:2044280.
Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, U
                                                                                                                                                                                                                                        AI390993 525 bp mRNA EST 02-FEB-1999 mb98d01.yl Soares mouse p3NMF19.5 Mus musculus cDNA clone IMAGE:337441 5' similar to SW:CASR_HUMAN P41180 EXTRACELLULAR CALCIUM-SENSING RECEPTOR PRECURSOR; mRNA sequence.
                                                                                                  Waterston, R. and Wilson, R. The WashU-NCI Mouse EST Pr
                                                                                                                                                                                                                                 AI390993
           Email: mouseest@watson.wustl.edu
This clone is available royalty-
                                                                                                                                                                                                                        AI390993.1
                                                                                                                                                                                                      house mouse.
clone is available royalty-free through LLNL; contact th
Consortium (info@image.llnl.gov) for further information
                              314 286 1800
314 286 1810
                                                                                                                                                                                                                                                                                                                                                      A1060029
FR0038287
AQ466269
CNS010RJ
CNS016FZ
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FR0044392
AI836682
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                                                                                                   Project 1999
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AL03103 Drosophil
AL131903 Fugu rubr
AL131976 Fugu rubr
Z90438 F.rubripes
AA170693 ma85h09.r
AL108611 Drosophil
AL004733 F.rubripe
AL131880 Fugu rubr
AI766210 wh68a04.x
AI893729 ma85h09.y
AL131884 Fugu rubr
AI836682 UI-M-APO-
AL060767 Drosophil
AL1131896 Fugu rubr
AL18996 DXFZP7611
AL118996 DXFZP7611
AL118996 DXFZP7611
AL118996 DXFZP7611
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AL1118996 DXFZP7611
AL105023 UI-M-AJ1-
AA170592 DXFSA6411.r
AL101789 DXFSA6411.r
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AQ615201 HS_5138_B
AV278654 AV278654
                                                  63108, USA
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GAACTGCCGGAGAACTATAACGAAGCCAAATGTGTCACCTTCAGCCTGCTCCTCCACTTC

gtcaatgtgctggcagggctggccactctgagtggcggcttcagcggctatttcctccct

418 2443

GTCAATGTGCTGGCAGGGCTGGCCACTCTGAGTGGCGGCTTCAGCGGCTATTTCCTCCCT

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Seq primer: -40RP from Gibco
High quality sequence stop: 481.
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/clone="IMAGE:337441"
/clone=Lib="Scares mouse p3NMF19.5"
/dev_stage="19.5 dpc total fetus"
/dev_stage="19.5 dpc total fetus"
/lab_host="DH10B (ampicillin resistant)"
/note="vector: pT7T3D (Pharmacia) with a modified
polylinker; Site-1: Not I; Site-2: Eco RI; Ist strand cDNA
polylinker; Site-1: Not I; Site-2: Eco RI; Ist strand cDNA
polylinker; Site-1: Not I; Site-2: Eco RI; Ist strand cDNA
polylinker; Site-1: Not I; Site-2: Eco RI; Ist strand cDNA
polylinker; Site-1: Not I; Site-2: Eco RI; Ist strand cDNA
polylinker; Site-1: Not I; Site-2: CDNA
polylinker; Site-1: Not I; Site-2: CDNA
polylinker; Site-2: CDNA
polylin
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Location/Qualifiers
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/db_xref="taxon:10090"
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Pred. No. 4.1e-83;
0; Mismatches 1
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AI562167/c
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 178
                                                                                                                                                  298
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hes 296;
                   agcttcggctgggtctggatctcgctcgttggcagctatggtgactacgggcagctgggc
                                                                    ttcttgcgcaccatccccagcgataagtaccaggtggaagtcatagtgcggctgctgcag
                                                                                                                                              CCACAGGTCAGCTATGAGGCGAGCAGCGTGATCCTCAGTGGGAAGCGCAAGTTCCCGTCC
                                                                                                                                                                     AGCTTCGGCTGGGTCTGGATCTCGCTCGTTGGCAGCTATGGTGACTACGGGCAGCTGGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1999)
On Mar 10, 1998 this sequence version replaced gi:2948814.
Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AI562167 298 bp mRNA EST 25-MAR-1999 vw73d10.x1 Stratagene mouse heart (#937316) Mus musculus cDNA clone IMAGE:1260595 3' similar to SW:CASR_HUMAN P41180 EXTRACELLULAR CALCIUM_SENSING RECEPTOR PRECURSOR ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R. Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AI562167
AI562167.1 GI:4513512
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MGI:663147 This clone was previously sequenced on the 5' data is from the 3' end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The WashU-NCI Mouse EST Project 1999
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l (bases 1 to 298)
                                                                                                                                                                                                                                         Similarity
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314 286 1810
                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                     /strain="NIH/Swiss"
/db_xref="taxon:10090"
/clone="IMAGE:1260595"
/clone_lib="Stratagene mouse heart (#937316)"
/sex="pooled"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Mus musculus"
                                                                                                                                                                                                                                         11.4%;
99.3%;
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                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                       Score 294.8; DB 4
Pred. No. 1.3e-68;
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AUTHORS
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                                                                                                                                                                        Query Match
Best Local Similarity 83.2
Matches 317; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM
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                     2219 atcetectetecateageaeetttgtetgeagetaeetgggtaaggaaetggeggagaae 2278
                                                                                                               2159 gtgattcttgagtgcacagaggtcaactctgtgggcttcctggtggctttcgcacacaac 2218
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502 GGCCTCCTCCATCAGTGCCTTTGCCTGCAGCTACCTGGGTAAGGACTTGCCAGAGAAC
                                                                                  562 GTGATGCTTGAGTGCACAGAGACCAACTCCNTGGGCTTCATACTGGCCTTCCTCTACAAT 503
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
This clone is available royalty-free tl
IMAGE Consortium (info@image.llnl.gov)
Seq primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1997)
On Dec 20, 1995 this sequence version Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AI742401 562 bp mRNA EST 21-JUN-1999 wg40e02.xl Soares_NSF_F8_9%_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2367578 3' similar to TR:093557 093557 PUTATIVE ODORANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 562)
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National Cancer Institute, Cancer Genome Ana
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AI742401
AI742401.1 GI:5110689
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                                                                                                                                                                                                                                                                                                        /note-"Organ: pooled; Vector: pT773D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from five normalized libraries were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 5 libraries. The pools consisted of the following libraries and cloneIDs: Scares NbHSF pool 1: 309384-310919, 33208-325895 Soares NbHSF pool 1: 150407, 151176-15327 Soares Nb2HFP pool 1: 758280-760583, 772104-774407 Soares NbHPA pool 1: 73820-760583, 772104-774407 Soares NbHPA pool 1: 73720-726407, 739800-740999 Subtraction by Bento Soares and M. Fatima Bonaldo." 1 others
                                                                                                                                                                                                                                                                                              pool 1: /_.
Soares and M. F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:9606"
/clone="IMAGE:2367578"
/clone_lib="Soarse_NSF_F8_9W_OT_PA_P_S1"
/lab_host="DH10B"
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83.2%;
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                                                                                                                                                                        Score 279.2; DB pred. No. 3e-54; 0; Mismatches
                                                                                                                                                                                                                       DB 51;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1999)
On Apr 21, 1998 this sequence version replaced gi:3073000.
Contact: Marra M/MashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Marra,M., Hiller,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Thelsing,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
The WashU-NCI Mouse EST Project 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A1415100 421 bp mRNA EST 09-FEB-199 mb98601.x1 Soares mouse p3NMF19.5 Mus musculus cDNA clone IMAGE:337441 3' similar to SW:CASR_RAT P48442 EXTRACELLULAR CALCIUM-SENSING RECEPTOR PRECURSOR ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                   Possible reversed clone: similarity on wrong strand High quality sequence stop: 373.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                   This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. This clone was previously sequenced on the 5' end only, this ne data is from the 3' end
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 421)
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314 286 1810
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               /clone_lib="Soares mouse p3NMF19.5"
/dev_stage="19.5 dpc total fetus"
/lab_host="DH10B (ampicillin resistant)"
/note="Vector: pT7T3D (Pharmacia) with a modified
/note="Vector: pT7T3D (Pharmacia) / Jst strand cDNA
/note="Vector: pT7T3D (Pharmacia) / Jst strand cloned into
the Not I and Eco RI sites of a modified pT7T3 vector
/pharmacia) / Library went through one round of
                                                                                                                                                                                                                                                               /organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:337441"
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constructed by Bento
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Query Match
Best Local Similarity
Matches 272; Conserv
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AA853967
                                                                                                                                                                                                                                                                                                                                                 on Jan 14, 1998 this sequence version replaced gi
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
cDNA_Library Preparation: M. Bento Soares, Ph.D.,
                                                                                                      Possible reversed clone: similarity on wrong strand Insert Length: 878 Std Error: 0.00 Seg primer: -40ml3 fwd. ET from Amersham High quality sequence stop: 223.
                                                                                                                                                                                                                                        Bonaldo, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-GGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 496)
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National Cancer Institute, Cancer Genome Anatomy
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1393866"
                                                                                      Location/Qualifiers
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clone IMAGE:1393866
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/sex="male"

/clone_lib="Soares_testis_NHT"

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BASE COUNT
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nes 260; Conserv
                               The WashU-HHMI Mouse EST Project
Unpublished (1996)
On May 9, 1995 this sequence version replaced gi
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, M
Tel: 314 286 1810
Fax: 314 286 1810
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W18663.1
                                                                                                                                                                                                                                                                                                                           Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                      Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 247)

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W18663 247 bp mRNA EST 10-SEP: mb98d01.rl Soares mouse p3NMF19.5 Mus musculus cDNA clone IMAGE:337441 5', mRNA sequence.
                                                                                                                                                                                                                        Waterston, R.
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clone is available royalty-free
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                     mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note-"Vector: pT7T3D-Pac (pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was prepared from mRNA obtained from Clontech Laboratories, Inc., and primed with a Not I - oligo(dT)
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81.5%;
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Pred. No. 3.3e-44;
D; Mismatches 57
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                                                                              Louis,
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LLVL
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464 bp mRNA

EST 09-JUN-1998

okl3f08.sl Soares_NSF_F8.9W_OT_PA_P_S1 Homo sapiens cDNA clone

IMAGE:1507719 3' similar to SW:CASR_HUMAN P41180 EXTRACELLULAR

CALCIUM-SENSING RECEPTOR PRECURSOR; mRNA sequence.

AA937218
                                                                            Tumor Gene Index
Unpublished (1997)
On Jan 19, 1998 this sequence v
Contact: Robert Strausberg, Ph
Tel: (301) 496-1550
Tel: (301) 495-1300 Email: Robert_Strausberg@nih.gov
Email: Robert_Strausberg@nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
IMAGE ----- Std Error: 0.00
                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 46)
NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Pro
                                                                                                                                                                                                                                                                                          EST
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Mus musculus"
/db_xref="taxon:10090"
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Pred. No. 4e-41;
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Matches 156; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AW051287 498 bp mrNA EST 20-SEP-1999 wy83g12.xl Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2555206 3' similar to SW:CASR_HUMAN P41180 EXTRACELLULAR
   Unpublished (1997)
On Dec 20, 1995 th
                                                     NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 498)
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AW051287.1
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                                        Tumor Gene Index
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h quality sequence stop: 398.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  libraries were mixed, and ss circles were made in vitro.
Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 5 libraries. The pools consisted of the following libraries and cloneIDs: Soares NbHSF pool 1:
309384-310919, 322208-325895 Soares NbHSF pool 1:
145022-147335, 147720-148103, 148872-149255, 15002-150407, 151176-152327 Soares NbHSF pool 1:
758280-760583, 777104-774407 Soares NbHSPA pool 1:
758280-760583, 777104-774407 Soares NbHSPA pool 1:
304776-306311, 320136-322823, 326280-32663 Soares NbHOP pool 1: 723720-726407, 739080-740999 Subtraction by Bento Soares and M. Fatima Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with
a modified polylinker; Site_1: Not I; Site_2: Eco RI;
Equal amounts of plasmid DNA from five normalized
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1507719"
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sequence version replaced gi:1134450
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Pred. No. 6.2e-11;
0; Mismatches 126;
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Query Match 3.1%;
Best Local Similarity 55.3%;
Matches 156; Conservative
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HS_518_B2_C04_SP6E_RPCI-11 Human Male BAC Library
genomic clone Plate-714 Col-8 Row-F, genomic survey
AQ615201
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40UP from Gibco
High quality sequence stop: 440.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 514)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S.
                                                                                                            Homo sapiens
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                                                                                                                                            human.
                                                                                                                                                                                               AQ615201.1
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/db_xref="taxon:9606"
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Pred. No. 6.5e-11;
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     Swartzell, S.,
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     Holzman, T.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAGAGATTCTGTATTCTGTTCCACATGTGAGCTGTCCTTTGACTTGGGCCCNTACGTGTG
Mus musculus
Eukaryota: Metazoa: Chordata; Craniata; Vertebrata; Mammalia;
Eukaryota: Metazoa: Chordata; Craniata; Vertebrata; Musmalia;
Eutheria; Rodentia: Sciurognathi; Muridae: Murinae: Mus.
1 (bases 1 to 260)
1 (bases 1 to 260)
Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Carninci, P., Endo, T.,
Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F.,
Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Kadota, K., Kagawa, I.,
Ishii, Y., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I.,
Kai, C., Kawai, J., Kikuchi, N., Kojima, Y., Koya, S., Kusakabe, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   128;
                                                                                                                                                                                                                        musculus
AV278654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Resear h Genetics (info@resgen.com). BAC end Web Server: http://www.htsc.washington.edu
plate: 714 row: F column: 8
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EST.
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University of Washington
401 Queen Anne Avenue Noz
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                                                                                                                                                                     house mouse.
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Hood,L.
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                                                                                                                                                                                                                                      260 bp mRNA EST 05-NOV-1999 RIKEN full-length enriched, adult male testis (DH10B) Mus cDNA clone 4933403B08 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organisme"Homo sapiens"
/db_xref="taxon:9606"
/clone="plate=714 Col=8 Row=F"
/clone_lib="RPCI-11 Human Male
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Pred. No. 2.
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Shibata,Y., Shigemoto,Y., Shirak,T., Sogabe,Y., Sugahara,Y.,
Suzuki,H., Suzuki,H., Tateno,M., Tominaga,N.,
Tsunoda,Y., Watahiki,A., Watanabe,S., Yamamura,T., Yasunishi,A.,
Yokota,T., Yoshiki,A., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.,
Yokota,T., Yoshiki,A., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
RIKEN Mouse ESTS (Konno,H., et al.)
Unpublished (1999)
On Mar 10, 1998 this sequence version replaced gi:2948605.
Contact: Yoshihide Hayashizaki
Genome Exploration Research Group, Life Science Tsukuba Center,
Genome Science Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Okazaki,Y. and Hayashizaki,Y.
Automated filtration based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
Please visit our web site (http://genome.rtc.riken.go.ip) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transcriptional sequencing: A method for DNA sequencing using RNA polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998) Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: genome-res@rtc.riken.go.jp,
URL:http://genome.rtc.riken.go.jp/
Sasaki,N., Izawa,M., Watahiki,M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hayashizaki,Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fax: +81-298-36-9098
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Tel: +81-298-36-9013
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                details.
                                                                                                                                                                                                                                                           was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sittes, 5 end: SalI; 3' end: BamHI." 55 c 74 g 67 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Site_1: Sall; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="4933403B08"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /dev_stage="adult"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="RIKEN full-length enriched, adult male testis
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Carninci,P., Muramatsu,M., Okazaki,Y. and
                              2.9%;
Score 74.2; D
Pred. No. 2e-0
0; Mismatches
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                              74.2; DB
No. 2e-09;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: zbrafish@watson.wustl.edu
CDNA Library Preparation: Matthew Clark. CDNA Library Arrayed by:
Matthew Clark. DNA Sequencing by: Washington University Genome
Sequencing Center Clone distribution: Genome Systems, St. Louis,
Missouri (web address: www.genomesystems.com) (email contact:
info@genomesystems.com) and Research Genetics, Huntsville, Alabama
(web address: www.resgen.com) (email contact: info@resgen.com) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis,
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M., Eddy,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Dowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., matter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
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1 (bases 1 to 573)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    On Jun 5, 1998 this sequence version replaced gi:3189643 Other_ESTs: fc14h06.x1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mRNA sequence.
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Location/Qualifiers
/lab_bst="%LI-blue MRF"
/lab_b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             stage embryos"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Danio rerio"
/db_xref="taxon:7955"
/clone_lib="Zebrafish WashU MPIMG EST"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="26 somite embryos, adult livers, shield
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /sex="mixed"
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                                                                                                                                                                                   Query Match
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                  AACTCCCTGATAATTTCAACGAAGCCAAAATGATCACCTTCAGCATGCTGATATTCTGTG 105
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gcactcattgggcctgataacactgaccacgctgtcaccactgctgccctgctgagccct 496
                                                                                                                                                                                                                                                                                                                                      ttcccgtccttcttgcgcaccatccccagcgataagtaccaggtggaagtcatagtgcgg 616
                                                                                                                                                                                                                                                                                                                                                                                                          TACCTCGTTCCTCAGGTCAGCACGTCCTCCTCTTCTCCGGTTCTGAGTGATAAACTGCGC 325
                                                                                                                                                                                                                                                                                                                                                                                                                                        tttctgatgcccctggtcagctatgaggcgagcagcgtgatcctcagtgggaagcgcaag 556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCAATCCTGGGAGAAACATACTCTGAGCTATCCATCGCTATCGCCAAGCTCCTCAGCCTC 265
                                                                                                                                                                                                                           CTCATGTCTCATTTCTCCTGGAACTGGGTCGGTGTCGTGTACGGAGATGATGACTATGG
                                                                                                                                                                                                                                                                                                                 TACCCGTCCTTCATGCGTGATTCCCAGTGATGTTGTACCAGGCTCAGGCGCTGGTCAAG
                                                                                      FR0044379 619 bp DNA GSS Fugu rubripes GSS sequence, clone 184F17aE5,
GSS; genome survey sequence
                       AL131871.1
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3.3e-06;
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genomic survey
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Centre, Hinxton, Cambridge, biohelp@hgmp.mrc.ac.uk
Vector: pBluescript II KS
V_type: phagemid
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1 (bases 1 to 619)

Elgar,G., Clark,M.S., Smith,S., Meek,S., Warner,S., Edwards,Y.J.K., Umrania,Y., Williams,G. and Brenner,S.
                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (11-OCT-1999) MRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fugu rubripes
                                                                                                                                                                                                   sequence
                                                                                                                                                                                                                                 One pass dye-terminator sequencing of cosmid cloned genomic
        166
/organism="Fugu rubripes"
/db_xref="taxon:31033"
/clone=lib="cosmid 184F17"
/clone="184F17aE5"
/clone="184F17aE5"
126 c 132 q 187 t
                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                  .619
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        187 t
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Conservative

0;

Score 62.2; DB 80; Pred. No. 5.7e-06; 0; Mismatches 105;

Indels Length 619;

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REFERENCE
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VERSION
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TACATCCTGCTGGGTGGTCTTCCTCTGCTACTGCATGACCTTCATCTTCATTGCCAAG
                                                                                  ttcctcatgctgggttccttggtagctgggagttgcagcctctacagcttcttcggggaag
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DRFZp434C2213_r1 434 (synonym: htes3)
DRFZp434C2213_5', mRNA sequence.
AL040113
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1 (bases 1 to 732)
Koehrer, K., Beyer, A., Mewes, H.W., Gassenhuber, J. and Wiemann, SET (Koehrer, et al.)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      No s1 sequence available.
This clone is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
Location/Qualifiers
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Am Klopferspitz 18a D-82152 Martinsried, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by BMFZ within the cDNA sequencing consortium of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              On Jul 7, 1999 th
Contact: Koehrer
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                                                                                                                                                                                                                                                                                                   /lab_host="DH108"
/note="Vector: pSport1; Site_1:
245 c 191 g 169 t
                                                                                                                                                                                                                                                                                                                                                    /dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="434 (synonym:
/tissue_type="testis"
                                                                                                                                                                                                                                                                                                                                                                                                     /clone="DKFZp434C2213"
                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
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Koehrer K
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Pred. No. 2.2e-05;
0; Mismatches 318;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tumor Gene Index
Unpublished (1997)
On May 7, 1998 this sequence version
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 602) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Pro
                                                                                                                                                                                                      Seq I
                                                                                                                                                                                                                                                                                      Tissue Procurement: Christopher Moskaluk, M.D., PEmmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
cDNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G. Consorthum/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AI434785 602 bp mRNA EST 30-MAR-1999 ti20c10.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2131025 similar to SW:CASR_HUMAN_P41180 EXTRACELLULAR CALCIUM-SENSING
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Sea primer: -40UP from Gibco
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                                                                                                                                                                                                      quality sequence stop: 453.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Robert_Strausberg@nih.gov
/note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with
a modified polylinker; Site_1: Not I; Site_2: Eco RI;
Plasmid DNA from the normalized library NCI_CGAP_Kid3 was
                                                          /lab_host-"DH10B"
                                                                         /clone="IMAGE:2131026"
/clone_lib="NCI_CGAP_Kid11"
                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                   Location/Qualifiers
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                                                                        196 ttgtgacaggtctgacagcttcaacggccatggctatcacctcttccaagccatgcggtt 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   266 gagataaacaactccacagctctgcttcccaacatcaccctggggtatgaactgtatgac 325
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256 caccgttgaggagataaaccaactccacagctctgcttcccaacatcaccctggggtatga 315
                                            245 TICTGTCATGATGTGCAGCATCAACCATCGTGAATTGCGACTGTCTCATGCAATGGTCTT 304
                                                                                                                                  y Match 2.0%; Score 52.6; DB 80; Local Similarity 60.7%; Pred. No. 0.0021; hes 85; Conservative 0; Mismatches 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (11-OCT-1999) MRC Human Genome Mapping Project Resource Centre, Hinxton, Cambridge, CB10 1SB. UK Email: biohelp@hgmp.mrc.ac.uk Vector: pBluescript II KS V_type: phagemid V_type: Phagemid
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Fugu rubripes GSS sequence, clone 184F17aG8, genomic survey
sequence.
AL131864
AL131864.1 GI:6113810
GSS; genome survey sequence.
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1 (bases 1 to 615)
Elgar,G., Clark,M.S., Smith,S., Meek,S., Warner,S., Edwards,Y.J.K., Umrania,Y., Williams,G. and Brenner,S.
                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence
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/db_xref="taxon:3103"
/clone_11bb"cosmid 184F17"
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133 c 144 g 153 t
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Db 305 CGCCATCGAGGAGTCAACANCAGCACGGAGCTGCTTCCTGGAATCAAACTCGGTTACCA 364
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Search completed: March 18, 2000, 10:28:19
Job time: 2304 sec

Qy 316 actgtatgacgtgtgctcag 335

Db 365 GATCCACGACTCGTGCGCAG 384

Sequence Sequence Sequence Sequence Sequence

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Patent No. 5688938
GENERAL INFORMATION:
APPLICANT: Edward M. Brown
APPLICANT: Steven C. Hebert
APPLICANT: Forrest H. Fuller
APPLICANT: James E. Garrett, Jr.
TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
TITLE OF INVENTION: MOLECULES
NUMBER OF SEQUENCES: 20
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US-08-485-588-3
                                                           OPERATING SYSTEM: OCCUPACIONES
OPERATING SYSTEM: OCCOS/MS-DOS
OPERATING SYSTEM: OCCOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,588
FILING DATE: 7 June, 1995
CLASSIFICATION UNSEER: US/08/485,588
FILING DATE: 7 June, 1995
PRIOR APPLICATION DATA: including applic
PRIOR APPLICATION DATA: including applic
PRIOR APPLICATION NUMBER: 08/353,784
FILING DATE: 9 December: 1994
APPLICATION NUMBER: US. 08/292,827
FILING DATE: 21 October: 1994
APPLICATION NUMBER: US. 08/292,827
FILING DATE: 22 October: 1994
APPLICATION NUMBER: US. 08/141,248
FILING DATE: 22 October: 1993
APPLICATION NUMBER: US. 08/09,389
FILING DATE: 12 February, 1993
APPLICATION NUMBER: US. 08/017,127
FILING DATE: 12 February, 1993
APPLICATION NUMBER: US. 07/934,161
FILING DATE: 11 February, 1992
APPLICATION NUMBER: US. 07/834,044
FILING DATE: 11 February, 1992
APPLICATION NUMBER: US. 07/834,044
FILING DATE: 11 February, 1992
APPLICATION NUMBER: US. 07/834,044
FILING DATE: 12 August, 1991
APPLICATION NUMBER: US. 07/749,451
FILING DATE: 23 August, 1991
APPLICATION SCHOOL 1995
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APPLICATION SCHOOL 
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STREET: First Interstate World o
STREET: Suite 4700
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
CCUNTRY: USA
ZCUNTRY: OSA
ZCUNTRY: USA
ZCUNTRY: OSA
ZCUNTRY
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  NAME: Heber, Sheldor
REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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PCT-US91-09422-15
PCT-US91-99422-20
US-02-486-770-1
US-08-486-770-1
US-08-072-574-9
US-08-072-574-1
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US-08-485-588-3
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Best Local Similarity 46.3%;
Matches 1130; Conservative
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TELEPHONE: (213) 489-1600
TELEPAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 3:
   1264
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LENGTH: 3809 base pairs
TYPE: nucleic acid
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LOCATION: 373..3606
OTHER INFORMATION:
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                    cagctgggcgtacaggcgctggaggagctggccactccacggggcatctgcgtcgccttc
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                                                                   gtgttcttcaggtctgtggtgctggccaacctgactggcaaagtgtggatcgcctccgaa
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Pred. No. 1.9e-37;
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                                                                                                       CTCTTTGCCGTGCTGGCATTTTCCTGACAGCCTTTGTGCTGGGTGTGTTTATCAAGTTC
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US-08-484-565-3
                                                                                                         SOFTWARE: FASTSEQ
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/C
FILING DATE: 7 June, 197
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 Diskette, 1.44 Mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ADDRESSEE: Lyon & Ly
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PRIOR APPLICATION DATA: PRIOR APPLICATION DATA: PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Lyon & Lyon
STREET: First Interstate World
STREET: Suite 4700
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: UZIP: 90071
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80 DЪ δÃ DЬ Q DЪ δÃ DЬ δÃ Вb

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; FEATURE:
, NAME/KEY: CDS
; LOCATION: 373..3606
; OTHER INFORMATION:
US-08-484-565-3
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Best Local Similarity 46.3%;
Matches 1130; Conservative
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FILING DATE: 12 February, 1993
APPLICATION NUMBER: U.S. 07/934,151
FILING DATE: 21 August, 1992
APPLICATION NUMBER: U.S. 07/834,044
FILING DATE: 11 February, 1992
APPLICATION NUMBER: U.S. 07/749,451
FILING DATE: 23 August, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Heber, Sheldon O.

NAME: Heber, Sheldon O.

NAME: Heber, Sheldon O.

NAME: Heber, Sheldon O.
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TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
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LENGTH: 3809 base pairs
TYPE: nucleic acid
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
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RESULT 3
US-08-480-751-3
; Sequence 3, Application U; Sequence 3, Patent No. 5858684
; APPLICANT: Edward F. APPLICANT: Edward F. APPLICANT: Forrest H. APPLICANT: James E. G. Edward F. Nemeth Edward M. Brown Steven C. Hebert Forrest H. Fuller James E. Garrett, US/08480751 Jr.

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Ouery Match Ouery Match 6.4%; Score 166.2; DB 3; Length 3809; Best Local Similarity 46.3%; Pred, No. 1.9e-37; Matches 1130; Conservative 0; Mismatches 1143; Indels 168; Gaps 11; Oy 206 tetgacagettcaacggccatggetatcacctettccaagccatgcgftcaccgttgag 265 1	STREET. SLIE ADDRESS STREET. SAIL AND STORES STREET. SAIL AND STORES CORP. LOS Angels Fifth Street CITY. LOS Angels STREET. CAS	TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE TITLE OF INVENTION: MOLECULES NUMBER OF SEQUENCES: 20 CORRESPONDENCE ADDRESS: ADDRESSE: LYON
Qy 112 tytcacgctttcacgacatggaacctgcacgagcttggagccttctccatgagcgtgcc 177	Db 570 ACTIGNAACACCTITICHANGGCTIGGANGCANGCTGGGTTTTGTTGTTAAAAAAAA 729 97 379 -agggacaggcagctaggagatctttggaagctcttggagtgtgtgt	Db 510 GAGATAAACAGCAGCCCAGCCCTTCTTCCCAACTTGACGCTGGGATACAGGATATITGAC 559 Qy 326 gtgtgctcagagtcttccaatgtctatgccaccctgagggtgcccgccagca 379

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                                                                                                             APPLICATION NUMBER: 194
APPLICATION NUMBER: PCT/US/94/12117
FILING DATE: 21 October, 1994
APPLICATION NUMBER: U.S. 08/29,827
FILING DATE: 23 AUGUST, 1994
APPLICATION NUMBER: U.S. 08/141,248
FILING DATE: 22 October, 1993
APPLICATION NUMBER: U.S. 08/09,389
FILING DATE: 23 February, 1993
APPLICATION NUMBER: U.S. 08/017,127
FILING DATE: 12 February, 1993
APPLICATION NUMBER: U.S. 07/934,161
FILING DATE: 21 AUGUST, 1992
APPLICATION NUMBER: U.S. 07/934,161
FILING DATE: 11 February, 1992
APPLICATION NUMBER: U.S. 07/934,044
FILING DATE: 11 February, 1992
APPLICATION NUMBER: U.S. 07/834,044
FILING DATE: 13 AUGUST, 1991
APPLICATION NUMBER: U.S. 07/834,044
FILING DATE: 191
APPLICATION NUMBER: U.S. 07/834,044
FILING DATE: 191
APPLICATION NUMBER: U.S. 07/834,044
FILING DATE: 23 AUGUST, 1991
APPLICATION NUMBER: U.S. 07/834,044
FILING DATE: 23 AUGUST, 1991
APPLICATION NUMBER: U.S. 07/834,044
FILING DATE: 23 AUGUST, 1991
APPLICATION NUMBER: U.S. 07/834,044
FILING DATE: 31 FEBRUARY
APPLICATION NUMBER: U.S. 07/834,044
FILING DATE: 31 FEBRUARY
APPLICATION NUMBER: U.S. 07/834,044
FILING DATE: 191
APPLICATION NUMBER: U.S. 07/834,044
FILING DATE: 23 AUGUST, 1991
APPLICATION NUMBER: U.S. 07/834,044
FILING DATE: 191
APPLICATION UMBER: U.S. 07/834,044
FILING DATE: 191
APPLICATION UMBER: U.S. 07/834,161
APPLICATION UMBER: U.S. 07
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Patent No. 596231
INFORMATION FOR SEQ
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ZIP: 90071
ZOMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FASTSEQ
SOFTWARE: FASTSEQ
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CITY: Los Angeles
STATE: California
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APPLICANT: James E. Garrett, Jr.
TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
TITLE OF INVENTION: MOLECULES
NUMBER OF SEQUENCES: 20
                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2881
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                        TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOK AFFILE.

APPLICATION NUMBER: 08/4

TOTTEN DATE: 7-June-1995
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STREET: 633 West Fifth
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  1324
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LENGTH: 3809 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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                                                 aaggacgtggtgcctctctccgcccaggcgggtgacccaaggatgcagcgcatgatgctg
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cgctccttccaactggtcatcatcttcaagttttctaccaaggtacccacattctaccac 2026	ttgetgegteagecectettttetetegggtttgecaittteeteteetgtetgacaate 1966	ttggtagctgggagttgcagcctctacagcttcttcgggaagcccacggtgcccgcgtgc 1906	cttcacacgcctgttgtgaggtcagctgggggtaggctgtgtgttcctcatgctgggttcc 1846	gcagctaacacgctattgctgctgctgctgattgggactgcttggcctgtttgcctggcgt 1786	tgcttctcacgcaccgtggagttcttgggggtggcatgaacccatctctttggtgctatta 1726	gagetteacacetgecageettgtggaacagaagaatggggecectgaggggagetcagee 1666	toccaccactgotgottogagtgoatgocotgtgaagottgggacatttotoaacacgagt 1605	cctgtgtcagtgtgtaccagggactgtctcgaagggcaccacaggttggtcatgggt 1546	ccagttcatctagacataaataagacaaaaatccagtggcacgggaagaacaatcaggtg 1489 	ggacctgaatggacctttgaggtcattggttctgcctcactgtct 1429	gcattcgatgacaagggggaccctctaggttattatgacatcatcgcctgggactggaat 1384	tggcagcttcttcagcagatctacaaggtgaatttccttctacataagaagactgta 1324 	acctctgggacctgtgccagaggcccagtctacccc 1267	tacaatgtgtatgaggctgtgtatgctgtggcccacggcctccaccagctcctgggatgt 1231	tgtcacgctttcacgacatggaacatgcccgagcttggagccttctccatgagcgctgcc 1171	GAAGAAAGTGGCGACAGGTTTAGCAACAGCTCGACAGCCTTCCGACCCTCTGTACAGGG 1563	TGCCACCTCCAAGAAGGTGCAAAAGGACCTTTACCTGTGGACACCTTTCTGAGAGGTCAC 1503	TCCCAGGAAGTCTGTCCACAATGGTTTTGCCAAGGAGTTTTGGGAAGAAACATTTAAC 144

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RESULT 5
US-08-353-784-3
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APPLICANT: Brown, Steven C. Hebert,
APPLICANT: Bradford C. Van Wagenen, Manuel
APPLICANT: F. Balandrin, Forrest H. Fuller,
APPLICANT: Eric G. DelMar, and Scott T. Moe
TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
TITLE OF INVENTION: MOLECULES
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Edward
PRIOR APPLICATION DATA: including application PRIOR APPLICATION DATA: described below: 8 APPLICATION NUMBER: PCT/US/94/12117 FILING DATE: 21 October, 1994 APPLICATION NUMBER: U.S. 08/292,827
                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: ILLENT, COMPATIBLE
COMPUTER: COMPATIBLE
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                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
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STREET: Soite 4700
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/353,784 FILING DATE: 9 December, 1994 CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC of OPERATING SYSTEM: SOFTWARE: FASTSEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
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Best Local 9
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TELEX: 67-3510
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: U.S. 08/009,389
FILING DATE: 23 February, 1993
APPLICATION NUMBER: U.S. 08/017,127
FILING DATE: 12 February, 1993
APPLICATION NUMBER: U.S. 07/934,161
FILING DATE: 21 August, 1992
APPLICATION NUMBER: U.S. 07/834,044
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1500
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FILING DATE: 11 February, 1992
APPLICATION NUMBER: U.S. 07/749,451
FILING DATE: 23 August, 1991
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US-08-485-588-1
US-08-485-588-1
Sequence 1, Application US/08485588
Patent No. 5688938

APPLICANT: Steven C. Hebert
APPLICANT: Forrest H. Fuller
APPLICANT: Dymmes E. Gazrett, Tr.
APPLICANT: Dymmes E. Gazrett, Tr.
TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
TITLE OF INVENTION: MOLECULES
UMMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: First Interstate World Center

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LOCATION: 515..3769
; OTHER INFORMATION:
US-08-485-588-1
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                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 1136; Conserv
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APPLICATION NUMBER: U.S. 08/292,827
FILING DATE: 23 August, 1934
APPLICATION NUMBER: U.S. 08/292,827
FILING DATE: 23 August, 1994
APPLICATION NUMBER: U.S. 08/009,389
FILING DATE: 22 October, 193
APPLICATION NUMBER: U.S. 08/017,127
FILING DATE: 22 February, 193
APPLICATION NUMBER: U.S. 08/017,127
FILING DATE: 12 February, 193
APPLICATION NUMBER: U.S. 07/934,161
FILING DATE: 11 February, 193
APPLICATION NUMBER: U.S. 07/834,044
FILING DATE: 11 February, 1992
APPLICATION NUMBER: U.S. 07/84,451
FILING DATE: 13 August, 1992
APPLICATION NUMBER: U.S. 07/49,451
FILING DATE: 13 August, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Heber, Sheldon O.
REGISTRATION NUMBER: 38,179
REFERENCE/DOCKET NUMBER: 213/005
TELEFAX: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
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FILING DATE: 7 June, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA: including app
PRIOR APPLICATION DATA: described bel
APPLICATION NUMBER: 08/353,784
APPLICATION NUMBER: 08/353,784
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FASTSEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 5275 base pair
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
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STREET: 633 West Fifth Street
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    CACTTGTAACACCGTCTCTAAAGCCTTGGAGGCCACCCTGAGTTTTGTGGCCCCAGAACAA 873
                           ggagataaacaactccacagctctgcttcccaacatcaccctggggtatgaactgtatga 324
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A: described below: 9
08/353,784
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Pred. No. 8e-35;
0; Mismatches 1168;
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                          INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                           FILING DATE: 9 December, 1994

APPLICATION NUMBER: DCT/US/94/12117

FILING DATE: 21 October, 1994

APPLICATION NUMBER: U.S. 08/292,827

FILING DATE: 23 AUGUST, 1994

APPLICATION NUMBER: U.S. 08/141,248

FILING DATE: 22 October, 1993

APPLICATION NUMBER: U.S. 08/017,127

FILING DATE: 23 February, 1993

APPLICATION NUMBER: U.S. 08/017,127

FILING DATE: 12 February, 1993

APPLICATION NUMBER: U.S. 07/934,161

FILING DATE: 21 AUGUST, 1992

APPLICATION NUMBER: U.S. 07/934,044

FILING DATE: 11 February, 1992

APPLICATION NUMBER: U.S. 07/749,451

FILING DATE: 21 AUGUST, 1991

APPLICATION NUMBER: U.S. 07/749,451

FILING DATE: 23 AUGUST, 1991

APTLORNEY AGGENT INCORMATION.
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FASTSEQ
CURRENT APPLICATION DATA:
                                                                                                                                                                             ATTORNEY/AGENT INFORMÁTION:
NAME: Heber, Sheldon O.
REGISTRATION NUMBER: 38,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" D1
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CITY: Los Angeles
STATE: California
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APPLICANT: Steven C. Hebert
APPLICANT: James S. Garrett, Jr.
TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
TITLE OF INVENTION: MOLECULES
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                     SEQUENCE
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PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 0
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                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
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STREET: First Interstate World
STREET: Suite 4700
STREET: 633 West Fifth Street
                                                                                                                                                              REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GEAGGTGATCGCCATCCTGGCGGCCAGCTTTGGCTTGCTGGCCTGTATCTTCTAACAA 3084
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; LOCATION: 515..3769
; OTHER INFORMATION:
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Best Local Similarity 46.0%;
Matches 1136; Conservative
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STRANDEDNESS: single
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Pred. No. 8e-35;
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 -CAATCGGGTCCTCCTGGTGTTTGAGGCCAAGATTCCCACCAGCTTCCACCG
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APPLICANT: Edward M. Brown
APPLICANT: Steven C. Hebert
APPLICANT: Forrest H. Fuller
APPLICANT: James E. Garrett, Jr.
TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
TITLE OF INVENTION: MOLECULES
NUMBER OF SEQUENCES: 20
CLASSIFICATION: 435
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below: 9
APPLICATION NUMBER: 08/353,784
                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FASTSEG
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,751
FILING DATE: 7 June, 1995
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STREET: First Interstate World
STREET: Suite 4700
STREET: 533 West Fifth Street
CITY: Los Angeles
STATE: California
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NAME/KEY: CDS
LOCATION: 515..37
OTHER INFORMATION:
US-08-480-751-1
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Best Local Similarity 46.0%;
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEEX: 67-3510
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 11 February, 1992
APPLICATION NUMBER: U.S. 07774
FILING DATE: 23 AUGUST, 1991
ATTORNEY,ACENT INFORMATION:
NAME: Heber, Sheldon O.
REGISTRATION NUMBER: 38,179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                         1054 ATTCAAGTCCTTCCTCCGCÁCCATACCCAATGATGAACÁCCAGGCCACGGCCATGGCTGA 1113
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APPLICATION NUMBER: U.S. 08/292,827
FILING DATE: 23 August, 1994
APPLICATION NUMBER: U.S. 08/141,248
FILING DATE: 22 October, 1993
APPLICATION NUMBER: U.S. 08/009,389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: U.S. 19
APPLICATION NUMBER: U.S. 19
TING DATE: 11 February, 19
TING DATE: U.S. 07/
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APPLICATION NUMBER: U.S. 08/009,389
FILING DATE: 23 February, 1993
APPLICATION NUMBER: U.S. 08/017,127
FILING DATE: 12 February, 1993
APPLICATION NUMBER: U.S. 07/934,161
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UMBER: PCT/US/94/12117
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-	796 1288	gcgtctggctcgagccaggacca	35
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US-08-943-986-1
US-08-943-986-1
; Sequence 1, Ap
; Patent No. 596
; PATENT INFOR
APPLICANT:
; APPLICANT:

Sequence 1, Application US/08943986
Patent No. 5962314
GENERAL INFORMATION:
APPLICANT: Edward M. Brown
APPLICANT: Steven C. Hebert

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: NAME/KEY: CDS
: LOCATION: 515..37
: OTHER INFORMATION:
US-08-943-986-1
                                                                                           Query Match
Best Local Similarity 45.
Matches 1135; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Heber, Sheldon O.
REGISTRATION NUMBER: 38,179
REFERENCE/POCKET NUMBER: 213/
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AFFILING DATE:
FILING DATE:
APPLICATION NUMBER: U.S. 1993
FILING DATE: 12 February, 1993
APPLICATION NUMBER: U.S. 07/934,161
APPLICATION NUMBER: U.S. 07/834,044
.... 1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 08/353,784
FILING DATE: 9 December, 1994
APPLICATION NUMBER: PCT/US/94/12117
FILING DATE: 21 October, 1994
APPLICATION NUMBER: U.S. 08/292,827
FILING DATE: 23 AUGUST, 1994
APPLICATION NUMBER: U.S. 08/141,248
FILING DATE: 22 OCTOBER; 1993
APPLICATION NUMBER: U.S. 08/09,389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: James E. GAITETT, Jr.
TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
TITLE OF INVENTION: MOLECULES
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 5275 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 21 August, 1992
APPLICATION NUMBER: U.S. 07/834,044
FILING DATE: 11 February, 1992
APPLICATION NUMBER: U.S. 07/749,451
FILING DATE: 23 August, 1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FASTSEQ
                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                              MOLECULE TYPE:
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CITY: Los Angeles
STATE: California
COUNTRY: USA
                        694
                                                           205
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APPLICATION NUMBER: U.S. 08/009,389
FILING DATE: 23 February, 1993
FLING DATE: U.S. 08/017,127
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STREET: Suite 4700
STREET: 633 West Fifth Street
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STRANDEDNESS: single
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APPLICANT:
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                                                                                                                                                APPLICATION NUMBER: PCT/US/94/12117
FILING DATE: 21 October, 1994
APPLICATION NUMBER: U.S. 08/29/28/27
FILING DATE: 23 August, 1994
APPLICATION NUMBER: U.S. 08/0141,248
FILING DATE: 22 October, 1993
APPLICATION NUMBER: U.S. 08/009,389
FILING DATE: 23 February, 1993
APPLICATION NUMBER: U.S. 08/017,127
FILING DATE: 12 February, 1993
APPLICATION NUMBER: U.S. 08/017,127
FILING DATE: 12 February, 1993
APPLICATION NUMBER: U.S. 07/934,161
FILING DATE: 13 February, 1993
APPLICATION NUMBER: U.S. 07/934,161
FILING DATE: 11 S 07/934,044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FASTSEQ
CURRENT APPLICATION DATA:
                  ATTORNEY/AGENT INFORMATION:
NAME: Heber, Sheldon O.
REGISTRATION NUMBER: 38,
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APPLICANT: Bradford C. Van Wagenen, Manuel
APPLICANT: F. Balandrin, Forrest H. Fuller,
APPLICANT: Eric G. DelMar, and Scott T. Moe
TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
TITLE OF INVENTION: MOLECULES
NUMBER OF SEQUENCES: 20
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                                             FILING DATE: 21 AUGUSTA 1992
APPLICATION NUMBER: U.S. 07/834, va.
FILING DATE: 11 February, 1992
APPLICATION NUMBER: U.S. 07/749,451
TITME DATE: 23 AUGUST, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE: 9 Dece CLASSIFICATION: 514
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STATE:
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REFERENCE/DOCKET NUMBER:
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NAME/KEY: CDS
LOCATION: 515..3769
OTHER INFORMATION:
US-08-353-784-1
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TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEFX: 67-3510
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5275 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 6.1%;
Best Local Similarity 46.0%;
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GGCCTGGGCCAGCTCTTCCCTGATTGCTATGCCCGAGTATTTCCATGTGGTCGGAGGCAC 1467
               caaggacgtggtgcctctctccgcccaggcgggtgacccaaggatgcagcgcatgatgct 795
                                                                                                                                                                                                                               CCGGCCAGGGATCGAGAAGTTTCGAGAGGAAGCTGAGGAGAGGGACATCTGCATCGACTT
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α	CGCAACACGCCCATCGTCAAGGCCACCAACCGGGAGCTCTCCTATCTCCTTCTCTCT	42	Db
1845	acacgcctgttgtgaggtcagctggggggtaggctgtgcttcctcatgctgg	1786	γQ
1785	agcagctaacacgctattgctgctgctgctgattgggactgctggctg	1726 2368	Qy Db
	TGCATCGCCAAGGAGATCGAGTTTCTGTCGTGGACCGAGCCCTTCGGGATCGCAC	2308	Дb
1725	ctgcttctcacgcaccgtggagttcttggggtggcatgaacccatctctttggtgctatt	1666	γQ
2307		2248	Dъ
1665	agottoacacotgocagoottgtggaacagaagaatgggccoctgaggggagotcago	1606	Qy
2247	CCTGATGGGGAGTACAGCGACGAGA	2188	מם
1605	accactgotgottogagtgoatgocotgtgaagotgggacatttotcaacacg	1546	Qy
2187	AGTCGAGACTGCCTGGCAGGGACCAGGAAAGGAATCATTGAGG	2128	da
1545	cctqtgtcagtgtgtaccagggactgtctcgaagggcaccacaggttggtcatg	1489	Qy
2127	AGGAGAGACTCTTCATCATGATGAAAAATTCTGTGGAGTGGATTCTCAAGGGAGGT	2068	Db
1489	gttcatctagacataaataagacaaaatccagtggcacgggaagaacaatcagg	1429	Qy
2057	CCCAGAGGACGGCTCCATAGTGTTTAAGGAAGTTGGATATTACAATGTCTATGCCAAGAA	2008	Db
1428	ctgaatggacctttgaggtcattggttctgcctcactgtc	1384	Qy
2007	AACTTTCGATGAATGTGGAGACCTGGCAGGGAACTATTCCATCATCAACTGGCACCTCTC	1948	Db
1383	cattogatgacaagggggacocototaggttattatgacatcatogcottgggaa	1324	Qy
9		œ	Db
1323	ggcagcttcttcagcagatctacaaggtgaatttccttctacataagaagactgt	1267	Qγ
		00 N3	Db
1266	cctctgggagtgtgcagaggcccagtctaccc	1231	Qy
1827	TTAGCCGTCTACTCCATTGCTCATSCCCTACAAGATATATACACCTG	1768	Db Db
1230	tacaatgtgtatgaggctgtgtatgctgtgggccacggcctccaccagctcctgggatg	1171	Qy
1767	GGAGGAGAACATCAGCAGTGTCGAGACTCCTTACATGGATTATACACATTTACGGATATC	1708	Дb
1170		1170	Qy
1707	AGCAACAGTCCCACTGCCTTCCGACCTCTGTGCACTGG	1648	Дb
1170	gacatggaacatgcccgagcttggagccttctccatgagcgctg	1125	Qy
1647	CCTGCAAGAGGTGCTAAAGGCCCATTACCGGTGGACACCTTCCTGAGAGGTCA	1588	Дb
1124	cagasgsstcctgstgcggcactaaccagctgtgcagggagtgtcacgctttca	1067	Qy
1587	GGTTTTGCCAAGGAGTTTTGGGAAGAAACATTTAA	1528	ФФ
1066	agagtcctatgtccaggcagtgatggtgctcccagaact	1024	Qy
1527		1468	Db
1024	gggggtggccatccagcagagacaagtccctggcctgaaggagtt	976	Qy

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Patent No. !
                                                                                                                                 STREET: First Interstate World Center STREET: Suite 4700
STREET: 633 West Fifth Street CITY: Los Angeles
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
APPLICANT:
APPLICANT:
               COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FASTSEQ
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                            APPLICANT: James E. Garrett, Jr.
TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
TITLE OF INVENTION: MOLECULES
NUMBER OF SEQUENCES: 20
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APPLICATION NUMBER:
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Steven C. Hebert
Forrest H. Fuller
US/08/485,588
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TELEPHONE: (213) 489-1600
TELEPAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 5006 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 5.9%;
Best Local Similarity 48.4%;
Matches 487; Conservative
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APPLICATION NUMBER: DCT/US/94/12117
FILING DATE: 21 October, 1994
APPLICATION NUMBER: U.S. 08/292,827
APPLICATION NUMBER: U.S. 08/141,248
FILING DATE: 23 August, 1994
APPLICATION NUMBER: U.S. 08/141,248
FILING DATE: 22 October, 1993
APPLICATION NUMBER: U.S. 08/009,389
FILING DATE: 23 February, 1993
APPLICATION NUMBER: U.S. 08/017,127
FILING DATE: 12 February, 1993
APPLICATION NUMBER: U.S. 07/934,161
FILING DATE: 21 August, 1992
APPLICATION NUMBER: U.S. 07/934,044
FILING DATE: 11 February, 1992
APPLICATION NUMBER: U.S. 07/834,044
FILING DATE: 11 February, 1992
APPLICATION NUMBER: U.S. 07/749,451
FILING DATE: 11 FEBRUARY, 1991
APPLICATION SAME U.S. 07/749,451
FILING DATE: 23 August, 1991
ATTORNET/AGENT INFORMATION:
NAME: Heber: Sheldon O.
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LOCATION: 436..3699
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Heber, Sheldon O. REGISTRATION NUMBER: 38,179
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CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                    GAGACAGATGCCAGTGCCTGTAACAAGTGCCCAGATGACTTCTGGTCCAATGAGAACCAC
AAGTTCCGCAACACCCCATTGTCAAGGCCACCAACCGAGAGCTCTCCTACCTCCTCCTC
                                                                                                                                    ctattagcagctaacacgctattgctgctgctgctgattgggactgctggtctgtttgcc 1780
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ON: 435
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Pred. No. 1.6e-33;
0; Mismatches 514;
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RESULT 12
US-08-484-565-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
APPLICANT:
                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FASTSEQ
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                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3028 AACAAGATCTACATCATTCTTCTAAGCCATCCCGCAACACCATCGA 3074
                                              CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                 STREET: First Interstate World
STREET: Suite 4700
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
    FILING DATE:
       APPLICATION NUMBER: FILING DATE: 7 Jun
                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
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                                                                                                                                                                                        90071
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Steven C. Hebert
James E. Gairett, Jr.
NVENTION: CALCIUM RECEPTOR-ACTIVE
NVENTION: MOLECULES
                                                                                                                                                                                                                USA
                                                                                                                                                                                                                                                                                                                                                      Lyon & Lyon
    June,
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    US/08/484,565
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEFAX: (213) 955-0440
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 487; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: U.S. 08/017,127
FILING DATE: 12 February, 1993
APPLICATION NUMBER: U.S. 07/934,161
FILING DATE: 21 August, 1992
APPLICATION NUMBER: U.S. 07/834,044
FILING DATE: 11 February, 1992
APPLICATION NUMBER: U.S. 07/749,451
FILING DATE: 23 August, 1991
FILING DATE: 23 August, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 21 October, 1994
APPLICATION NUMBER: U.S. 08/292,827
FILING DATE: 23 AUGUST, 1994
APPLICATION NUMBER: U.S. 08/141,248
FILING DATE: 22 October, 1993
APPLICATION NUMBER: U.S. 08/009,389
FILING DATE: 23 February, 1993
APPLICATION NUMBER: U.S. 08/017,127
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PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
  1841
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Heber, Sheldon O.
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LOCATION: 436..36
OTHER INFORMATION
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TYPE: n
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STRANDEDNESS: single
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ggttccttggtagctgggagttgcagcctctacagcttcttcgggaagcccacggtgccc
                                              AAGTTCCGCAACACACCCATTGTCAAGGCCACCAACCGAGAGCTCTCCTACCTCCTCCTC
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ON DATA: described below:
IUMBER: 08,753,784
9 December, 1994
IUMBER: PCT/US/94/12117
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Pred. No. 1.6e-33;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/08480751 Patent No. 5858684
                                                                                                                                                          STREET: First Interstate World Center STREET: Suite 4700
STREET: Suite 4700
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
APPLICANT:
        ZIP: 90071

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: FASTSEQ

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Forrest H. Fuller
APPLICANT: James E. Garrett, Jr.
TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
TITLE OF INVENTION: MOLECULES
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Edward M. Brown
Steven C. Hebert
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US/08/480,751
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US-08-480-751-2
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Best Local Similarity 48.4%;
Matches 487; Conservative
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APPLICATION NUMBER: U.S. 08/292,827
FILING DATE: 23 August, 1994
APPLICATION NUMBER: U.S. 08/141,248
APPLICATION NUMBER: U.S. 08/00,389
FILING DATE: 23 February, 1993
APPLICATION NUMBER: U.S. 08/017,127
FILING DATE: 12 February, 1993
APPLICATION NUMBER: U.S. 09/017,127
FILING DATE: 12 February, 1993
APPLICATION NUMBER: U.S. 07/934,161
FILING DATE: 12 February, 1993
APPLICATION NUMBER: U.S. 07/934,044
FILING DATE: 11 February, 1992
APPLICATION NUMBER: U.S. 07/84,044
FILING DATE: 11 February, 1992
APPLICATION NUMBER: U.S. 07/749,451
FILING DATE: 12 August, 1991
ATTORNEY/AGENT INFORMATION
NAME: Heber, Sheldon O.
REFERENCE-DOCKET NUMBER: 213/004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:

NAME/KEY: CDS

LOCATION: 436.
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TELECOMMUNICATION INFORMATION:
TELEPHONE: {213} 489-1500
                                                                                                                                                                                                                                                                                                             1601 acgagtgagcttcacacctgccagccttgtggaacagaagaatgggcccctgaggggagc 1660
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LENGTH: 5006 base pair
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FILING DATE: 9 December, 1994
APPLICATION NUMBER: PCT/US/94/12117
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CLASSIFICATION:
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                    AAGTTCCGCAACACCCCATTGTCAAGGCCACCAACCGAGAGCTCTCCTACCTCCTC
                                              tggcgtcttcacacgcctgttgtgaggtcagctgggggtaggctgtgcttcctcatgctg 1840
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Pred. No. 1.6e-33;
0; Mismatches 514;
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Indels Length 5006;

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RESULT 14
US-08-943-986-2
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FASTSEQ
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,986
FILING DATE: 03-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Edward M. Brown
APPLICANT: Steven C. Hebert
APPLICANT: James E. Garrett, Jr.
TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
TITLE OF INVENTION: MOLECULES
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2021
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                                                                                                                                                                                                                                     STREET: First Interstate World
STREET: Suite 4700
STREET: 531 West Fifth Street
CITY: Los Angeles
STATE: California
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US-08-943-986-2
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Best Local S
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APPLICATION NUMBER: U.S. 08/017,127
FILING DATE: 12 February, 1993
APPLICATION NUMBER: U.S. 07/934,161
FILING DATE: 21 August, 1992
APPLICATION NUMBER: U.S. 07/834,044
FILING DATE: 11 February, 1992
APPLICATION NUMBER: U.S. 07/749,451
AFILING DATE: 23 August, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Heber, Sheldon O.
PETATORNEYN NUMBER: 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 67-3510 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/484,565
FILING DATE: 7-Unne-1995
APPLICATION NUMBER: 08/353,784
FILING DATE: 9 December: 1994
APPLICATION NUMBER: POT/US/94/1
FILING DATE: 21 October: 1994
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APPLICATION NUMBER: U.S. 1993
FILING DATE: 22 October, 1993
APPLICATION NUMBER: U.S. 08/009,389
APPLICATION NUMBER: U.S. 08/017,127
TILING DATE: 23 February, 1993
TILING DATE: 23 February, 1993
TILING DATE: 1993
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REFERENCE/DOCKET NUMBER: 211
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEPAX: (213) 955-0440
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LENGTH: 5006 base pairs
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TTTING DATE: 23 August, 1994
TTTING DATE: 23 August, 1994
1993
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LOCATION: 436..3699
OTHER INFORMATION:
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ggttccttggtagctgggagttgcagcctctacagcttcttcgggaagcccacggtgccc 1900
                                                       AAGTTCCGCAACACACCCATTGTCAAGGCCACCAACCGAGAGCTCTCCTACCTCCTCCTC
                                                                                       tggcgtcttcacacgcctgttgtgaggtcagctgggggtaggctgtgcttcctcatgctg 1840
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Pred. No. 1.5e-33;
0; Mismatches 514;
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US-08-353-784-2
; Sequence 2, Ap
; Patent No. 601
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APPLICANT: Edward
APPLICANT: Brown,
APPLICANT: Bradfor
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                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3028 AACAAGATCTACATCATTCTCTTCAAGCCATCCCGCAACACCATCGA 3074
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    CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: CALCIUM R
                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                    STREET: First Interstate World Center STREET: Suite 4700
STREET: 633 West Fifth Street
CITY: Los Angeles
                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: FASTSEQ
                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CACCGCAAGTGGTGGGGGCTCAACCTGCAGTTCCTGCTGGTTTTCCTCTGCACCTTCATG
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Brown, Steven C. Hebert,
Bradford C. Van Wagenen, Manuel
F. Balandrin, Forrest H. Fuller,
Eric G. DelMar, and Scott T. Moe
CALCIUM RECEPTOR-ACTIVE
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LOCATION: 436..36
OTHER INFORMATION:
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TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
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REGISTRATION NUMBER: 38,179
REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1500
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DB 5; 514;

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PRIOR APPLICATION

PRIOR APPLICATION NUMBER: PCT/vv/A

APPLICATION NUMBER: U.S. 08/29,827

FILING DATE: 23 August, 1994

APPLICATION NUMBER: U.S. 08/141,248

APPLICATION NUMBER: U.S. 08/009,389

TITING DATE: 22 October, 1993

TITING DATE: 22 October, 1993

TITING DATE: 1993

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TITING DATE: 1993
APPLICATION NUMBER: U.S. 08/009,389
FILING DATE: 23 February, 1993
APPLICATION NUMBER: U.S. 08/017,127
FILING DATE: 12 February, 1993
APPLICATION NUMBER: U.S. 07/934,161
FILING DATE: 21 August, 1992
APPLICATION NUMBER: U.S. 07/834,044
FILING DATE: 11 February, 1992
APPLICATION NUMBER: U.S. 07/84,044
APPLICATION NUMBER: U.S. 07/749,451
FILING DATE: 23 August, 1991
ATTORNEY/AGENT INFORMATION:
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T61382 standard; cDNA to T61382; standard; cDNA to T61382; standard; cDNA to T61382; standard; cDNA to T61382; standard; clim rece Calcium receptor; human primary hyperparathyroid calcium-activated chlori variant; untranslated re alternative transcription human CaR gene; iscform; Homo sapiens. Location Cds Cds 2-MAY-1996; U13704. 21-OCT-1994; WO-U12117. OB-DEC-1994; WO-U12117. OB-DEC-1994; US-353784. (NPSP) NPS PHARM INC. Balandrin MF, Delmar Ed PFSDB; W11889. New disarylalkyl amine o receptor activities - es calcium on cell surface hyperparathyroidism, Page These sequences diven in I These sequences were isc tumour using pBoPCaR1 as a 3 year old caucasian and two clones of approx finjected into Xenopus of functional calcium receptors as as e.g. MPS R-467 and NPS F indicated the existence the 3' untranslated regipolyadenylation. Sequence transcription initiation sequence variation occur pHupCaR5.2 and pHupCaR4. proteins. Sequence anal additional 30 bp in clon from alternative mRNA spr to insert 10 additional pHupCaR4.0. In addition at positions These pharmacologically distin sequence	188 882 188 188 882
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2581 GTCATCTGTGTGATCTGGCTCTACACCGCGCCCCCTCAAGCTACCGCAACCAGGAGCTG 2	
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2404 CGCCTGCGCCAGCCGGCCTTTGGCATCAGCTTCGTGCATCTCATGCATCCTGGTG 246	
1907 tigetgegteageegetettttetetetggggtttgeeatttteetetetgtgggate 1	
Qy 1847 ttggtagctgggagttgcagcctctacagcttcttcgggaagcccacggtgcccgcgtgc 1906	
2284 CGCAACACACCATTGTCAAGGCCACCAACCGAGAGCTCTCCTACCTCCTCCTCCTTCTCC	
1787	
Db 2224 CTCTTTGCCGTGCTGGCATTTTCCTGACAGCCTTTGTGCTGGGTGTGTTTATCAAGTTC 2283	
Qy 1727 gcagctaacacgctattgctgctgctgctgattgggactgctggcctgtttgcctggcgt 1786	
Db 2164 TGCATTGCCAAGGAGATCGAGTTTCTGTCGTGGACGGAGCCCTTTGGGATCGCACTCACC 2223	
Qy 1667 tgcttctcacgcaccgtggagttcttggggtggcatgaacccatctctttggtgctatta 1726	
Db 2104 GATGCCAGTGCCTGTAACAAGTGCCCAGATGACTTCTGGTCCAATGAGAACCACACCTCC 2163	
Qy 1607 gagetteacacetgeeageettgtggaacagaagaatgggeeecetgaggggageteagee 1666	
Db 2044 GAGCCCACCIGCTITGAGTGTGTGGGGAGTGTCCTGATGGGGAGTATAGTGAGACA 2103	
Qy 1547 tcccaccactgctgcttcgagtgcatgccctgtgaagctgggacatttctcaacacgagt 1606	
1984 CCCTTCTCCAACTGCAGCCGAGACTGCCTGGCAGGACCAGGAAAGGGATCATTGA	
Qy 1490 cctgtgtcagtgtgtaccagggactgtctcgaagggcaccacaggttggtcatgggt 1546	
Db 1924 GGAGAAAGACTCTTCATCAACGAGGAGAAAATCCTGTGGAGTGGTTCTCCAGGGAGGTG 1983	
Oy 1430 ccagitcaictagacataaataagacaaaaatccagiggcacgggaagaacaatcaggig 1489	
1864 CCAGAGGATGGCTCCATCGTGTTTAAGGAAGTCGGGTATTACAACGTCTATG	
Qy 1385 ggacctgaatggacctttgaggtcattggttctgcctcactgtct 1429	
Db 1804 ACCTTGATGAGTGTGGTGACCTGGTGGGGAACTATTCCATCATCAACTGGCACCTCTCC 1863	
Qy 1325 gcattcgatgacaagggggaccctctaggttattatgacatcatcgcctgggactggaat 1384	
Db 1744 TGGCAGGTCCTGAAGCACCTACGGCATCTAAACTTTACAAACAA	
Qy 1268 tggcagcttcttcagcagatctacaaggtgaatttccttctacataagaagactgta 1324	
Db 1684 TTACCTGGGAGAGGGCTCTTCACCAATGGCTCCTGTGCAGACATCAAGAAAGTTGAGGCG 1743	
Oy 1232 acctctgggacctgtgccagaggcccagtctacccc 1267	
Db 1624 TACAATGTGTACTTAGCAGTCTACTCCATTGCCCACGCCTTGCAAGATATATAT	
Oy 1172 tacaatgtgtatgaggctgtgtatgctgtggcccacggcctccaccagctcctgggatgt 1231	
Db 1564 GATGAGAACATCAGCAGTGTCGAGACCCCTTACATAGATTACACGCATTTACGGATATCC 1623	
Qy 1112 tgtcacgctttcacgacatggaacatgcccgagcttggagccttctccatgagcgctgcc 1171	_

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                                                                                                            DNA encoding calcium receptor polypeptide(s) - useful for therapeutic purposes, e.g. hyperparathyroidism and osteoporosis (claim 15; Columns 125-134; 174pp; English.

The present sequence encodes human parathyroid cell calcium receptor 4.0 (HuPCaR 4.0).

The specification includes details of molecules that can modulate one or more inorganic ion receptor activities, and antibodies and antibody fragments targetted to inorganic ion receptor proteins. The proteins, nucleic acids and antibodies may be used to treat disorders by modulating one or more inorganic ion receptor activities, preferably disorders of calcium homeostasis, e.g. hyperparathyroidism and osteoporosis.

Sequence 3809 BP; 910 A; 1071 C; 979 G; 849 T;
  Query Match
Best Local Similarity
Matches 1130; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-NOV-1997

17-JUN-1995

17-JUN-1995

17-JUN-1995

17-JUN-1995

23-AUG-1991

11-FEB-1993

12-FEB-1993

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12-CCT-1994

21-OCT-1994
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WPI; 9
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Key
CDS
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US-485588

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US-934121

US-017127

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US-141248

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Score 166.2; DB 1
Pred. No. 1.6e-33;
0; Mismatches 1143
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Query Match
Best Local Similarity
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Score 166.2; DB 1; Pred. No. 1.6e-33; 0; Mismatches 1143;

Length Indels 168;

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PT antibody production

PS Example 27: Fig 49: 174pp; English.

CC The Human parathyroid calcium receptor gene encodes a 1078 amino acid

CC protein. The tissue from which the receptor and receptors from bovine

CC parathyroid and rat kidney are derived, respond to changes, and control

CC changes, in calcium ion concentration, e.g. parathyroid hormone regulates

CC Ca2+ homeostasis in blood and extracellular fluid, and kidney function

CC claim to the compound to change for the compound to change for the compound to change for the compound to compound to compound the calcium

CC recombinantly) can be used to screen for compounds that modulate calcium

CC receptor activity, especially those that can be used to treat diseases

CC associated with the receptors in these tissues. They can also be used

CC traise antibodies for use in detection assays.

SQ Sequence 3809 BP; 910 A; 1071 C; 979 G; 849 T;
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09-JUN-1998.
07-JUN-1995;
07-JUN-1995;
23-AUG-1991;
11-FEB-1992;
12-FEB-1993;
                                                                                                                                                                                                                                                                                                                                       21-OCT-1994;
08-DEC-1994;
                                                                                                                                                                                                                                       Calcium receptor poly:peptide(s) - useful for drug screening
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                                                                                                                                                                                                                                                                                         Brown
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Human parathyroid calcium receptor 4.0 gene 4Kb fragment
ss; calcium ion concentration; parathyroid hormone; home
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22-OCT-1993;
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6	917 gactgggccatctccacgtacatcaccaatgtgcccgggatccagggcattgggacggtg 976	Qy
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6	677 cagctgggcgtacaggcggtggaggagctggccactccacggggcatctgcgtcgccttc 736	Qy
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9	0 TTCTACATTCCCCAGGTCAGTTATGCCTCCTCCAGCAGCTCCTCAGCAACAAGAATCAA 90	D
	97 tttetgatgeeettggteagetatgaggegageagegtgatceteagtgggaagegeaag 5	Qy
9	GAGCAACTGGCTCAGGCGTCTCCACGGCAGTGGCAAATCTGCTGGGGCTC 84	Db
о —	437 gcactcattgggcotgataacactgaccacgctgtcaccactgctgccctgctgagccct 496	Qy
9	GATGAGTTCTGCAACTGCTCAGAGCACATTCCCTCTACG	Db
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        PT Screening for calcium receptor-active compounds - by recombinant PT expression of nucleic acid encoding calcium receptor and determining PT the effect of compounds on calcium receptor activity the effect of compounds on calcium receptor activity PS Claim 1; Fig 49; 179pp; English.

CC A method has been developed of screening for a compound able to affect CC one or more activities of a calcium receptor (CR) comprises: (A) CC contacting a recombinant cell with a test compound, where the CC recombinant cell comprises a recombinant nucleic acid expressing the CR, CC provided that the cell does not have functional CR expression from CC endogenous nucleic acid; (B) determining the ability of the test CC compound to affect one or more activities of the calcium receptor; and CC (C) comparing the ability with the ability of the test compound to CC affect the one or more CR activities in a cell not comprising the CC comparathyroid CR, designated a pHuPCaR 4.0. The nucleic acid sequence of CC pHuPCaR 4.0 can be used as part of the recombinant nucleic acid in the CC method described above. The compounds identified can be used to treat CC diseases or disorders characterised by abnormal calcium homeostasis, e.g. Cd disorders. They can also be used for the treatment of diseases and CC disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-JUN-195; 480751.
07-JUN-195; US-400751.
27-AUG-1991; US-749451.
11.FEB-1992; US-834044.
21.AUG-1992; US-934161.
12.FEB-1993; US-017127.
23.FEB-1993; US-017127.
23.FEB-1993; US-0171248.
19.AUG-1994; US-292827.
21.OCT-1994; WG-012117.
21.OCT-1994; WG-353784.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human parathyroid calcium receptor pHuPCaR 4.0 encoding cDNA.

Parathyroid calcium receptor; inorganic ion receptor; osteoporosis;

calcium homeostasis; hyperparathyroidism; selzure; stroke; epilepsy;

spinal cord injury; hypoxia-induced nerve cell damage; cardiac arrest;

neonatal distress; neurodegenerative disease; Alzheimer's disease;
                                                                                                                                                                                                                                                                                                                                                                                                    Balandrin MF, Brown EM, Del Mar EK
Hebert SC, Nemeth EF, Van Wagenen
WPI: 99-119871/10.
                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB; W89565.
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hyperparathyroidism,
disorders. They can
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Best Local Similarity 46.3
Matches 1130; Conservative
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11-FEB-1992; US-834044.
21-AUG-1992; US-934161.
12-FEB-1993; US-017127.
23-FEB-1993; US-009389.
22-OCT-1993; US-141248.
19-AUG-1994; US-292827.
21-OCT-1994; WS-12117.
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Bos sp.
Key
CDS
The present sequence encodes bovine parathyroid cell calcium receptor I (BoPCaR I).

The specification includes details of molecules that can modulate one or more inorganic ion receptor activities, and antibodies and antibody fragments targetted to inorganic ion receptor proteins. nucleic acids and antibodies may be used to treat disorders by modulating one or more inorganic ion receptor activities, preferably disorders of calcium homeostasis, e.g.
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Bovine
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The present sequence encodes bovine parathyroid cel
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parathyroid cell calcium receptor 1; BoPCaR 1;
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Qy	Db Qy	9d 63	4 d	da Vy	o da Vy	da da	d Qy	gg Qy	da da	Qy Db	d dd (y	d dd y	מם עט	Db Qy	9 d Q) B 2	Qy Db	Db
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23-AUG-1991; US-749451.
11-FEB-1992; US-934161.
12-FEB-1993; US-934161.
12-FEB-1993; US-017127.
23-FEB-1993; US-01248.
22-OCT-1993; US-141248.
19-AUG-1994; US-292827.
21-OCT-1994; WG-292827.
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09-JUN-1998.
07-JUN-1995;
07-JUN-1995;
                 Calcium receptor poly:peptide(s) - useful for drug screening or antibody production

Example 25; Fig 47; 174pp; English.

The bowine parathyroid calcium receptor gene encodes a 1085 amino acid protein. The tissue from which this receptor and receptors from human parathyroid and rat kidney are derived, respond to changes, and control changes, in calcium ion concentration, e.g. parathyroid hormone regulates ca2+ homeostasis in blood and extracellular fluid, and kidney function alters through changes in Ca2+ levels in juxtaglomerular and proximal tubule cells in the kidney. The purified receptors (produced that the case of th
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(NPSP-) NPS PHARM INC.
Brown EM, Garrett JE, Hebert
WPI; 98-347412/30.
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                 tgcccagaggggtcctggtgcgca--ctaaccagctgtgcagggagtgtcacgctttca
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07-JUN-1995; US-480751.
23-AUG-1991; US-749451.
11-FEB-1992; US-834044.
21-AUG-1992; US-934161.
12-FEB-1993; US-017127.
23-FEB-1993; US-017127.
23-FEB-1993; US-017127.
23-CCT-1994; WC-012117.
08-DEC-1994; US-353784.
(BGHM) BRIGHAM & WOMENS HO:
(NPSP-) NPS PHARM INC.
BALANDRIN MF, BROWN EM, Del
Hebert SC, Nemeth EF, Van WART; 99-119871/10.
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12-JAN-1999.
07-JUN-1995;
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Bos sp.
Key
CDS
Screening for calcium receptor-active compounds - by expression of nucleic acid encoding calcium receptor the effect of compounds on calcium receptor activity Claim 1; Fig 47; 176pp; English.

A method has been developed of screening for a compounds of the comp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-MAR-1999 (first entry)
Bovine parathyroid calcium receptor BoPCaR 1 encoding cDNA.
Bovine parathyroid calcium receptor; inorganic ion receptor; osteoporosis;
calcium homeostasis; hyperparathyroidism; seizure; stroke; epilepsy;
capinal cord injury; hypoxia-induced nerve cell damage; cardiac arrest;
neonatal distress; neurodegenerative disease; Alzheimer's disease;
Huntington's disease; Parkinson's disease; dementia; muscle tension;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            V82483 standard; cDNA to mRNA;
V82483;
19-MAR-1999 (first entry)
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Matches 1136; Conser-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   recombinant nucleic acid. The present sequence encodes boving parathyroid CR, designated a BoPCaR 1. The nucleic acid sequence of BoPCaR 1 can be used as part of the recombinant nucleic acid in the method described above. The compounds identified can be used to treat diseases or disorders characterised by abnormal calcium homeostasis, e.g. hyperparathyroidism, osteoporosis and other bone and mineral-related disorders. They can also be used for the treatment of diseases and disorders associated with disrupted Ca2+ responses, e.g. seizures, stroke, spinal cord injury, hypoxia-induced nerve cell damage such as in cardiac arrest or neonatal distress, epilepsy, neurodegenerative diseases such as Alzheimer's disease, Huntington's disease and Parkinson's disease, dementia, muscle tension, depression, and anxiety. Sequence 5275 Bp; 1277 A; 1475 C; 1316 G; 1207 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 contacting a recombinant cell with a test compound, where the recombinant cell comprises a recombinant nucleic acid expressing the provided that the cell does not have functional CR expression from endogenous nucleic acid; (B) determining the ability of the test compound to affect one or more activities of the calcium receptor; (C) comparing the ability with the ability of the test compound to affect the one or more CR activities in a cell not comprising the affect the one or more CR activities in a cell not comprising the
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                                  tottoacacgootgitgigaggicagcigggggitaggoigigcitcotcatgoigggitco
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                                                                                                                  agcagctaacacgctattgctgctgctgctgattgggactgctggcctgtttgcctggcg
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                                                                                                                                                                                                              Parathyroid calcium receptor coding sequence clone pHuPCaR5.2. Calcium receptor; human parathyroid gland adenoma tumour; pBoPCaR1 primary hyperparathyroidism; Xenopus oocyte; alternative splicing; calcium-activated chloride current; agonist; NPS R-467; NPS R-568; variant; untranslated region; alternative polyadenylation; probe; alternative transcription initiation; pHuPCaR5.2; pHuPCaR4.0;
                                                                                                                                                                                                                                                                                                                           T61381 standard;
T61381;
22-APR-1997 (fir
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                                                                                                                                                                                                 alternative transcription initiation; human CaR gene; isoform; ss.
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21-OCT-1994; WO-U12117.
08-DEC-1994; US-353784.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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The sequences given in T61381-82 encode functional calcium receptors.

These sequences were isolated from human parathyroid gland adenoma tumour using pBoPCaR1 as a hybridisation probe. mRNA was isolated from a 39 year old caucasian male diagnosed with primary hyperparathyroidism and two clones of approx. 5 and 4 kb were identified. These cDNA's were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        these positions. These two
pharmacologically distinct.
Sequence 5006 BP; 1228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pHuPCaR4.0. In addition pHuPCaR4.0 encodes Gln at position 925 and Glat position 930, whereas pHuPCaR5.2 encodes Arg at both equivalent positions. The human CaR gene encodes for Gln and Arg respectively at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New di:arylalkyl amine cpds. useful for modulating inorganic id receptor activities - esp. for modulating effect of extracellul calcium on cell surface calcium receptors, useful for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New d1:arylalkyl amine cpd receptor activities - esp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hyperparathyroidism, Paget's disease or osteoporosis
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WPI; 96-230520/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
mes 487; Conserv
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                                                            TTCTCCCTGCTCTGCTTCTCCAGCTCCCTGTTCTTCATCGGGGAGCCCCAGGACTGG
                                                                                                                                                                              tggcgtcttcacacgcctgttgtgaggtcagctggggggtaggctgtgcttcctcatgctg
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                                   11-FEB-1992; US-334044.
21-AUG-1992; US-334161.
12-FEB-1993; US-017127.
23-FEB-1993; US-009389.
23-GCT-1993; US-02827.
21-GCT-1994; WS-292827.
21-GCT-1994; WS-292827.
21-GCT-1994; WS-353784.
(BGHM ) BRIGHAM & WOMENS HOSPIT (NPSP-) NPS PHARM INC.
BFOWN EM, Fuller FH, Garrett JE WPI: 98-008040/01.
P-PSDB; W38273.
DNA encoding callium receptor p
                                                                                                                                                                                                                                                                                                                               Human parathyroid cell calcium receptor 5.2 (Human parathyroid cell calcium receptor 5.2; calcium homeostasis; hyperparathyroidism; ost Homo sapiens.
                                                                                                                                                                                                                           18-NOV-1997.
07-JUN-1995;
07-JUN-1995;
23-AUG-1991;
 DNA encoding calcium receptor polypeptide(s) - therapeutic purposes, e.g. hyperparathyroidism Claim 15; Columns 117-126; 174pp; English The present sequence encodes human parathyroid
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GHAM & WOMENS
PHARM INC.
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Matches
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The specification includes details of molecules that can modulate one or more inorganic ion receptor activities, and antibodies and antibody fragments targetted to inorganic ion receptor proteins. I proteins, nucleic acids and antibodies may be used to treat disorders by modulating one or more inorganic ion receptor activities, preferably disorders of calcium homeostasis, e.g. hyperparathyroidism and osteoporosis.

Sequence 5006 BP; 1227 A; 1378 C; 1219 G; 1182 T;
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nilarity 48.48;
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Sequence 5006 BP; 1228 A; 1376 C; 1770 C.
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22-OCT-1993;
19-AUG-1994;
19-OCT-1994;
08-DEC-1994;
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11-FEB-1992;
21-AUG-1992;
12-FEB-1993;
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09-JUN-1998.
07-JUN-1995;
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Example 27; Fig 48; 174pp; English.
The Human parathyroid calcium receptor gene encodes a 1088 amino protein. The tissue from which this receptor and receptors from the tissue from which this receptor and receptors from the tissue from which this receptor and receptors from the tissue from the tis
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US-934161.

US-017127.

US-009389.

US-141248.

US-292827.

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                        Huntington's disease; depression; anxiety; s Homo sapiens.
                                                                                       Human parathyroid calcium receptor pHuPCaR 5.2 encoding cDNA. Parathyroid calcium receptor; inorganic ion receptor; osteoporosis; calcium homeostasis; hyperparathyroidism; seizure; stroke; epilepsy; spinal cord injury; hypoxia-induced nerve cell damage; cardiac arrest; neonatal distress; neurodegenerative disease; Alzheimer's disease;
                                                                                                                                                                                                  V82484;
19-MAR-1999 (first entry)
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Location/Qualifiers
                                                                      Parkinson's
                                                                      disease; dementia;
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muscle

tension;

2487

2440

2967

2907

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2727 2140 2080 2607 2550 1960 2490

2020

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В
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Best Local S
Matches 487
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07-JUN-1995; US-480751.
23-AUG-1991; US-749451.
111-FEB-1992; US-834044.
21-AUG-1992; US-934161.
12-FEB-1993; US-017127.
23-FEB-1993; US-009389.
22-OCT-1993; US-141248.
19-AUG-1994; US-292827.
21-OCT-1994; US-292827.
21-OCT-1994; WS-292827.
21-OCT-1994; WS-33784.
(BGHM ) BRIGHAM & WOMENS H
(NPSP-) NPS PHARM INC.
Balandrin MF, Brown EM, De
                                                                                                                                                  2191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                diseases or disorders characterised by abnormal calcium homeostasis, e. hyperparathyroidism, osteoporosis and other bone and mineral-related disorders. They can also be used for the treatment of diseases and disorders associated with disrupted Ca2+ responses, e.g. seizures, stroke, spinal cord injury, hypoxia-induced nerve cell damage such as i cardiac arrest or neonatal distress, epilepsy, neurodegenerative diseases such as Alzheimer's disease, Huntington's disease and Parkinson's disease, dementia, muscle tension, depression, and anxiety. Sequence 5006 Bp; 1228 A; 1376 C; 1220 G; 1182 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  endogenous nucleic acid; (B) determining the ability of the test compound to affect one or more activities of the calcium receptor; and (C) comparing the ability with the ability of the test compound to affect the one or more CR activities in a cell not comprising the recombinant nucleic acid. The present sequence encodes human parathyroid CR, designated a pHuPCaR 5.2. The nucleic acid sequence of pHuPCaR 5.2 can be used as part of the recombinant nucleic acid in the method described above. The compounds identified can be used to treat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Screening for calcium receptor-active compounds - by recombinant expression of nucleic acid encoding calcium receptor and determining the effect of compounds on calcium receptor activity Claim 1; Fig 48; 176pp; English.

A method has been developed of screening for a compound able to affec one or more activities of a calcium receptor (CR) comprises: (A) contacting a recombinant cell with a test compound, where the recombinant cell comprises a recombinant nucleic acid expressing the provided that the cell does not have functional CR expression from
                                      1721
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   2311
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CTCACCCTCTTTGCCGTGCTGGGCATTTTCCTGACAGCCTTTGTGCTGGGTGTGTTTATC
                                ctattagcagctaacacgctattgctgctgctgattgggactgctggcctgtttgcc
                                                                                                tcagcctgcttctcacgcaccgtggagttcttggggttgcatgaacccatctctttggtg
                                                                                                                                                GAGACAGATGCCAGTGCCTGTAACAAGTGCCCAGATGACTTCTGGTCCAATGAGAACCAC
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487; Conserv
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Pred. No. 5.8e
0; Mismatches
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25-JUL-1996; U12336.
26-JUL-1995; US-001526.
26-JUL-1995; US-001526.
(NPSP-) NPS PHARM INC.
Fuller FH, Hammerland L
                                                                                                                                                                                                                                                                                                                                                                                                      Chimeric receptor; extracellular domain; seven transmembrane domain; intracellular cytoplasmic tail domain; metabotropic glutamate receptor; MGR; calcium receptor; CR; mGluR; G protein-coupled receptor; neurological disease; ss.

Chimeric - Homo sapiens.
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T86166;
02-DEC-1997 (first
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      Chimeric
                                WPI; 97-145690/13.
P-PSDB; W25763.
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Nucleotide sequence of pCaR/R1
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comprising metabotropic glutamate receptor and
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Query Match
Best Local Sim.
Matches 427;
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gactgggccatctccacgtacatcaccaatgtgcccgggatccagggcattgggacggtg
                                                gtgttcttcaggtctgtggtgctggccaacctgactggcaaagtgtggatcgcctccgaa
                                                                                                                                                       GTGATTCAAAATTCCACGGCCAAAGTCATCGTGGTTTTCTCCAGTGGCCCAGATCTTGAG
                                                                                                                                                                                     aaggacgtggtgcctctctccgcccaggcgggtgacccaaggatgcagcgcatgatgctg
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51.6%;
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Pred. No. 1.4e-29;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1010 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The chimeric receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               907 T;
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                                                                                                                                                                                                                                                                                                                                                                                                              This cDNA clone codes for dogfish shark kidney calcium receptor related protein (SKCaR-RP, see W32059), an aquatic polyvalent cation sensing receptor (PVCR). It was isolated from a shark kidney cDNA library using a rat kidney calcium receptor cDNA as probe. Also claimed are: a probe comprising the 4131 bp SKCaR-RP sequence; an isolated PVCR present in the plasma membranes of aquatic species, especially on the apical membrane of epithelial cells of elasmobranch fish, particularly from cells found in the collecting duct or late distal tubule in the kidney, intestine, gill, rectal gland, gonad or brain; an antibody that specifically binds to a PVCR; and a method of screening for aquatic PVCR aquatic PVCR advants or inhibits aquatic pVCR mediated ion transport and endocrine changes that permit fish to adapt to fresh or salt water. The method facilitates the aquaculture of marine
                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                       1439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Squalus
Key
                                                                                                                                                                                                                                                                                                                                                               fish and can provide for the development of marine fish that are easily adaptable to fresh water aquaculture. Sequence 4131 BP; 1028 A; 1161 C; 1019 G; 923 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated Aquatic polyvalent cation-sensing receptor - used to develop products for increasing or decreasing the salinity toleran of fish for use in aquaculture claim 2; Fig 4A-F; 57pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-MAR-1998 (first entry)

Dogfish shark kidney calcium receptor related protein cDk
Calcium receptor related protein; CaR-RP; dogfish shark;
polycation-sensing receptor; aquaculture; fish farming;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               T89290;
27-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 97-489640/45.
P-PSDB; W32059.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     salinity tolerance; ss.
                    1616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Brown
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27-MAR-1996; US-622738
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   T89290 standard;
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Brown E, Harris HW, Hebert S:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 932
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acctgccagccttgtggaacagaagaatgggcccctgaggggagctcagcctgcttctca
                                                                                                                                                                                                                        ctagacataaataagacaaaatccagtggcacgggaagaacaatcaggtgcctgtgtca 1498
                                                                           tgotgottogagtgoatgocotgtgaagotgggacatttotoaacaogagtgagottoao
                                                                                                                                                        gtgtgtaccagggactgtctcgaagggcaccacaggttggtcat---gggttcccaccac 1555
                                                                                                                                                                                                   CTCAACATCAACGAAAAGAAAATCCTCTGGAGTGGCTTCTCCAAAGTGGTTCCTTTCTCC 2079
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                                                                                                                              AACTGCAGTCGAGACTGTGCCGGGCACCAGGAAGGGGATCATCGAGGGGGAGCCCACC
                                                                                                                                                                                                                                                                           514;
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                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers 439. .3519
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4076. .4113
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                                                                                                                                                                                                                                                                                            5.8%;
47.5%;
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                                                                                                                                                                                                                                                                                            Score 150.8; DB 1 Pred. No. 1.6e-29;
                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                              DB 1;
                                                                                                                                                                                                                                                                           562;
                                                                                                                                                                                                                                                                                                           Length 4131;
                                                                                                                                                                                                                                                                           Indels
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1676 2200

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08-MAY-1998 (first entry)
Rat kidney cell calcium receptor 3A; RakCaR 3A;
Rat kidney cell calcium receptor 3A; RakCaR 3A;
calcium homeostasis; hyperparathyroidism; osteo;
Rattus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   attototgoogtocagaactoaacaacaagaacactttoaggootocatocaggaotac
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                                                                                                                                standard; cDNA to mRNA;
     Location/Qualifiers
                                                                                                                                  4131
                                      osteoporosis;
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                                                                    Qy
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                                      밁
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Best Local Similarity
Matches 502; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-JUN-1995; 485588.
07-JUN-1995; US-484588.
23-AUG-1991; US-749451.
11-FEB-1992; US-834044.
21-AUG-1992; US-934161.
12-FEB-1993; US-009389.
23-FEB-1993; US-009389.
23-FEB-1993; US-141248.
22-OCT-1994; US-292827.
21-OCT-1994; US-353784.
(BGHM) BRIGHAM & WOMENS (NPSP-) NPS PHARM INC.
BTOM EM, FRIGHCY FH, GAIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US5688938-A.
18-NOV-1997.
07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The specification includes details of molecules that can modul one or more inorganic ion receptor activities, and antibodies antibody fragments targetted to inorganic ion receptor protein proteins, nucleic acids and antibodies may be used to treat disorders by modulating one or more inorganic ion receptor activities, preferably disorders of calcium homeostasis, e.g. sequence 4131 BP; 987 A; 1170 C; 1053 G; 921 T;
                                                                                                                                                                                   2434
                                                                                                                                                                                                                                                                                                                                                                                                                                                1556
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA encoding calcium receptor polypeptide(s) - useful for therapeutic purposes, e.g. hyperparathyroidism and osteopt Claim 15; Columns 133-142; 1799; English. The present sequence encodes rat kidney ceil calcium receptor 3A (RakCaR 3A).
 1916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P-PSDB; W38275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 98-008040/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ctagacataaataagacaaaaatccagtggcacgggaagaacaatcaggtgcctgtgtca 1498
                                                                                                                                                                                                              acgctattgctgctgctgattgggactgctggcctgtttgcctggcgtcttcacacg
                                                                                                                                                                                                                                                                                                                                                                                                                            tgctgcttcgagtgcatgccctgtgaagctgggacatttctcaacacgagtgagcttcac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gtgtgtaccagggactgtctcgaagggcaccacagggttggtcat---gggttcccaccac
GTGCTGGGCCATTTTCCTGACCGCCTTTGTGCTGGGTGTCTTCATCAAGTTCCGAAACACA
                                                                                                                                                                                                                                                                                         cgcaccgtggagttcttggggtggcatgaacccatctctttggtgctattagcagctaac
                                                                                                                                                                                                                                                                                                                                   GCCTGTGACAAGTGCCCGGATGACTTCTGGTCCAATGAGAACCACACTTCTTGCATTGCC
                                                                                                                                                                                                                                                                                                                                                                   acctgccagccttgtggaacagaagaatgggcccctgaggggagctcagcctgcttctca
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTCTTCATCAATGAGGAGAAGATCTTGTGGAGTGGGTTCTCCAGAGAGGTGCCTTTCTCC
                                      TGCTTCTCCAGCTCCTTGTTCTTCATTGGGGAGCCCCAGGACTGGACGTGCCGCCTGCGA
                                                             gggagttgcagcctctacagcttcttcgggaagcccanggtgcccgcgtgcttgctgcgt
                                                                                                            CCTATCGTCAAGGCCAACCGAGAACTGTCCTACCTCCTGCTCTTCTCCCTACTCTGC
                                                                                                                                                                                                                                                            AAGGAGATTGAGTTTCTGGCGTGGACCGAGCCCTTTGGAATCGCTCTCACTCTTTTGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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/product=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5.4%;
46.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 138.2; DB 1
Pred. No. 2.9e-26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JΞ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hebert
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
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Дb QY 망 Ş B QΥ g Qy Вb γQ В 20

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                                                                                        07-JUN-1995; US-484565.

23-AUG-1991; US-749451.

11-FEB-1992; US-834044.

21-AUG-1992; US-934161.

12-FEB-1993; US-017127.

23-FEB-1993; US-009389.

22-OCT-1994; US-292827.

21-CCT-1994; WO-012117.

21-CCT-1994; WO-012117.
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09-JUN-1998.
07-JUN-1995;
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Calcium receptor poly:peptide(s) -
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                                   n EM, Garrett JE, Hebert SC: 98-347412/30.
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parathyroid hormone;
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Matches 502; Conserv
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The rat kidney calcium receptor gene encodes a 1079 amino acid protein. The tissue from which this receptor and receptors from bovine parathyroid and rat kidney are derived, respond to changes, and control changes, in calcium ion concentration, e.g. parathyroid hormone regulates Ca2+ homeostasis in blood and extracellular fluid, and kidney function alters through changes in Ca2+ levels in juxtaglomerular and proximal tubule cells in the kidney. The purified receptors (produced recombinantly) can be used to screen for compounds that modulate calcium receptor activity, especially those that can be used to treat diseases associated with the receptors in these tissues. They can also be used to raise antibodies for use in detection assays.

Sequence 4131 BP; 988 A; 1170 C; 1052 G; 921 T;
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Search completed: March 18, 2000, 19:00:09 Job time: 3012 sec

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Title:
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-2223.608 Million cell updates/sec
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50: gb_pl3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

REFERENCE	ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	LOCUS	AF127389	KENOLI L
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. 1 (bases 1 to 2520)	Rattus norvegicus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;	Norway rat.		AF127389.1 GI:4337085	AF127389	Rattus norvegicus putative taste receptor TR1 mRNA, partial cds.	AF127389 2520 bp mRNA ROD 04-MAR-1999		

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JOURNAL
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Best Local Similarity 91.1%;
Matches 2301; Conservative
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Submitted (10-FEB-1999) Taste and
Drive MSC 1188, Bethesda, MD 2089;
Drive MSC 1187 Mnsalfflers
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Zuker,C.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 (bases 1 to 2520)
Hoon,M.A., Adler,E., Lindemeier,J.,
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LHGDCLQVRHRPLVTSCDRPDSFNGHGYHLFQAMRETVEEINNSSALLPNITLGYELY
DVCSESANVYATLRVLALGGFRHIEIGKDLRNHSSKVVAFIGFDNTDHAVTTAALLGF
FLMPLVSYEASSYVLSAKRKFESELRTVESDRHGYEVMYQLLQSFGWYMISLIGSYGD
YGQLGVGALEBLAVPRGIGVAFKDIVEFSARVGDPRMGMGHLAQARTTYVVVFSR
HLARVFFRSVVLANLIGKVWVASEDWAISTITSVTGIGOIGTVLGVAVQGQQVPGLK
EFEESYVRAVTAAPSACPEGSWCSTNOLCRECHTFTTRNMFTLGAFSMSAAYRVEAV
YAVAHGLHQLLGCTSEICSRGPVYPWQLLQQIYKVNFLLHENTVAFDDNGDTLGYYDI
IAWDWNGPEWTFEIIGSASLSFVHLDINKTKIQWHGKNNQVPVSYCTTDCLAGHHRVV
VGSHHCCFECVPCEAGTFLNMSELHICQPGGTEEMAPKESTTCFFRTVEFLAWHEPIS
LVLIAANTLLLLLLYGTAGLFAWHFHTPVVRSAGGRLCFUMLGSLYAGSCSFYSFGE
PTVPACLLRQPLESLGFAIFLSCLTIRSFQLVIIFKFSTKVPTYFTWAQNHGAGLFV
IVSSTVHLLICLTWLYMWTPRFTREYQRFPLVILECTEVNSVGFLLAFTHNILLSIS
TFYCSYLGKELPENYNEAKCVTTSLLNHFVSWLAFFTMASIYGGSYLPAVNVLAGLTT
LSGGFSGYFLPKCYVILCRPELNNTEHFQASIQDYTRRCGTT"

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/protein_id="AAD18069.1"
/db_xref="GI:4337086"
/trans1=+1-- "...
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/strain="Wistar"
/db_xref="taxon:10116"
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                                                                                                               GATGACAACGGGGACACTCTAGGTTACTACGACATCATCGCCTGGGACTGGAATGGACCT
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Pred. No. 6.4e-81;
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2231 TGCTGGGGTTTCAGCTTGGCTTACATGGGGAAGGAGCTGCCAACTACAACGAAGCCAACTACAACGAAGCAACCAAC	20 DD		1138 ccatgagoctgctacaatgtgratgaggctgtgtatgtgtgtgccacggcccacc 1217 1154 GGGAGCGCGTGGTCTACAGCGTGTACTCGGCAGTTTACGCGGTGGCCCATGCCCCACA 1213 1218 agctcctgggatgtacctctgggacctgtgccagaggcccagtctacccctggcagcttc 1277 1214 GACTCCTCGGCTGTAACCGGGTCCGCTGCACCAAAAAGGTCTACCCGTGGCAGCTAC 1278 ttcagcagatctaccaggtgaatttccttctacataagaagactgtagcattcgatgaca 1337 1278 ttcagcagatctacaaggtgaatttccttctacataagaagactgtagcattcgatgaca 1337 1274 TCAGGGAGATCTGGCACGACCTACGCTCGGGTAACCGGTCTTTGACCAAC 1333 1338 agggggacctctaggttattatgacatcatcgcctgggactggaatggacctgaatgga 1397 1
2112 tytygaccccacggcccaccacggagtaccagcgcttcccccatctgytyattcttgagt	\$\$\$ \$\$\$ \$\$\$	44. 8 4. 1	tccaggcagtgatgggtgctcccagaacttgcccagaggggtcctggtgcggcactaacc
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1755 tgattgggactgctggcctgtttgcctggggcttcaacqccctgttgtgaggtcaagtg 1751 CACTGGCCATTCTTTCATCTTCTGGAGACATTTCCAGACACCCATGGTGCGCTCGGCCG 1815 ggggtaggctgtgcttcctcatgctgggttccttgtagctggagttgcagcctctaca 1816 gggtaggctgtgcttcctcatgctgggttccttgtagctggagttgcagcctctaca 1811 GTGGCCCATGTGCTTCCTGATGCTCGTGCCCTGCTGCTGCGGTTTGGGATGGTGCCCG 1813 GGttttttaggaagaagaagaagaagaagaagaagaagaaga	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		696 tggaggagctggccactccacggggcatctgcgtcgccttcaaggacgtggtgcctct- 754
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                                                                                                                                                                                                                                                                                                                                                                    Primer A: CTCACCACAGGGGTGTCTAG
Primer B: TGCTGTTTTTGGCTTTGC
STS size: 124
PCR Profile:
                                                                                                                                                                                                                                                                                                                                                                                                                               The University of Iowa Department of Pediatrics, Tel: (319) 356-3508
Fax: (319) 356-3347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cooperative Human Linkage Center Unpublished (1995)
Synonyms: GCT15G02, CHLC.GCT15G02.T16713
Contact: Dr. Jeffrey C. Murray
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Catarrhini; Hominidae; Homo.

1 (bases 1 to 270)

Murray, J., Sheffield, V, Weber, J.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STS sequence; primer; sequence tagged site.
human vector=pJCPl host=E.coli dut+ung+ (DH10B) Marker
genomic DNA prepared from XY individual of French natio
                                                                                                                                                                                                                                     Buffer:
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STS CHLC.GCT15G02.
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KC1: 50mM

Tris: 10mM

pH: 8.3

Location/Qualifiers

1.270
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95. .218
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ATCATCGAGTATTTCCGCTGGAACTGGGGTGGGCACAATTGCAGCTGATGACGACTATGGG
                                  ctgctgcagagcttcggctgggtctggatctcgctcgttggcagctatggtgactacggg
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Brown, E.M., Hebert, S.C. and Garrett, J.
Calcium receptor-active molecules
Patent: US 5763569-A 3 09-JUN-1998;
Location/Qualifiers
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rom patent
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1666	1607 gagcttcacacctgccagccttgtggaacagaagaatgggcccctgaggggagctcagcc	Qy
2103	CCACCTGCTTCGAGTGTGTGGAGTGTCCTGATGGGGAGTATAGTGATGAGACA	DЪ
1606	gctgggacatttctcaacacgagt	Qy
2043	1990 CCCTCTCCCAACTGCAGCCGAGACTGCCTGGCAGGGACCAGGAAAGGGATCATTGAGGGG	B 2
98	924 GGAGAAAGACTCTTCATCAACGAGGAGAAAATCCTGTGGAGTGGGTTCTCCAGGGAGGTG	망
1489	30 ccagttcatctagacataaataagacaaaaatccagtggcacgggaagaacaatcaggtg	Qy
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36	677 cagctgggcgtacaggcgctggaggagctggccactccacggggcatctgcgtcgccttc	γ Q

RESULT 5
AR028467
LOCUS
DEFINITION
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VERSION
KEYWORDS
SOURCE
ORGANISM

AR028467 3809 bp DNA Sequence 3 from patent US 5858684. AR028467 AR028467.1 GI:5940440

PAT

29-SEP-1999

REFERENCE AUTHORS

Unknown.
Unknown.
Unknown.
Unclassified.
Unclassified.
1 (bases 1 to 3809)
1 Nemeth, E.F., Brown, E.M., Hebert, S.C., Garrett, J.E. Jr., Van Wagenen, B.C., Balandrin, M.F. and Del Mar, E.G.

1967 cgctccttccaactggtcatcatcttcaagttttctaccaaggtacccacattctaccac 202
1967 cgctccttccaactggtcatcatcttcaagttttctaccaaggtacccacattctaccac 202
1967 cgctccttccaactggtcatcatcttcaagttttctaccaaggtacccacattctaccac 202
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1967 ogotoottocaactggtcatcatcttcaagttttctaccaaggtacccacattctaccac 202
1967 ogotoottocaactggtcatcatcttcaagttttctaccaaggtacccacattctaccac 202
1967 cyctcottocaactyytcatcatcttcaayttttctaccaayytacccacattctaccac 202
Db 2404 CGCCTGCGCCAGCCGCCTTTGGCATCAGCTTCGTGCTCTGCATCTCATGCATCCTGGTG 2463
Qy 1907 ttgctgcgtcagcccctctttcctctcgggtttgccattttcctctcctgtctgacaatc 1966
Db 2344 CTGCTCTGCTGCTTCTCCAGCTCCCTGTTCTTCATCGGGGAGCCCCAGGACTGGACGTGC 2403
ggtagctgggagttgcagcctc
Db 2284 CGCAACACCCATTGTCAAGGCCACCAACCGAGAGCTCTCCTACCTCCTCCTCCTCTCTCC 2343
Qy 1787 cttcacacgcctgttgtgaggtcagctgggggtaggctgtgcttcctcatgctgggttcc 1846
Db 2224 CTCTTTGCCGTGCTGGGCATTTTCCTGACAGCCTTTGTGCTGGGTGTGTTTATCAAGTTC 2283
Qy 1727 gcagctaacacgctattgctgctgctgctgattgggactgctggcctgtttgcctggcgt 1786
Db 2164 TGCATTGCCAAGGAGATCGAGTTTCTGTTCGTGGACCCCTTTGGGATCGCACTCACC 2223
Qy 1667 tgcttctcacgcaccgtggagttctttggggtggcatgaacccatctctttggtgctatta 1726
Db 2104 GATGCCAGTGCCTGTAACAAGTGCCCAGATGACTTCTGGTCCAATGAGAACCACACCTCC 2163

L1 3809 ACTION OF THE PROPERTY OF THE PROPERT	PARTURES LOCATION/OWALIFIERS BASE COUNT 910 a 1071 c 979 g ORIGIN OUELY MATCH Matches 1130: Conservative 0: Mismatt Oy 266 gagatasacaactccacaagctctgctcccacactcacactcacactcacactcacacactccacactcacactcacactcacactcacacacactcacacactcacacactcacacactcacacactcacacactcacacactcacacactcacacacactcacacactcacacactcacacacactcacacacactcacacacactcacacactcacacacactcacacacactcacacacactcacacacactcacacacactcacacacactcacacacactcacacacactcacacacactcacacacacactcacacacactcacacacacacacactca
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Best Local Similarity 46.3%;
Matches 1130; Conservative
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                  ATTGATTCTTTGAACCTTGATGAGTTCTGCAACTGCTCAGAGCACATTCCCCTCTACGATT
                                             -- agggacaggccacctagagatgcagagatcttcgcaaccactcctccaaggtggtg
                                                                             ACTTGCAACACCGTTTCTAAGGCCTTGGAAGCCACCCTGAGTTTTGTTGCTCAAAACAAA
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                                                                                                                                                                                                                                                                                                                                                                                                l (bases 1 to 3809)
Brown,E.M., Fuller,F.H., Hebert,S.C
Calcium receptor-active molecules
Patent: US 5688938-A 3 18-NOV-1997;
Location/Qualifiers
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TGTATCAGGTATAATTTCCGTGGGTTTCGCTGGTTACAGGCTATGATATTTGCCATAGAG 265
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1 (bases 1 to 3361)
Aida, K., Koishi, S.,
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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SSKSNSSDPFPQPERQKQQQPLALTQOEQQQQPLCKQKVIFGSCT
VTFSLSFDEPQKNAMAHRNSTHQNSLEAQKSSDTLTRHQPLLPLQCGETDLDLTVQET
GLQGPVGGDQRPEVEDPEELSPALVVSSSQSFVISGGSTVTENVVNS*
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AFGISEVLCISCILVKINRVLLVEEAKIPTSEHKKMWGINLQELLVFLCCEMQIVICV
IWLYTAPPSSYRNOELEELIFITCHEGSLMALGELIGYTCLLAAICPFPAFKSRKLP
ENFNEAKFITESMLIFFIVMISFIPAYASTYGKFVSAVEVIAILAASFGLLACIFFNK
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Qy 2147 ttcccccatctggtgattcttgagtgcacagaggtcaactctgtgggcttcctggtggct 2206	9 1	tytcacyctttcacyacatygaacatycccyaycttgyayccttctccatyaycgctycc
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QY 1967 cyctcottccaactgytcatcatcttcaagttttctaccaagytacccacattctaccac 2026	· · · · · · · · · · · · · · · · · · ·	1024tgaagagtcctatgtccaggcagtgatg1052
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Indels Length

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2 (bases 1 to 3783)
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Submitted (07-FEB-1995) James E. Garrett, Molecular Biology, NPS Submitted (07-FEB-1995) James E. Garrett, Molecular Biology, NPS Pharmaceuticals, Inc., 420 Chipeta Way, Salt Lake City, UT 84108
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                                                                                                                                                                                                                                                                                              GenBank staff at the National Library of Medicine created entry [NCBI gibbsq 179653] from the original journal artic This sequence comes from Fig. 6.
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theria; Primates; Catarrhini; Hominidae; Homo.
(bases 1 to 3234)
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                                                                         /note="calcium-sensing reco
join(1. 185,493. 769)
/gene="CaSR"
/note="This sequence comes
           /product="calcium-sensing receptor
/protein_id="AAB46874.1"
/db_xref="GI:1836095"
                                                                                                                                                                                                                  /organism="Homo sapiens'
/db_xref="taxon:9606"
                                                             /codon_start=
                                                                                                                                        /gene="CaSR"
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translation="MAFYSCCWVLLALTWHTSAYGPDQRAQKKGDIILGGLFPIHFGV"
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KKYHRKSYHNGFAKEFWEETFNCHLOBGAKGPLPVDTFLRGHEESGGRFSNSSTAFR
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INLYTAFPSSYRNOELEDEIIFITCHEGSLAALGFLIGKTCLLAAIGFFRKSKIK
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INILFKPSRNIFETVWISFIPAYASTYGKEVSAVEVIAILAASFGLLAGIFFRK
INILFKPSRNIFEEVRGSTAAHAFKVAARAILRRSNVSRKRSSSLGGSTGSTPSSSI
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/product="calcium-sensing receptor"
/prodein_id="AAB46873.1"
/prodein_id="AAB46873.1"
/db_xref="Gi:1838694"
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VTFSLSSDEPOKNAMAHRNSTHONSLEAOKSSDTLTRHOPLLPLOCGETDLDLTVOET
GLOGPVGGDQRPEVEDPEELSPALVVSSSQSFVISGGGSTVTENVVNS"
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AGTGWAQLQLMTTMGGRGLRNSERKLRKGISASTSVNSSPSTLMRKRSSMW"
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/note="longer_isoform.
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Direct Submission
Submitted (16-AUG-1994) S.H.S. Pearce, MRC Molecular Medicine Group, Collier Bldg, Royal Postgrad Med School, London W12 ONI revised by [3] MAT 2 (bases 1 to 3234)
                                                                                           Eukaryota; Metazoa; Chordata; Vertebrata; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 3234)
                                                                                  Pearce, S.H.S.
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Location/Qualifiers
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PLCTGDENISSVETPY LDYTHLRISYNYLAVE SLAHALQDIYTCLPGGELFTNGSCA
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GYYNVZAKKGERLF INEEK ILMSGFSREVPFSNCSRDCLAGTRKGI IEGEPTCCFECV
ECPDGEY SDETDASACNKCPDDFWSNENHTSCIAKE IEFLSWTEPFGTALTLFAVLGI
FLTAFVLGVFIKFNNTPIVKATNRELSYLLFSLLCCFSSSLFFIGEPDDMTCRLRQP
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INLYTAPPSSTRNQELEDEII FITCHEGSLMALGFLIGYTCLLAAICFFFAFKSRKLPI
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/chromosome="3"
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Query Match 6.4
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Matches 1129; Conservative tctgacagcttcaacggccatggctatcacctcttccaagccatgcggttcaccgttgag tttctgatgcccctggtcagctatgaggcgagcgagcgtgatcctcagtgggaagcgcaag gtgtgctcagagtcttccaatgtct---atgccaccctgagggtgcccgcccagca----GAGATAAACAGCAGCCCAGCCCTTCTTCCCAACTTGACGCTGGGATACAGGATATTTGAC gagataaactaccacagototgottoccaacatcacootggggtatgaactgtatgac TGTATCAGGTATAATTTCCGTGGGTTTCGCTGGTTACAGGCTATGATATTTGCCATAGAG GCTGTGGTGGGAGCAACTGGCTCAGGCGTCTCCACGGCAGTGGCAAATCTGCTGGGGCTC gcactcattgggcctgataacactgaccacgctgtcaccactgctgccctgctgagccct ATTGATTCTTTGAACCTTGATGAGTTCTGCAACTGCTCAGAGCACATTCCCTCTACGATT ACTTGCAACACCGTTTCTAAGGCCTTGGAAGCCACCCTGAGTTTTGTTGCTCAAAACAAA --agggacaggccacctagagatgcagagatcttcgcaaccactcctccaaggtggtg 6.48; 46.38; 0; Score 164.6; DB 9; Pred. No. 1.1e-26; 0; Mismatches 1144; Length Indels 3234; 168; Gaps 496 417 436 357 297 325 237 379 11;

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1429 1551	1385 ggacctgaatggacctttgaggtcattggttctgcctcactgtct:	Db Db
1384 1491	tcatcgcctgggactggaat CATCAACTGGCACCTCTCC	dg VQ
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	.232 acctotyggacoty	dg VQ
\vdash ω	172 tacaatytytatyagyctytytatyctytygycccacygcotccaccagotcctyggatyt	dd VQ
1171 1251	acatgcccgagcttggagccttctccatgagcgctgcc 	Оy
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976 951	ggacggtg GCGGCACC	Qy Db
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856 831	797 cgtctggctcgagccaggaccaccgtggtcgttggtcttctctaaccggcacctggctgg	Db Oy
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736 717	gctggaggagctggccactccacggggcatctgcgtcgccttc 	Оу
676 657	617 ctgctgcagagcttcggctgggtctggatctcgctcgttggcagctatggtgactacggg (Оy
616 597	557 ttcccgtccttcttgcgcaccatccccagcgataagtaccaggtggaagtcatagtgcgg	ду
537	78 TTCTACATTCCCCAGGTCAGTTATGCCTCCTCCAGCAGACTCCTCAGCAACAAGAATCAA	Дb

RESULT AF1101 LOCUS	Qy Db	ДЪ	Db Qy	Оy	Qy Db	Qy	Qy	Qy Db	Qу	dd VQ	da VQ	Db Qy	ρρ	Db Db	dg VQ	Оy	Qy Qy
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AF110179	tgctacgtgattct ATCTACATCATTCT	aatgtgctggcagg GAGGTGATTGCCAT	tcctggatcgcttt GTCTGGATCTCCTT	ctgccggageacta CTGCCGGAGAACTT	ttogcacacaacat ATCGGCTACACCTG	tteccccatctggt GAGGATGAGATCAT	tteetetgteteae GTCATCTGTGTGAT	acttgggcccaaaa AAGTGGTGGGGGCT	cgctccttccaaci	ttgetgegteageec	ttggtagctgggag 	cttcacacgcctg1 CGCAACACCCCAC	gcagctaacacgct	tgetteteaegead 	gagetteacacets	teceaceactgetget	cctgtgtcagtgt:
4319 bp	ctgccgtcc	getggecae ccrggcage	cttcaccat	taacgaagc CAATGAAGC	cetectete CCTGCTGGC	gattettga CTTCATCAC	gtggettge CTGGCTCTA	ccatggtgc CAACCTGCA	rtggtcatcat rccrccrggr	setettt secenns	ttgcagcct 1 CTCCAGCTC	gttgtgaggtc ATTGTCAAGGC	attgctgct GGGCATTTT	accgtggagttct GAGATCGAGTTTC	gccagccttg 	tcgagtg TGAGTG	gtaccagggac GCAGCCGAGAC
mRNA	agaactcaacaacacaga ATCCCGCAACACCATCGA	tctgagtggcggcttcag CAGCTTTGGCTTGCTGGC	gtccagcatttaccaggg	caaatgtgtcaccttcag CAAGTTCATCACCTTCAG	catcagcacctttgtctg TGCCATCTGCTTCTTCTT	gtgcacagaggtcaactct 	aatgtggaccccccccggcc ACCGCGCCCCCCTAAG	ggaatattogtcatto	cttcaagttttctaccaag	tetetegggtttgeeatttte 	ctacagottottogggaagoco 	agetgggggtaggetgtget 	gctgctgattgggactgct CCTGACAGCCTTTGTGCTG	tggggtggcat rercereeace	tggaacagaagaatgggco 	catgccotgtgaagotgg 	otgtotogaagggcaccao
ROD	2487 2609	cggctatttc GTGCATCTTC	cagctaccta 	catgctcctc	cagctacctg	gtgggctt ATGGCCCT	caccagggag CTACCGCAAC	teagetecaes	ggtacccaca CCCCACCAGC	ctctcctg ATCTCATG	gcccacggtgc GCCCCAGGACT	cttcctcatgctgg CTACCTCCTCCTCT	ggcctgtt GGTGTGTT	gaacccatctctttgg -	cctgaggg AATGAGAA	gacatttct GGAGTATAG	caggttggtc GAAAGGGATC
02-MAY-19		CTTCAACAAG	acccgcggtc PTCTGCCGTA	ccacttcgta TTCTTCATC	gggtaaggaa srcccggaag	cctggtggct 	ytaccagcgc CCAGGAGCTG	ggtccatttg CATGCAGATT	attetaceae TTCCACCGC	rtctgacaatc CATCCTGGTG	geeegegtge TEGACGIGC	getgggttee CCTCTTCTCC	tgcctggcgt 	ggtgctatta CGCACTCACC	gageteagee 	Caacacgagt - - TGATGAGACA	catgggt carmgagggg
99		2445 2568	2386 2508	2326 2448	2266 2399	2206 2328	2146 2268	2086	2026 2148	1966 2091	1906	1846 1971	1786 1911	1726 1851	1666 1791	1606 1731	1546 1671

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                                                                                                                                                 CAGGTATAACTTCCGTGGATTCCGATGGTTACAAGCCATGATCTTTTGCCATAGAGGAGAT
                  TAACACCGTCTCCAAGGCTCTGGAGGCCACCTTGAGTTTTGTTGCCCCAGAACAAATCGA
                                 AAACAGCAGCCCCCCCCTTCTTCCCCAACATGACTCTGGGATATAGGATATTCGACACCTG
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
1 (bases 1 to 4319)
1 (bases 1 to 4319)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (10-NOV-1998) 190 Dermatology, VA Medical Center Francisco, 4150 Clement Street, San Francisco, CA 94121, US
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DIKKVERMQVPFSNCSKDCQAGTRKGILEGEFYCCFECVECPDGEYSGETDASACDKC
PDDFRSNENTSCIAKEIEFLAWTEBPGIALTLFAWLGIFILTARFVLGVFIKENNTPILV
KATNRELSYLLLESLLCCFSSSLFFIGEPQDMTCRLRQPAFGISFVLCISCILVKTNR
VLLVFERKIFTSSHRKWGLKLQFLVFLCTFMOIVICIIMLTAPPSSYRNHELEDE
IIFICHEGSIAMALGSLIGYTCLLAALGFFIRKSRKLPENFNEAKFITFSMLIFFIV
WISFIFAYASTYGKFVSAVEVLAILGFFFAKSRKLPENFNEAKFITFSMLIFFIV
WISFIFAYASTYGKFVSAVEVLAILGFFTAKSRKLPENFNEAKFITESMLIFFIV
TAAHAFKVAARATLRRENISKRASSSLGGSTGSNFSSSISKKNSEDREPGERGKOU
                                                                                                                                                                                                                                                                                                                      QPLALTQQEQQQQPTITLQPQQQQQPQQPRCKQKVIFGSGTVTFSLSFDEPQKNAMAHR NSMRQNSLEAQKSNDTLNRHQALLPLQCAEADSEMTIQETGLQGPMYGDHQPEIESPD EMSPALYVSTSRSFYISGGGSSYTENILHS"
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EPLIKEIVRRNITGRIWLASEAWASSSLIAMPEYFHVVGGTIGFGLKAGQIPGFREFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="mawfgyclallautwhssaygpdqraqkkgdiilgglfpihfgy
aakdqdlksrpesyecirynfrgfrwilqamifaieeinsspallpnwilgyrifdicn
tyskaleatlsfyaqnkidslnldefcncsehipstiayygatgsgystayanllglf
yipqysyasssrllsnknqfksflrtipndehqatamadiieyerwnwygtiaadddy
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525. .3533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="calcium-sensing receptor"
/protein_id="AAD28372.1"
/db_xref="GI:4731165"
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/strain="C57BL/6"
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1649 AAGTCACGAGGAAGGCGGCAACAGGTTACTCAATAGCTCCACTGCCTTCCGACCCCTCTG 1007 TATCCCCCAGGTGAGCTACGCCTCCTCTAGCAGGCTTCTCAGCAATAAGAACCAGTTCAA 1066 gagcgctgcctacaatgtgtatgaggctgtgtatgctgtggcccacggcctccaccagct 1221 gtgcagggagtgtcacgctttcacgacatggaacatgcccgagcttggagccttctccat 1161 GGCCAGTTCCTCCCTGATTGCCTATGCCTGAGTACTTCCATGTAGTCGGGGGGTACCATTGG CCAGAACTCTACAGCCAAGGTCATTGTCGTTTTCTCCAGCGGCCCAGACCTAGAACCTCT ccagtggcacgggaagaacaatcaggtgcctgtgtcagtgtgtaccagggactgtctcga GCACGCCTGCAAGATATATACACCTGC ggaccctctaggttattatgacatcatcgcctgggactggaatggacctgaatggacctt GATATCCTACAACGTGTACT----gcagatctacaaggtgaatttccttctacataagaagactgtagcattcgatgacaaggg cctgggatgtacctctgggacctgtgccagaggcccagtctacccctggcagcttcttca 1281 ggcagtgatggtgctcccagaacttgcccagaggggtcctggtgcggcactaaccagct GTTCGGTCTGAAGGCTGGGCAGATTCCAGGCTTCCGAGAATTCCTACAGA---AAGTCCA ggtggccatccagcagagacaagtccctggcctgaaggagtttgaagagtcctatgtcca ggccatctccacgtacatcaccaatgtgcccgggatccagggcattgggacggtgctggg cttcaggtctgtggtgctggccaacctgactggcaaagtgtggatcgcctccgaagactg cgtggtgcctctctccgcccaggcgggtgacccaaggatgcagcgcatgatgctgcgtct gggcgtacaggcgctggaggagctggccactccacggggcatctgcgtcgccttcaagga 741 CGAGTATTTCCGTTGGAACTGGGTGGGCACAATTGCAGCCGACGACTATGGCAGGCC 1186 gcagagcttcggctgggtctggatctcgctcgttggcagctatggtgactacgggcagct 681 GTCCTTCCTCCGCACCATTCCCAACGACGACGACCAGGCCACCGCGATGGCTGACATTAT 1126 gtccttcttgcgcaccatccccagcgataagtaccaggtggaagtcatagtgcggctgct 621 gatgcccctggtcagctatgaggcgagcagcgtgatcctcagtgggaagcgcaagttccc gcctgataacactgaccacgctgtcaccactgctgc-----cctgctgagcccttttct 501 CACGGGGGATGAAAACATCAATAGTGTCGAGACCCCTTACATGGGCTACGAACATTTACG CCACCTGCAAGACGGCGCAAAAGGACCTTTACCCGTGGAC TCCCAGGAAGTCTGTCCACAATGGTTTTGCCAAAGAGTTTTTGGGAAGAAACATTTAATTG -----GCTCATCTCCCAGTACTCTGATGAGGAAGAGATCCAGCAGGTGGTGGAAGTGAT TGGCATTGAGAAGTTCCGAGAGGAAGCCGAGGAGAGGGACATCTGCATTGACTTCAGCGA TTCTCTGAACCTGGATGAGTTCTGCAACTGCTCCGAGCATCCCTTCAACCATCGCAGT ccacctagagatgcagagatcttcgcaaccactcctccaaggtggtggcactcattgg ----TAGCCGTCTACTCCATTGC -TGCAGACATCAAGAAG -----ACCTTCGTGAG TTACCCGGAAGAGGGCTT 1401 1807 1341 1597 1101 1041 921 861 1246 1853 1768 1648 1537 1480 1420 1300 801 561 1887 981 1360 946

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Brown, E.M., Gamba, G., Riccardi, D., Lombardi, M., Butters, R., Kifor, O., Sun, A., Hediger, M.A., Lytton, J. and Hebert, S.C. Cloning and characterization of an extracellular Ca(2+)-sense receptor from bovine parathyroid Nature 366 (6455), 575-580 (1993)
94077182
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/note="This sequence comes from
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2965 CGTCTGGATCTCTTTCATCCCCGCCTACGCCAGCACTTACGGCAAGTTCGTCTCTGCCGT 2386 Caatgtgctggcagggctggccactctgagtggcggcttcagcggctatttcctccctaa	da Qy	
2905 2326	Оу	1231 tacctctggga
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2086 gttcctctgtctcacgtggcttgcaatgtggacccacgggcccaccagggagtaccagcg	Qy dd	cgacatggaacatgcccgagcttggagccttctccatgagcgctg
2026 cacttgggcccaaaaccatggtgccggaatattcgtcattgtcagctccacggtccattt	Qy Db	tgccagaggggtcctggtgcggcactaaccagctgtgcagggagtgtcacgctttca
1966 ocgotoottocaacotggtoatcatottoaagttttotaccaaggtacocacattotacca	ф	CCACCCCAGGAAGTCTGTCCCACATGGTTTTGCCAAGGAGTTTTGGGAAGAAAACATTTAA
1906 ottgotgogtoagococtottttototoggttttgocattttoctototgtotgacaat	Оу	976 gctgggggtggccatccagcagagacaagtccctggcctgaaggagtt 1024
1846 cttggtagctgggagttgcagcctctacagcttcttcgggaagcccacggtgcccgcgtg	Ду	916 agactgggccatctccacgtacatcaccaatgtgcccgggatccagggcattgggacggt 975
1786 2428	Ф	856 agtgttcttcaggtctgtggtgctggccaacctgactggcaaagtgtggatcgcctccga 915
1726 agcagctaacacgctattgctgctgctgctgattgggactgctggtgtgctgtttgcctggcg 1785	ду	
1666 otgottotcacgcaccgtggagttottggggtggcatgaacccatctotttggtgctatt	Оу	caaggacgtggtgcctctctccgcccaggcggtgacccaaggatgcagcgcatgatgct
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Brown,E.M., Hebert.S.C. and Garrett,J.
Calcium receptor-active molecules
Patent: US 5763569-A 1 09-JUN-1998;
Location/Qualifiers
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Nemeth,E.F., Brown,E.M., Hebert,S.C., Garrett,J.E.
Wagenen,B.C., Balandrin,M.F. and Del Mar,E.G.
Method of screening calcium receptor-active molecul
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                             CACTTGTAACACCGTCTCTAAAGCCTTGGAGGCCACCCTGAGTTTTGTGGCCCCAGAACAA
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Brown, E.M., Fuller, F.H., Hebert, S.C.
Calcium receptor-active molecules
Patent: CS 5588938-A 1 18-NOV-1997;
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Qy 2206 tttcgcacacaacatcctcctcctccatcagcacctttgtctgcagctacctgggtaagga 2265	
Qy 2146 cttcccccatctggtgattcttgagtgcacagaggtcaactctgtgggcttcctggtggc 2205	
Qy 2086 gttcctctgtctcacgtggcttgcaatgtggacccacggcccaccagggagtaccagcg 2145	
Qy 2026 cacttgggcccaaaaccatggtgccggaatattcgtcattgtcagctccacggtccattt 2085	
Qy 1966 ccgctccttccaactggtcatcatcttcaagttttctaccaaggtacccacattctacca 2025	
Qy 1906 cttgctgcgtcagcccctcttttctctctgggtttgccattttcctctcctgtctgacaat 1965	
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Qy 1786 tottcacacgcotgttgtgaggtcagctggggtaggctgtgcttcctcatgctgggttc 1845	
Qy 1726 agcagctaacacgctattgctgctgctgctgctgattgggactgctggtctgtttgcctggcg 1785	
Qy 1666 ctgcttctcacgcaccgtggagttcttggggtggcatgaacccatctctttggtgctatt 1725	
Qy 1606 tgagcttcacacctgccagccttgtggaacagaatgggcccctgagggggagctcagc 1665	
Qy 1546 ttcccaccactgctgcttcgagtgcatgccctgtgaagctgggacatttctcaacacgag 1605	
Qy 1489 goctgtgtcagtgtgtaccagggactgtctcgaagggcaccacaggttggtcatggg 1545	
Qy 1429 tocagttcatctagacataaataagacaaaaatocagtggcacgggaagaacaatcaggt 1488 	
Oy 1384 tggacctgaatggacctttgaggtcattggttctgcctcactgtc 1428	
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   /cgn2_5/ptodata/Z/ina/5C_COMB.seq:*
   /cgn2_6/ptodata/Z/ina/5D_COMB.seq:*
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US-08-943-986-3

2 US-08-943-986-3

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US-08-943-986-4

US-08-972-55-8

US-08-972-57-5

US-08-972-57-5

US-08-33-784-5

US-08-33-784-5

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PCT-US3-01640-1

PCT-US3-01640-1
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PCT-US94-14989-1	US-08-072-574-9	US-08-072-574-7	US-08-072-574-1	PCT-US91-09422-16	PCT-US91-09422-1	US-08-465-157-1	US-08-455-602-1	US-08-463-642-1	US-08-041-538-1	US-08-367-264-1	US-08-587-289A-4	US-08-687-289A-3
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ALIGNMENTS

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                                                                                   APPLICATION NUMBER: US/08/485,588
FILING DATE: 7 June, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA: including applic prior APPLICATION DATA: including applic prior APPLICATION NUMBER: 08/355,784
APPLICATION NUMBER: 08/355,784
APPLICATION NUMBER: 08/355,784
APPLICATION NUMBER: PCT/09/94/12117
FILING DATE: 21 October, 1994
APPLICATION NUMBER: U.S. 08/292,827
FILING DATE: 22 October, 1994
APPLICATION NUMBER: U.S. 08/41,248
FILING DATE: 22 October, 1993
APPLICATION NUMBER: U.S. 08/009,389
FILING DATE: 23 FEBTUARY, 1993
APPLICATION NUMBER: U.S. 08/017,127
FILING DATE: 21 FEBTUARY, 1993
APPLICATION NUMBER: U.S. 07/934,161
FILING DATE: 21 August, 1992
APPLICATION NUMBER: U.S. 07/934,044
FILING DATE: 11 FEBTUARY, 1993
APPLICATION NUMBER: U.S. 07/749,451
FILING DATE: 11 FEBTUARY, 1992
APPLICATION NUMBER: U.S. 07/749,451
FILING DATE: 11 FEBTUARY, 1991
ATTORNEY ACREST TEXPORMATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: Suite 4700
STREET: Suite 4700
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: Califor-
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MEDJUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: FASTSEO
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Edward M. Brown
APPLICANT: Steven C. Hebbert
APPLICANT: Forrest H. Fuller
APPLICANT: James E. Garrett, Jr.
TITLE OF INVENTION: CALCUUM RECEPTOR-ACTIVE
TITLE OF INVENTION: MOLECULES
                                                                   FILING DATE: 23 August, ATTORNEY/AGENT INFORMATION:
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                    NAME: Heber, Sheldon O. REGISTRATION NUMBER: 38,179
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION:
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: described below: 9
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TELECOMMUNICATION INFORMATION: TELEPHONE: (213) 489-1600

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TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5275 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 6.1%;
Best Local Similarity 47.3%;
Matches 501; Conservative
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LOCATION: 515..3769
OTHER INFORMATION:
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Pred. No. 5.5e-28;
0; Mismatches 553;
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Sequent No. 5/00-1
; Patent No. 5/00-1
; GENERAL INFORMATION:
; APPLICANT: Edward M. Brown
; APPLICANT: Steven C. Hebert
; APPLICANT: James E. Garrett, Jr.
APPLICANT: James E. Garrett, Jr.
CALCIUM RECEPTOR-ACTIVE
CALCIUM RECEPTOR-ACTIVE
CALCIUM RECEPTOR-ACTIVE
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US-08-484-565-1
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 APPLICATION NUMBER: U.S. 07/834
APPLICATION NUMBER: U.S. 07/834
FILING DATE: 11 February, 1992
APPLICATION NUMBER: U.S. 07/74
TTTING DATE: 23 August, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2915
                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2250
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FILING DATE: ATTORNEY/AGENT
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FILING DATE: 23 ru.
APPLICATION NUMBER: U.S. Ub, L.
APPLICATION NUMBER: U.S. 07/934,161
1992
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FILING DATE: 22 UCC...
APPLICATION NUMBER: U.S. UB/U.
APPLICATION NUMBER: U.S. UB/U.
APPLICATION NUMBER: U.S. UB/U.
1993
16.16.
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FILING DATE: 21 October, 1994
APPLICATION NUMBER: U.S. 08/292,827
FILING DATE: 23 August, 1994
FILING DATE: 23 August, 1994
                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: FILING DATE: 9 Dece
                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: U
ZIP: 9007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: First Interstate World
STREET: Suite 4700
STREET: 633 West Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     atcctctgccgcccagacctcaacagcacagagcacttcc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Los Angeles
California
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Lyon & Lyon
                                                                      21 August, 1992
JMBER: U.S. 07/834,044
                                                                                                                                                                                                                                                                                                          9 December,
                                                                                                                                                                                                                                                                                                                                                                                                                7 June,
                                                                                                                                                                                                                                                                                                                                                                                                                                     US/08/484,565
                                                                                                                                                                                                                                                                                                                           08/353,784
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 5275 base pair:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 5275 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 21:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1500
TELEPAX: (213) 955-0440
TELEX: 67-3510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1233 ctaaacataaatgagaccaaaatccagtggcacggaaagaaccaccaggtgcctaagtct 1292
2735 GCCATTTGGCTCAATACAGCGCCCCCCTCGAGCTACCGCAACCACGAGCTGGAGGACGAG
                          1890 ctaacttggctggtggtgtggaccccactgcctgctagggaataccagcgcttcccccat
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hes 501; Conserv
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APPLICANT: EGWARD
APPLICANT: EdWard
APPLICANE: Steven
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                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FASTEED
CURRENT APPLICATION DATA:
APPLICATION NUMBER: U5/08/480,751
FILLING DATE: 7 June 1995
CLASSIFICATION: 435
         APPLICATION NUMBER: 08/353,784
APPLICATION NUMBER: 9 December, 1994
APPLICATION NUMBER: PCT/US/94/12117
FILING DATE: 21 October, 1994
APPLICATION NUMBER: U.S. 08/292.827
FILING DATE: 23 AUGUST, 1994
APPLICATION NUMBER: U.S. 08/141,248
FILING DATE: 22 October, 1993
APPLICATION NUMBER: U.S. 08/009,389
FILING DATE: 23 February, 1993
APPLICATION NUMBER: U.S. 08/017,127
FILING DATE: 12 February, 1993
APPLICATION NUMBER: U.S. 08/017,127
FILING DATE: 12 February, 1993
APPLICATION NUMBER: U.S. 08/017,127
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ADDRESSE: Lyon & Lyon
STREET: First Interstate World Center
STREET: Suite 4700
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
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APPLICANT: EGWARD M. Brown
APPLICANT: Steven C. Hebert
APPLICANT: Forrest H. Fuller
APPLICANT: James E. Gerrett, Jr.
APPLICANT: James E. Gerrett, Jr.
TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
TITLE OF INVENTION: MOLECULES
UNMBER OF SEQUENCES: 20
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DATE:
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21 August,
                                                                                                                                                                                                                                                                                        A: including
A: described
08/353,784
                                                                                                                                                                                                                                                                                                                    application below: 9
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NAME/KEY: CDS
LOCATION: 515..3769
OTHER INFORMATION:
US-08-480-751-1
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INFORMATION FOR SEQ ID NO: 1:
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FILING DATE: 11 February, 1992
APPLICATION NUMBER: U.S. 07/749,451
FILING DATE: 23 August, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Heber, Sheldon O.
REGISTRATION NUMBER: 38,179
REGERENCE DESCRIPTION NUMBER: 38,179
     2675
                                                                                                 1770 caactaatcatcatcatcatgttttccaccaaggtacctacattctaccacgcctgggtc
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LENGTH: 5275 base pairs
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEPAX: (213) 955-0440
                                                                                                                                                                                                                                 2498 TGCTTCTCCAGCTCCCTGTTCTTCATCGGGGAGCCCCAGGACTGGACGTGCCGCCTGCGC
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nes 501; Conserv
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                                                                                                                                                      CAGCCGGCCTTTGGCATCAGCTTCGTGCTCTGCATCTCGTGCATCCTGGTGAAAACCAAT
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Pred. No. 5.5e-28;
0; Mismatches 553;
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APPLICANT: S
                                                                                                                                                                                                                           CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/484,565
                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                             SOFTWARE: FASTSEQ CURRENT APPLICATION DATA:
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CITY: L
               APPLICATION NUMBER: U.S. (FILING DATE: 23 February,
                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/943,986 FILING DATE: 03-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: First Interstate World
STREET: Suite 4700
APPLICATION NUMBER:
                                                                                                                                                                                          FILING DATE: 7-June-1995
APPLICATION NUMBER: 08/353,784
                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM:
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APPLICATION NUMBER: PCT/US/94/12117
FILING DATE: 21 October, 1994
APPLICATION NUMBER: U.S. 08/292,827
FILING DATE: 23 August, 1994
APPLICATION NUMBER: U.S. 08/141,248
FILING DATE: 22 October, 1993
***TOATION NUMBER: U.S. 08/09,389
***TOATION NUMBER: U.S. 08/09,389
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Steven C. Hebert
James E. Gairett, Jr.
VENTION: CALCIUM RECEPTOR-ACTIVE
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US-08-943-986-1
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Best Local Similarity
Matches 501; Conserv
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TELEPHONE: (213) 489-1600
TELEPAN: (213) 955-0440
TELEX: 67-3510
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APPLICATION NUMBER: U.S. 07/834,044
FILING DATE: 11 February, 1992
APPLICATION NUMBER: U.S. 07/749,451
FILING DATE: 23 August, 1991
ATTORNEY/AGENT INFORMATION:
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LOCATION: 515..37
OTHER INFORMATION:
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TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
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                                                       GTGCTGGGCATTTTCCTCACAGCCTTCGTGCTGGGCGTCTTCATCAAGTTCCGCAACACG
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                              CGGGTCCTCCTGGTGTTTGAG----GCCAAGATTCCCACCAGCTTCCACCGGAAGTGGTGG
                                                                                                                              CAGCCGGCCTTTGGCATCAGCTTCGTGCTCTGCATCTCGTGCATCCTGGTGAAAACCAAT
                                                                                                                                                                      IGCTTCTCCAGCTCCCTGTTCTTCATCGGGGAGCCCCAGGACTGGACGTGCCGCCTGCGC
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NUMBER: U.S. 07/934,161

21 August, 1992

NUMBER: U.S. 07/834,044

11 February, 1992
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Pred. No. 5.5e-28;
0; Mismatches 553;
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COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb st
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FASTSEQ
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/353,784
FILING DATE: 9 December, 1994
CLASSIFICATION DATA:
PRIOR APPLICATION DATA: including applic
PRIOR APPLICATION DATA: hocked below:
APPLICATION NUMBER: PCT/US/94/12117
FILING DATE: 21 October, 1994
APPLICATION NUMBER: U.S. 08/292,827
FILING DATE: 23 August, 1994
APPLICATION NUMBER: U.S. 08/41,248
FILING DATE: 22 October, 1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Edward F. Nemeth, Edward M.
APPLICANT: Brown, Steven C. Hebert,
APPLICANT: Bradford C. Van Wagenen, Manuel
APPLICANT: E. Balandrin, Forrest H. Fuller,
APPLICANT: Eric G. DelMar, and Scott T. Moe
TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
TITLE OF INVENTION: MOLECULES
NUMBER OF SEQUENCES: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Lyon & Lyon
STREET: First Interstate World Control of STREET: Suite 4700
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
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\: described below: 8
    PCT/US/94/12117
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Query Match 6.1%;
Best Local Similarity 47.3%;
Matches 501; Conservative
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INFORMATION FOR SEQ ID NO: 1:
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FILING DATE: 23 February, 1993
APPLICATION NUMBER: U.S. 08/017,127
FILING DATE: 12 February, 1993
APPLICATION NUMBER: U.S. 07/934,161
FILING DATE: 21 August, 1992
APPLICATION NUMBER: U.S. 07/834,044
FILING DATE: 11 February, 1992
APPLICATION NUMBER: U.S. 07/749,451
FILING DATE: 23 August, 1991
APPLICATION NUMBER: U.S. 07/749,451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1293 gtgtgttccagcgactgtcttgaagggcac---cagcgagtggttacgggtttccatcac
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LENGTH: 5275 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: (213) 489-1600 TELEFAX: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMÁTION:
NAME: Heber, Sheldon O.
REGISTRATION NUMBER: 38,179
REFERENCE/DOCKET NUMBER: 20
                                                                                                                                                                                                                                                                                               1590 cctgtggtgaggtcagcagggggccgcctgtgctttcttatgctgggctccctggcagca
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: CDS
LOCATION: 515..3769
OTHER INFORMATION:
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                                                   CAGCCGGCCTTTGGCATCAGCTTCGTGCTCTGCATCTCGTGCATCCTGGTGAAAACCAAT 2617
                                                                                     TGCTTCTCCAGCTCCCTGTTCTTCATCGGGGAGCCCCAGGACTGGACGTGCCGCCTGCGC
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Pred. No. 5.5e-28;
0; Mismatches 553;
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APPLICANT: Edward M. Brown
APPLICANT: Steven C. Hebert
APPLICANT: Forrest H. Fuller
APPLICANT: James E. Garrett, Jr.
TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
TITLE OF INVENTION: MOLECULES
                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 ME
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FASTEEQ
CURRENT APPLICATION DATA:
APPLICATION UNDER: US/08/485,588
FILING DATE: 7 June, 1995
                                      NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3095 ATCCTCTTCAAGCCTTCCCGGAACACCATCGAGGAGGTGC
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STREET: Suite 4700
STREET: 633 West Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 9007
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ER: PCT/US/94/12117
October, 1994
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Best Local S
Matches 498
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FILING DATE: 23 February, 1993
APPLICATION NUMBER: U.S. 08/017,127
FILING DATE: 12 February, 1993
APPLICATION NUMBER: U.S. 07/934,161
FILING DATE: 13 APPLICATION NUMBER: U.S. 07/834,044
FILING DATE: 13 AUGUST, 1992
FILING DATE: 13 AUGUST, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
TELLEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1233 ctaaacataaatgagaccaaaatccagtggcacggaaagaaccaccaggtgcctaagtct 1292
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 23 August, ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 3809 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: U.S. 07/834,044
FILING DATE: 11 February, 1992
APPLICATION NUMBER: U.S. 07/749,451
FILING DATE: 23 AUGUST, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: CDS
LOCATION: 373..3606
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
nes 498; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: FILING DATE: 22 OC
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                                   TGCTTCTCCAGCTCCCTGTTCTTCATCGGGGAGCCCCAGGACTGGACGTGCCGCCTGCGC
                                                                  CCCATTGTCAAGGCCACCAACCGAGAGCTCTCCTACCTCCTCCTCTTCTCCCTGCTCTGC
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TE: 23 August, 1994
TON NUMBER: U.S. 08/141,248
ATE: 22 October, 1993
ATE: 27 OKTOBER: U.S. 08/009,389
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Pred. No. 8.4e-27;
0; Mismatches 556;
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RESULT 7
US-08-484-565-3
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                               CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/484,565
FILING DATE: 7 June, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA: including approximate approxima
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MEDIUM TYPE: 3.5" Diskette, 1.44 %b
COMPUTER: IBM PC compatible
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APPLICANT: Steven C. Hebert
APPLICANT: James E. Garrett, Jr.
APPLICANT: James E. Garrett, Jr.
TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
TITLE OF INVENTION: MOLECULES
NUMBER OF SEQUENCES: 20
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STREET: Suite 4700
STREET: 633 West Fifth Street
                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM:
SOFTWARE: FASTSEC
    APPLICATION NUMBER:
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08/353,784
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Best Local Similarity 47.0%;
Matches 498; Conservative
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SEQUENCE CHARACTERISTICS:
LENGTH: 3809 base pair
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APPLICATION NUMBER: PCT/US/94/12117
FILING DATE: 21 October, 1994
APPLICATION NUMBER: U.S. 08/292,827
FILING DATE: 23 AUGUST, 1994
APPLICATION NUMBER: U.S. 08/141,248
FILING DATE: 22 October, 1993
APPLICATION NUMBER: U.S. 08/017,127
FILING DATE: 23 February, 1993
APPLICATION NUMBER: U.S. 08/017,127
FILING DATE: 12 February, 1993
APPLICATION NUMBER: U.S. 07/34,161
FILING DATE: 21 AUGUST, 1992
APPLICATION NUMBER: U.S. 07/834,044
FILING DATE: 11 February, 1992
APPLICATION NUMBER: U.S. 07/749,451
FILING DATE: 11 February, 1992
APPLICATION NUMBER: U.S. 07/749,451
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APPLICATION NUMBER: U.S. 07/749,451
FILING DATE: 23 AUGUST, 1991
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FILING DATE: 23 AUGUST, 1991
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ATTORNEY/AGENT INFORMATION:
NAME: Heber, Sheldon O.
REGISTRATION NUMBER: 38,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1933 CTCTTCATCAACGAGGAGAAAATCCTGTGGAGTGGGTTCTCCAGGGAGGTGCCCCTTCTCC 1992
REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: cDNA to mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: CDS
LOCATION: 373..3606
OTHER INFORMATION:
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TELEX: 67-3510
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                                                                                                                                                                  GTGCTGGGCATTTTCCTGACAGCCTTTGTGCTGGGTGTGTTTATCAAGTTCCGCAACACA
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                                                                       CCCATTGTCAAGGCCACCAACCGAGAGCTCTCCTACCTCCTCCTCCTCTCCCTGCTCTGC
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                                                                                               cctgtggtgaggtcagcaggggccgcctgtgctttcttatgctgggctccctggcagca 1649
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Pred. No. 8.4e-27;
0; Mismatches 556;
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2950 ATTCTCTTCAAGCCATCCCGCAACACCATCGAGGAGGTGC
                  atectetgeegeecagaeeteaaeageaeagageaettee
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US-08-480-751-3

ISEQUENCE 3, APPLICATION US/08480751

PATENT NO. 5858684

GENERAL INFORMATION:
APPLICANT: Edward F. Nemeth
APPLICANT: Edward M. Brown
APPLICANT: Edward M. Brown
APPLICANT: Steven C. Hebert
APPLICANT: James E. Garrett, Jr.
TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
TITLE OF INVENTION: MOLECULES
NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:
NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:
NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:
STREET: First Interstate World Center
STREET: Suite 4700
STREET: Suite 4700
STREET: G33 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTR: USA
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 33.5" Diskette, 1.44 Mb storage
COMPUTER: LIEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FASTSEO
CURRENT APPLICATION NUMBER: US/08/480,751
FILING DATE: 7 June, 1995

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; LOCATION: 373..36
; OTHER INFORMATION:
US-08-480-751-3
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NAME: Heber, Sheldon O.
REGISTRATION NUMBER: 213/
REFERENCE/DOCKET NUMBER: 213/
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEFAX: (213) 955-0440
INFORMATION FOR SEQ ID NO: 3:
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Best Local S
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APPLICATION NUMBER: PCT/US/94/1/11/
FILING DATE: 21 October, 1994
APPLICATION NUMBER: U.S. 08/292,827
FILING DATE: 23 August, 1994
APPLICATION NUMBER: U.S. 08/141,248
FILING DATE: 22 October, 1993
APPLICATION NUMBER: U.S. 08/009,389
FILING DATE: 23 February, 1993
APPLICATION NUMBER: U.S. 08/017,127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08
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APPLICATION NUMBER: U.S. 08/017,127
FILING DATE: 12 February, 1993
APPLICATION NUMBER: U.S. 07/934,161
FILING DATE: 21 August, 1992
APPLICATION NUMBER: U.S. 07/834,044
FILING DATE: U.S. 07/834,044
FILING DATE: U.S. 07/749,451
FILING DATE: 23 August, 1991
FILING DATE: 23 August, 1991
                                                                                                                                                                                                                                                                                                                                                                      1233 ctaaacaatgagaccaaaatccagtggcacggaaagaaccaccaggtgcctaagtct 1292
                                                                                                                                                                                                                                                                                        1993 AACTGCAGCCGAGACTGCCTGGCAGGGACCAGGAAAGGGGATCATTGAGGGGGGAGCCCCACC
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LENGTH: 3809 base pair
   1590
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hes 498;
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                              agatgccagccttgtggaacagaagagtgggcacctgagggaagccagacctgcttcccg
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                                                             acgctgctgctgctgctgcttgggactgctggcctgtttgcctggcacctagacacc
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                               GTGCTGGGCATTTTCCTGACAGCCTTTGTGCTGGGTGTGTTTATCAAGTTCCGCAACACA
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Similarity 47.0%;
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h: described below: 9
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Pred. No. 8.4e-27;
0; Mismatches 556;
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                                                                                                                                                                                                                                                                                                                    Sequence 3, Application Patent No. 5962314 GENERAL INFORMATION:
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                                           ZIP: 90071

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette,
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CORRESPONDENCE ADDRESS:
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 COMPUTER:
OPERATING
SOFTWARE:
                                                                                              COUNTRY:
                                                                               90071
                                                                                                USA
   FASTSEQ
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APPLICANT: Edward M. Brown
APPLICANT: Steven C. Hebert
APPLICANT: James E. Garrett, Jr.
TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
TITLE OF INVENTION: MOLECULES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1710 caggocotottttgocottggtttcaccatottcotgtootgootgacagttcgotcatto 1769
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                                                                                                                                                                    ADDRESSEE: Lyon & Lyon
STREET: First Interstate World
STREET: Suite 4700
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
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CURRENT APPLICATION DATA:

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; NAME/KEY: CDS;
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; OTHER IMPORMATION:
US-08-943-986-3
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Best Local Similarity
Matches 498; Conserv
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FILING DATE: 21 October, 1994
APPLICATION NUMBER: U.S. 08/29,827
FILING DATE: 23 August, 1994
APPLICATION NUMBER: U.S. 08/141,248
FILING DATE: 22 October, 1993
APPLICATION NUMBER: U.S. 08/00,389
FILING DATE: 23 February, 1993
APPLICATION NUMBER: U.S. 08/017,127
FILING DATE: 12 February, 1993
APPLICATION NUMBER: U.S. 07/934,161
FILING DATE: 11 February, 1992
APPLICATION NUMBER: U.S. 07/834,044
FILING DATE: 11 February, 1992
APPLICATION NUMBER: U.S. 07/834,044
FILING DATE: 11 February, 1992
APPLICATION NUMBER: U.S. 07/749,451
FILING DATE: 11 February, 1992
APPLICATION NUMBER: U.S. 07/749,451
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1530 acgctgctgctgctgcttgcttgggactgctgttttgccttggcacctagacacc 1589
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
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NAME: Heber, Sheldon O.
REGISTRATION NUMBER: 38,179
                                                                                                                          2173 AAGGAGATCGAGTTTCTGTCGTGGACGGAGCCCTTTGGGATCGCACTCACCCTCTTTGCC
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THE PROPERTY OF THE PROPERTY
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APPLICATION NUMBER: U8/40
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Pred. No. 8.4e-27;
0; Mismatches 556;
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                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Edward
APPLICANT: Brown,
APPLICANT: Bradfor
APPLICANT: F. Bala
                                                                                                                                                                                                                                                                                                       Sequence 3, Application US/08353784 Patent No. 6011068
                                                                                                              APPLICANT: Eric G. DelMar, and Scott T. Moe
TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
TITLE OF INVENTION: MOLECULES
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
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                                                           ADDRESSEE: Lyon & Lyou
STREET: First Interstate World
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                                       633 West Fifth Street
                                                                                                                                                                                         Bradford C. Van Wagenen, Manuel F. Balandrin, Forrest H. Fuller, Eric G. DelMar, and Scott T. Moe
                                                                                                                                                                                                                                                    Brown,
                                                                                                                                                                                                                                                Edward F. Nemeth, Edward M. Brown, Steven C. Hebert,
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COUNTRY:

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                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 498; Conserv
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PRIOR APPLICATION DATA: including applic
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER: PCT/US/94/12117
FILING DATE: 21 October: 1994
APPLICATION NUMBER: U.S. 08/292.827
FILING DATE: 23 August: 1994
FILING DATE: 23 Cottober: 1993
APPLICATION NUMBER: U.S. 08/141,248
FILING DATE: 22 October: 1993
APPLICATION NUMBER: U.S. 08/00,389
FILING DATE: 23 February, 1993
APPLICATION NUMBER: U.S. 08/071127
FILING DATE: 12 February, 1993
APPLICATION NUMBER: U.S. 07/934.161
FILING DATE: 12 February, 1993
APPLICATION NUMBER: U.S. 07/934.161
FILING DATE: 12 August: 1992
APPLICATION NUMBER: U.S. 07/934.161
FILING DATE: 13 August: 1992
APPLICATION NUMBER: U.S. 07/934.161
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
  2173
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APPLICATION NOWBER: U.S. 07/834,044
FILING DATE: 11 February, 1992
APPLICATION NOWBER: U.S. 07/749,451
FILING DATE: 23 August, 1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: 11 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 3809 base pairs TYPE: nucleic acid STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: FILING DATE: 9 Dece
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                          CTCTTCATCAACGAGGAGAAAATCCTGTGGAGTGGGTTCTCCAGGGAGGTGCCCTTCTCC
AAGGAGATCGAGTTTCTGTCGTGGACGGAGCCCTTTGGGGATCGCACTCACCCTCTTTGCC
                                                                                  GCCTGTAACAAGTGCCCAGATGACTTCTGGTCCAATGAGAACCACACCTCCTGCATTGCC
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                      cgcactgtggtgttttttggctttgcgtgagcacacctcttgggtgctgctggcagctaac
                                                                                                                      agatgccagccttgtggaacagaagagtgggcacctgagggaagccagacctgcttcccg
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9 December, 1994
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47.0%;
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Pred. No. 8.4e-27;
0; Mismatches 556;
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RESULT 11
US-08-485-588-2
US-08-485-588-2
Sequence 2, Application US/08485588
Patent No. 5688938
GENERAL INFORMATION:
APPLICANT: Edward M. Brown
APPLICANT: Steven C. Hebert
APPLICANT: Forrest H. Fuller
APPLICANT: James E. Garrett, Jr.
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APPLICANT: Edward M. Brown
APPLICANT: Steven C. Hebert
APPLICANT: Forrest H. Fuller
APPLICANT: James E. Garrett, Jr.
TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
TITLE OF INVENTION: MOLECULES
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:

STREET: STREET: ADDRESSEE:

First Interstate World Suite 4700 633 West Fifth Street Lyon & Lyon

Los Angeles California

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; LOCATION: 436..3699
; OTHER INFORMATION:
US-08-485-588-2
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TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 5006 hasc
                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                              Matches 414;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 11 February, 1992
APPLICATION NUMBER: U.S. 07/749,
FILING DATE: 23 August, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Heber, Sheldon O.
REGISTRATION NUMBER: 38,179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: U.S. 08/009,389
FILING DATE: 23 February, 1993
APPLICATION NUMBER: U.S. 08/017,127
FILING DATE: 12 February, 1993
APPLICATION NUMBER: U.S. 07/934,161
FILING DATE: 21 August, 1992
APPLICATION NUMBER: U.S. 07/834,044
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: FASTSEQ CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: cDNA to mRNA
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                                     178
     799
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APPLICATION NUMBER: U.S. 08/292,827
FILING DATE: 23 August, 1994
APPLICATION NUMBER: U.S. 08/141,248
FILING DATE: 22 October, 1993
APPLICATION NUMBER: U.S. 08/009,389
                                                                                                                                                         70 aacaactccacggccctgctgcccaacatcaccctggggtaccagctgtatgatgtgtgt 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
TOPOLOGY: 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/485,588 FILING DATE: 7 June, 1995
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SOFTWARE: FASTSEQ
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                     gggcaacaccacatagagctccaaggagaccttctccactattccccctacggtgctggca 237
                                                                                         tctgactctgccaatg---tgtatgccacgctgagagtgctctccc-----tgcca 177
TCTTTGAACCTTGATGAGTTCTGCAACTGCTCAGAGCACATTCCCTCTACGATTGCTGTG 858
                                                                                                                                      AACAGCAGCCCAGCCCTTCTTCCCAACTTGACGCTGGGATACAGGATATTTGACACTTGC 738
                                                                                                                                                                                                          AGGTATAATTTCCGTGGGTTTCGCTGGTTACAGGCTATGATATTTGCCATAGAGGAGATA 678
                                                                  AACACCGTTTCTAAGGCCTTGGAAGCCACCCTGAGTTTTGTTGCTCAAAAACAAATTGAT 798
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IBM PC compatible
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UMBER: PCT/US/94/12117
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: described below: 9
.08/353,784
                                                                                                                                                                                                                                                                          Score 132.6; DB 1;
Pred. No. 3.1e-25;
0; Mismatches 389;
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US-08-484-565-2
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Patent No. 5763569
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FASTSEQ
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,565
FILING DATE: 7 June, 1995
CLASSIFICATION DATA: including application
PRIOR APPLICATION DATA: including application
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                          STREET: First ....
STREET: Suite 4700
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: James E. Garrett, Jr.
TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
TITLE OF INVENTION: MOLECULES
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
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Steven C. Hebert
                                                                                                                                                                                                                                                                                                                                                                                                                                    Lyon & Lyon
                                                                                                                                                                                                                                                                                                                                                                                                            Interstate World Center
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LOCATION: 436..3699
OTHER INFORMATION:
US-08-484-565-2
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Best Local Similarity 50.4
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1500
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: U.S. 08/009,389
FILING DATE: 23 February, 1993
APPLICATION NUMBER: U.S. 08/017,127
FILING DATE: 12 February, 1993
APPLICATION NUMBER: U.S. 07/934,161
FILING DATE: 12 August, 1992
APPLICATION NUMBER: U.S. 07/934,044
FILING DATE: 11 February, 1992
APPLICATION NUMBER: U.S. 07/749,451
FILING DATE: 13 February, 1992
APPLICATION NUMBER: U.S. 07/749,451
FILING DATE: 23 August, 1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: CDNA to mRNA
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APPLICATION NUMBER: (
FILING DATE: 9 Decemb
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APPLICATION NUMBER: U.S. 08/292,827
FILING DATE: 23 August, 1994
APPLICATION NUMBER: U.S. 08/141,248
FILING DATE: 22 October, 1993
APPLICATION NUMBER: U.S. 08/009,389
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                     tctttcctgcgcaccatccccaatgacaagtaccaggtggagaccatggtgctgctgctg 417
                                                                                                                                                                          gtgattgggcctgacagcaccaaccgtgctgccaccacagccgccctgctgagccctttc
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                                                                                             ctggtgcatattagctatgcggccagcagcgagacgctcagcgtgaagcggcagtatccc
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                                                                                                                                                                                                                                                                                                                                                                      AACAGCAGCCCAGCCCTTCTTCCCAACTTGACGCTGGGATACAGGATATTTGACACTTGC 738
TCTTTCCTCCGAACCATCCCCAATGATGAGCACCAGGCCACTGCCATGGCAGACATCATC
                                                                                                                                               GTGGGAGCAACTGGCTCAGGCGTCTCCACGGCAGTGGCAAATCTGCTGGGGCTCTTCTAC
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BER: PCT/US/94/12117
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50.4%;
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RESULT 13
US-08-480-751-2
; Sequence 2, Application
; Patent No. 5858684
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                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Dis
COMPUTER: 1BM PC comp
OPERATING SYSTEM: PC-
SOFTWARE: FASTSEQ
APPLICATION NUMBER: 08/353,784
FILING DATE: 9 December, 1994
APPLICATION NUMBER: PCT/US/94/12117
FILING DATE: 21 October, 1994
APPLICATION NUMBER: U.S. 08/292,827
FILING DATE: 23 AUGUST, 1994
APPLICATION NUMBER: U.S. 08/141,248
FILING DATE: 22 October, 1993
APPLICATION NUMBER: U.S. 08/09/389
FILING DATE: 23 February, 1993
                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,751
FILING DATE: 7 June, 1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Edward M. Brown
APPLICANT: Steven C. Hebert
APPLICANT: Forrest H. Fuller
APPLICANT: James E. Garrett, Jr.
TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
TITLE OF INVENTION: MOLECULES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1393 TICGCICIGAAGGCIGGGCAGATCCCAGGCIICCGGGAATI 1433
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PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
ZIP: 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Lyon & Lyon
STREET: First Interstate World
STREET: Suite 4700
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gccctctccaggcacatcactggggtgcccgggatccagcgcattgggatggtgctgggc
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SYSTEM: PC-DOS/MS-DOS
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A: described below: 9
08/353,784
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; NAME/KEY: CDS
; LOCATION: 436..3699
; OTHER INFORMATION:
US-08-480-751-2
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Best Local Similarity 50.4%;
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FILING DATE: 12 February, 1993
APPLICATION NUMBER: U.S. 07/934,161
FILING DATE: 21 August, 1992
APPLICATION NUMBER: U.S. 07/834,044
FILING DATE: 11 February, 1992
APPLICATION NUMBER: U.S. 07/749,451
FILING DATE: 13 August, 1991
ATTORNEY/ACENT INFORMATION:
ANABE: Heber, Sheldon O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
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REGISTRATION NUMBER:
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CTCATCTCCCAGTACTCTGATGAGGAAGA-----GATCCAGCATGTGGTAGAGGTGATT 1212
                                                                                                                                                                                     GGGATTGAGAAATTCCGAGAGGAAGCTGAGGAAAGGGATATCTGCATCGACTTCAGTGAA 1158
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RESULT 14
US-08-943-986-2
; Sequence 2, Applic
; Patent No. 5962314
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                                                                                                                                         APPLICATION NUMBER: PCT/US/94/12117
FILING DATE: 21 October, 1994
APPLICATION NUMBER: U.S. 08/292,827
FILING DATE: 23 August, 1994
APPLICATION NUMBER: U.S. 08/141,248
FILING DATE: 22 October, 1993
APPLICATION NUMBER: U.S. 08/009,389
FILING DATE: 23 February, 1993
APPLICATION NUMBER: U.S. 08/017,127
FILING DATE: 12 February, 1993
APPLICATION NUMBER: U.S. 08/017,127
FILING DATE: 12 February, 1993
APPLICATION NUMBER: U.S. 07/934,161
FILING DATE: 12 August, 1992
APPLICATION NUMBER: U.S. 07/834,044
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APPLICATION NUMBER: US,
FILING DATE: 03-OCT-199
CLASSIFICATION: 530
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MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
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APPLICANT: Steven C. Hebert
APPLICANT: James E. Garrett
                                  ATTORNEY/AGENT INFORMATION:
NAME: Heber, Sheldon O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: James E. Garrett, Jr.
TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
TITLE OF INVENTION: MOLECULES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: First Inters
STREET: Suite 4700
STREET: 633 West Fil
CITY: Los Angeles
                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 11 February, 1992
APPLICATION NUMBER: U.S. 07/74
FILING DATE: 23 August, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: FASTSEQ
REGISTRATION NUMBER: 38
REFERENCE/DOCKET NUMBER:
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Los Angeles
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Best Local Similarity
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LENGTH: 5005 base pair
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TYPE: nucleic acid
STRANDEDNESS: single
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TELEFAX: (213) 955-0440
TELEX: 67-3510
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                                                                                                                                                CAAAATTCCACGGCCAAAGTCATCGTGGTTTTCTCCAGTGGCCCAGATCTTGAGCCCCTC
                                                                                                                                                                   gcccaggccggggccaccgtcgtggttgtttttttccagccggcagttggccagggtgttt 657
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GCCAGCTCCTCCCTGATCGCCATGCCTCAGTACTTCCACGTGGTTGGCGGCACCATTGGA 1392
                                    gccctctccaggcacatcactggggtgcccgggatccagcgcattgggatggtgctgggc 777
                                                                           CTCATCTCCCAGTACTCTGATGAGGAAGA-----GATCCAGCATGTGGTAGAGGTGATT
                                                                                                                                                                                                                                                                                                GGGATTGAGAAATTCCGAGAGGAAGCTGAGGAAAGGGATATCTGCATCGACTTCAGTGAA 1158
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                                                                                                                                                                                                                                                                                                                                                                                                                                               TCTTTCCTCCGAACCATCCCCAATGATGAGCACCAGGCCACTGCCATGGCAGACATCATC 1038
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Pred. No. 3.1e-25;
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US-08-687-289A-2
: Sequence 2, Application US/08687289A
: Patent No. 5981195
: GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 220/
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEFAX: (7-3510
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 4000 base pairs
                                                                                                                                                                                                                Query Match
Best Local S
Matches 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08, FILING DATE: July 25, 1990 CLASSIFICATION: 435 PRIOR APPLICATION DATA: APPLICATION NUMBER: 60/001 FILING DATE: July 26, 1990 ATTORNEY_AGENT INFORMATION: NAME: Warburg, Richard J. REGISTRATION NUMBER: 32,33 REGISTRATION NUMBER: 32,33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
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OPERATING SYSTEM: IBM P.C. DOS 5
SOFTWARE: FastSEO for Windows 2.
CURRENT APPLICATION DATA:
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MEDIUM TYPE: 3.5" Diskette,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Lyon 6 Lyon
STREET: 633 West Fifth S
STREET: Suite 4700
CITY: Los Angeles
STATE: California
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344
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                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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                                                                                                                                                                                                                                  Local Similarity
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                  tctgactctgccaatg---tgtatgccacgctgagagtgctctccc-----tgcca
                                                                                        aacaactccacggccctgctgcccaacatcaccctggggtaccagctgtatgatgtgtgt 129
AACACCGTTTCTAAGGCCTTGGAAGCCACCCTGAGTTTTGTTGCTCAAAACAAAATTGAT
                                                                     AACAGCAGCCCAGCCCTTCTTCCCAACTTGACGCTGGGATACAGGATATTTGACACTTGC 343
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Hammerland, Lance G.

VENTION: CHIMERIC RECEPTORS AND METHODS FOR VENTION: IDENTIFYING COMPOUNDS ACTIVE AT VENTION: METABOTROPIC GLUTAMATE RECEPTORS AND VENTION: THE USE OF SUCH COMPOUNDS IN THE VENTION: TREATMENT OF NEUROLOGICAL DISORDERS WENTION: AND DISEASES
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Pred. No. 2.8e-25;
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938 GCCAGCTCCTCCCTGATCGCCATGCCTCAGTACTTCCACGTGGTTGGCGGCACCATTGGA 997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            704 GGGATTGAGAAATTCCGAGAGGAAGCTGAGGAAAGGGATATCTGCATCGACTTCAGTGAA 763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              644 GAGTATTTCCGCTGGAACTGGGTGGGCACAATTGCAGCTGATGACGACTATGGGCGGCCG 703
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Search completed: March 19, 2000, 18:11:12 Job time: 1471 sec B 64

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Result
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The encoding calcium receptor polypeptide(s) - useful for therapeutic purposes, e.g. hyperparathyroidism and osteoporosis claim 1; Columns 107-116; 174pp; English.

The present sequence encodes bovine parathyroid cell calcium receptor 1 (BoPCaR 1).

The specification includes details of molecules that can modulate one or more inorganic ion receptor activities, and antibodies and antibody fragments targetted to inorganic ion receptor proteins. The proteins, nucleic acids and antibodies may be used to treat disorders by modulating one or more inorganic ion receptor activities, preferably disorders of calcium homeostasis, e.g. hyperparathyroidism and osteoporosis.

Sequence 5275 BP; 1277 A; 1476 C; 1315 G; 1207 T;
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Best Local Sim
Matches 501;
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Key

Location (**CDS**)
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18-NOV-1997.
07-JUN-1995; US-485588.
07-JUN-1995; US-485588.
07-JUN-1995; US-349451.
11-FEB-1992; US-934161.
11-FEB-1992; US-934161.
11-FEB-1993; US-017127.
23-FEB-1993; US-017127.
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23-FEB-1993; US-017127.
23-FEB-1993; US-017127.
23-FEB-1994; US-292827.
21-OCT-1994; WS-292827.
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08-DEC-1994; WS-11711.
08-DEC-1994; US-353784.
(LGHM ) BRIGHAM & WOMENS H.
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BEOWN EM, Fuller FH, Garre,
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                           gtgtgttccagcgactgtcttgaagggcac---cagcgagtggttacgggtttccatcac 1349
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PT Calcium reverse.

PT antibody production

PS Example 25; Fig 47; 174pp; English.

CC The bovine parathyroid calcium receptor gene encodes a 1085 amino acid

CC protein. The tissue from which this receptor and receptors from human

CC protein. The tissue from which this receptor and receptors from human

CC protein. The tissue from which this receptor and receptors from human

CC protein. The tissue from which this receptor changes, and control

CC changes, in calcium ion concentration, e.g. parathyroid hormone regulates

CC C2+ homeostasis in blood and extracellular fluid, and kidney function

CC alters through changes in C2+ levels in juxtaglomerular and proximal

CC tubule cells in the kidney. The purified receptors (produced

CC receptor activity, can be used to screen for compounds that modulate calcium

CC receptor activity, especially those that can be used to treat diseases

CC associated with the receptors in these tissues. They can also be used

CC to raise antibodies for use in detection assays.

CC carmence 5275 BP; 1277 A; 1475 C; 1316 G; 1207 T;
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08-DEC-1994; US-353:

(BGHM) BRIGHAM & WI

(NPSP-) NPS PHARM II

BIOWN EM, GAITETE UPI; 98-347412/30.

P-PSDB; W54844.
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                                                                                                                               GTGCTGGGCATTTTCCTCACAGCCTTCGTGCTGGGCGTCTTCATCAAGTTCCGCAACACG
                                                                                                                                                                                                                CCCATCGTCAAGGCCACCAACCGGGAGCTCTCCTATCTCCTTCTCTTCTCCCTGCTCTGC
                                                                                            cctgtggtgaggtcagcagggggccgcctgtgctttcttatgctgggctccctggcagca
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 TGCTTCTCCAGCTCCCTGTTCTTCATCGGGGAGCCCCAGGACTGGACGTGCCGCCTGCGC
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US-017127.

US-009389.

US-141248.

US-292827.

WO-U12117.

US-353784.
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23-FEB-1993

23-FEB-1993

23-GCT-1994

21-OCT-1994
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Bovine parathyroid calcium receptor BoPCaR 1 encoding cDNA.

Bovine parathyroid calcium receptor; inorganic ion receptor; osteoporosis;

Parathyroid calcium receptor; inorganic ion receptor; osteoporosis;

calcium homeostasis; hyperparathyroidism; seizure; stroke; epilepsy;

spinal cord injury; hypoxia-induced nerve cell damage; cardiac arrest;

neonatal distress; neurodegenerative disease; Alzheimer's disease;

neonatal distress; parkinson's disease; dementia; muscle tension;
                                                    (NPSP-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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Matches 501;
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A method has been developed of screening for a compound able to affect one or more activities of a calcium receptor (CR) comprises: (A) contacting a recombinant cell with a test compound, where the
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                                       caactaatcatcatcttcaagttttccaccaaggtacctacattctaccacgcctgggtc
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23-OCT 1995; U13704.
21-OCT 1994; WO-U12117.
08-DEC-1994; US-353784.
(NPSP-) NPS PHARM INC.
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These sequences given in T61381-82 encode numerical gland adenoma
These sequences were isolated from human parathyroid gland adenoma
These sequences were isolated from human parathyroid gland adenoma
tumour using pBopCaR1 as a hybridisation probe. mRNA was isolated from
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The sequences given in T61381-82 encode functional calcium receptors.
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/product- Calcium receptor
/product- "Pages 94-95 are missing from the specification,
/note- "Pages 94-95 are missing from the EPO"
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Matches

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Conservative

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CC functional calcium receptors.

CC calcium receptors as assessed by the stimulation of calcium-activated CC chloride currents upon addition of appropriate calcium receptor agonists, CC e.g. NPS R-467 and NPS R-558. Sequence analysis of the two cDNA clones indicated the existence of at least two sequence variants differing in CC the 3' untranslated region and which may result from alternative CC polyadenylation. Sequence variation also exists in the 5' end of the CC inserts. These sequence differences may have arisen due to alternative transcription initiation and/or splicing. These additional sites of sequence variation occur within the coding regions of cDNA clones CC phuPCaR5.2 and phuPCaR4.0 demonstrating that they encode distinct proteins. Sequence analysis of the human CaR gene indicates that the coding regions of cDNA clones of cDNA clones of cDNA clones of cDNA clones. Sequence analysis of the human CaR gene indicates that the proteins. Sequence analysis of the human CaR gene indicates that the coding regions of cDNA clones of cDNA clones. Sequence analysis of the human CaR gene indicates that the proteins. Sequence analysis of the human CaR gene encoded by compared to phuPCaR4.0, results from alternative mRNA splicing. This alternative splicing is predicted to insert 10 additional amino acids into the CaR protein encoded by phuPCaR5.2 between residues 536 and 537 of the protein encoded by chuPCaR5.2 between residues 536 and 537 of the protein encoded by chuPCaR5.0. In addition phuPCaR4.0 encodes Gln at position 925 and Gly at positions. The human CaR gene encodes for Gln and Arg respectively at these two receptor isoforms may be functionally and/or
                                                                                                                                                       Query Match
Best Local
                                                                                                                                                    pharmacologically distinct.
Sequence 3809 BP; 910 A;
                               Similarity
                            5.98;
Score 138.4; Pred. No. 3.6e

O; Mismatches
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1; DB 1;
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11-FEB-1992; US-934461.
11-FEB-1992; US-93461.
12-FEB-1993; US-017127.
12-FEB-1993; US-017127.
12-FEB-1993; US-017127.
12-FEB-1993; US-017127.
12-OCT-1994; US-292827.
19-AUG-1994; WG-U12117.
08-DEC-1994; WG-U12117.
08-DEC-1994; WG-U12117.
08-DEC-1994; US-353744.
(BGHM ) BRIGHAM & WOMENS HC (NPSP-) NPS PHARM INC.
BROWN - BRIGHAM FH, GARIET
proteins, nucleic acids and ancounter may a disorders by modulating one or more inorganic ion receptor activities, preferably disorders of calcium homeostasis, e hyperparathyroidism and osteoporosis.

Ann BP: 910 A; 1071 C; 979 G; 849
                                                                                                                                                                   DNA encoding calcium receptor polypeptide(s) - useful for therapeutic purposes, e.g. hyperparathyroidism and osteoporosis Claim 15: Columns 125-134: 174pp; English.

The present sequence encodes human parathyroid cell calcium receptor 4.0 (HuPCaR 4.0).

The specification includes details of molecules that can modulate one or more inorganic ion receptor activities, and antibodies and antibody fragments targetted to inorganic ion receptor proteins. The specification includes and antibodies may be used to treat includes that the sequence of the sequence o
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P-PSDB; W38274.
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Pred. No. 3.5e-25;
0; Mismatches 556;
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19-AUG-1994; 1
21-OCT-1994; 1
08-DEC-1994; 1
(BGHM ) BRIGH
                                                                                                                                                                                                                                                                                                                                                                                                                                    The Human parathyroid calcium receptor gene encodes a 1078 amino acid protein. The tissue from which the receptor and receptors from bovine parathyroid and rat kidney are derived, respond to changes, and control changes, in calcium ion concentration, e.g. parathyroid hormone regulates ca2+ homeostasis in blood and extracellular fluid, and kidney function alters through changes in Ca2+ levels in juxtaglomerular and proximal tubule cells in the kidney. The purified receptors (produced recombinantly) can be used to screen for compounds that modulate calcium receptor activity, especially those that can be used to treat diseases associated with the receptors in these tissues. They can also be used to raise antibodies for use in detection assays. sequence 3809 BP; 910 A; 1071 C; 979 G; 849 T;
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11-FEB-1992;
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Example 27; Fig 49; 174pp; English.
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Brown EM, Garrett JE,
WPI; 98-347412/30.
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US-934161.

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Pred. No. 3.6e-7
0; Mismatches 5
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                                                      19-MAR 1999 (first entry)

Human parathyroid calcium receptor pHupCaR 4.0 encoding cDNA.

Parathyroid calcium receptor; inorganic ion receptor; osteoporosis;

Parathyroid calcium receptor; inorganic ion receptor; osteoporosis;

calcium homeostasis; hyperparathyroidism; seizure; stroke; epilepsy;

spinal cord injury; hypoxia-induced nerve cell damage; cardiac arrest;

neonatal distress; neurodegenerative disease; Alzheimer's disease;
                                                                                                                                                                                                                                           V82485
V82485;
Huntington's disease; Parkinson's disease; dementia; depression; anxiety; ss.
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Matches 498
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A method has been developed of screening for a compound of the compound 
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CC injected into Xenopus oocytes which were assayed for the presence of the functional calcium receptors. Both clone types gave rise to functional calcium receptors as assessed by the stimulation of calcium-activated calcium receptors as assessed by the stimulation of calcium-activated calcium receptors as assessed by the stimulation of calcium-activated calcium receptor agonists, compared to the currents upon addition of appropriate calcium receptor agonists, compared to the existence of at least two sequence variants differing in the 3' untranslated region and which may result from alternative the golyadenylation. Sequence variation also exists in the 5' end of the compared compared part of the compared to alternative transcription initiation and/or splicing. Three additional sites of sequence variation occur within the coding regions of cDNA clones of sequence variation occur within the coding regions of cDNA clones of the proteins. Sequence analysis of the human CaR gene indicates that the proteins. Sequence analysis of the human CaR gene indicates that the additional anino acids into the CaR protein encoded by phuPCaR5.2 between residues 536 and 537 of the protein encoded by phuPCaR5.2 between residues 536 and 537 of the protein encoded by consistion 90, whereas phuPCaR4.0 encodes Gln and position 925 and Gly contained to the care protein encoded by the positions. The human CaR gene encodes for Gln and Arg respectively at these positions. These two receptor isoforms may be functionally and/or characterically distinct.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New di:arylalkyl amine cpds. useful for modulating inorganic ion receptor activities - esp. for modulating effect of extracellular calcium on cell surface calcium receptors, useful for treating e. hyperparathyroidism, Paget's disease or osteoporosis Example 1; Page 85-93; 231pp; English.

The sequences given in T61381-82 encode functional calcium receptors.
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                                                                                                                                     This sequence encodes a chimeric receptor. The chimeric receptor comprises an extracellular domain, a seven transmembrane domain, and an intracellular cytoplasmic tail domain, and a sequence of at least 6 contiguous amino acids is homologous to a sequence of a metabotropic glutamate receptor (MGR), and a sequence of at least 6 contiguous amino acids is homologous to a sequence of at least 6 contiguous amino acids is homologous to a sequence of a calcium receptor (CR). The chimeric receptor may be used for screening for compounds that bind to or modulate the activity of MGR or CR and for determining the site-of-action of a CR active compound. The compounds can be used in the treatment of neurological diseases and disorders. They can also be
                                                                                                                                                                                                                                                                                                                                                          conpounds

Example 3; Fig 3; 177pp; English.

Example 3; Fig 3; 177pp; English.

The chimeric receptor. The chimeric receptor and a sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chimeric receptor; extracellular domain; seven transmembrane domain; intracellular cytoplasmic tail domain; metabotropic glutamate recept MGR; calcium receptor; CR; mGluR; G protein-coupled receptor; neurological disease; ss.

Chimeric - Homo sapiens.
                                                      used as diagnostic agents. Chimeric receptors such as this, allow the coupling of certain functional aspects of an MGR with certain functional aspects of a CR. They allow for more efficient high-throughput screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chimeric receptors comprising calcium receptor - used for s
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P-PSDB; W25763.
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25-JUL-1996; U12336.
26-JUL-1995; US-001526.
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Human parathyroid cell calcium receptor 5.
Human parathyroid cell calcium receptor 5.
calcium homeostasis; hyperparathyroidism;
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07-JUN-1995; US-485588.
07-JUN-1995; US-485588.
23-AUG-1991; US-749451.
11-FEB-1992; US-934044.
21-AUG-1992; US-934161.
12-FEB-1993; US-017127.
23-FEB-1993; US-0171248.
19-AUG-1994; US-292827.
21-OCT-1994; US-292827.
21-OCT-1994; US-353784.
(BGIM ) BRIGHAM & WOMENS H (NPSP-) NPS PEARM INC.
35-CN-198-008040/01.
35-CN-198-008040/01.
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RESULT T95858 ID T0 AC T1 AC T1 AC T1 OD DT OD DE HI KW OS HI KW OS HI KW OS ST T1 OS T1 O

γQ B 20 Вb Qy рь δÃ g 20 В Ωy DЪ γQ

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DNA encoding calcium receptor polypeptide(s) - useful for therapeutic purposes, e.g. hyperparathyroidism and osteoporosis (laim 15; Columns 117-126; 174pp; English.

C Talim 15; Columns 117-126; 174pp; English.

C The present sequence encodes human parathyroid cell calcium receptor 5.2 (HuPCaR 5.2).

C The specification includes details of molecules that can modulate one or more inorganic ion receptor activities, and antibodies and antibody fragments targetted to inorganic ion receptor proteins. The proteins, nucleic acids and antibodies may be used to treat disorders by modulating one or more inorganic ion receptor activities, preferably disorders of calcium homeostasis, e.g. hyperparathyroidism and osteoporosis.

Sequence 5006 BP; 1227 A; 1378 C; 1219 G; 1182 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  agetteaatgageatggetaeceacetetteeaggetatgeggetttgggggttgaggagata
                                  ggggtgcaggcactggagaaccaggccctggtcaggggcatctgcattgcatttcaaggac
                                                                                                                                                    cagaagttogggtggacotggatotototggtttggcagcagtgacgaotatgggcagota
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Best Local S
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                                                                                               The Human parathyroid calcium receptor gene encodes a 1088 amino acid protein. The tissue from which this receptor and receptors from bowine parathyroid and rat kidney are derived, respond to changes, and control changes, in calcium ion concentration, e.g. parathyroid hormone regulates ca2+ homeostasis in blood and extracellular fluid, and kidney function alters through changes in Ca2+ levels in jux taglomerular and proximal tubule cells in the kidney. The purified receptors (produced recombinantly) can be used to screen for compounds that modulate calcium receptor activity, especially those that can be used to treat diseases associated with the receptors in these tissues. They can also be used to raise antibodies for use in detection assays.

Sequence 5006 BP; 1228 A; 1376 C; 1220 G; 1182 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-JUN-1995;
07-JUN-1995;
07-JUN-1991;
23-AUG-1992;
11-FEB-1992;
21-AUG-1992;
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23-FEB-1993;
22-OCT-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human parathyroid calcium receptor 5.2 gene ss; calcium ion concentration; parathyroid hkidney; calcium receptor; detection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1333
                                                                                                                                                                                                                                                                        Calcium receptor poly:peptide(s) - antibody production Example 27; Fig 48; 174pp; English.
                                                                                                                                                                                                                                                                                                                   Brown EM, Garrett JE,
WPI; 98-347412/30.
P-PSDB; W54845.
                                                                                                                                                                                                                                                                                                                                                                                          21-OCT-1994;
08-DEC-1994;
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                            Match 5.7%;
Local Similarity 50.4%;
Local Similarity 50.4%;
Local Similarity 50.4%;
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agcttcaatgagcatggctaccacctcttccaggctatgcggcttggggttgaggata 69
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US-009389.
US-141248.
US-292827.
WO-U12117.
US-353784.
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US-749451.
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                            Score 132.6; D
Pred. No. 1.1e-
0; Mismatches
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                             DB 1;
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389;
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                             Indels
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                             18;
                            Gaps
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                                                                                                        19-MAR-1999 (first entry)
Human parathyroid calcium receptor pHuPCaR 5.2 encoding cDNA.
Parathyroid calcium receptor; inorganic ion receptor; osteoporosis;
Parathyroid calcium receptor; inorganic ion receptor; osteoporosis;
calcium homeostasis; hyperparathyroidism; seizure; stroke; epilepsy;
spinal cord injury; hypoxia-induced nerve cell damage; cardiac arrest;
neonatal distress; neurodegenerative disease; Alzheimer's disease;
neonatal distress; neurodegenerative disease;
                                                                                                                                                                                                           V82484
V82484;
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                                                                             depression;
                                                                                          Huntington's disease;
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                                                                                                                                                                                                                                                                                                                                                                           GCCAGCTCCTCCTGATCGCCATGCCTCAGTACTTCCACGTGGTTGGCCGCCACCATTGGA 1392
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                                                                                                                                                                                                                          standard;
                                                                             anxiety;
                            Location/Qualifiers 436. .3702
                                                                                                                                                                                                                            CDNA
                                                                             SS
                                                                                              Parkinson's
                                                                                                                                                                                                                          to mRNA;
                                                                                                                                                                                                                            5006
                                                                                              disease;
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                                                                                              dementia;
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                                                                                              muscle tension;
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Best Local S
Matches 414
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23-AUG-1991 US-749451
11-FEB-1992 US-844044
21-AUG-1992 US-934161
12-FEB-1993 US-017127
23-FEB-1993 US-007127
23-FEB-1993 US-009389
22-OCT-1993 US-11248
19-AUG-1994 US-929827
21-OCT-1994 WO-U12117
08-DEC-1994 US-353784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        provided that the cell does not have functional CR expression from endogenous nucleic acid; (B) determining the ability of the test compound to affect one or more activities of the calcium receptor; and (C) comparing the ability with the ability of the test compound to affect the one or more CR activities in a cell not comprising the recombinant nucleic acid. The present sequence encodes human parathyroid CR, designated a pHuPCAR 5.2 The nucleic acid sequence of pHuPCAR 5.2 can be used as part of the recombinant nucleic acid in the method described above. The compounds identified can be used to treat diseases or disorders characterised by abnormal calcium homeostasis, e hyperparathyroidism, osteoporosis and other bone and mineral-related disorders. They can also be used for the treatment of diseases and disorders associated with discribers the treatment of diseases and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               p-PSDB; W89564.

Screening for calcium receptor-active compounds - by recombinant expression of nucleic acid encoding calcium receptor and determin the effect of compounds on calcium receptor activity Claim 1; Fig 48; 176pp; English.

A method has been developed of screening for a compound able to a one or more activities of a calcium receptor (CR) comprises: (A) contacting a recombinant cell with a test compound, where the recombinant cell comprises a recombinant nucleic acid expressing
                                                                                                                                                                                                                                                                                                                                                                                                                                                   disorders associated with disrupted Ca2+ responses, e.g. seizures, stroke, spinal cord injury, hypoxia-induced nerve cell damage such cardiac arrest or neonatal distress, pellepsy, neurodegenerative diseases such as Alzheimer's disease, Huntington's disease and Parkinson's disease, dementia, muscle tension, depression, and anxi Sequence 5006 Bp; 1228 A; 1376 C; 1220 G; 1182 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Balandrin MF, Brown EM, Del Mar EG, Hebert SC, Nemeth EF, Van Wagenen E WPI; 99-119871/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (BGHM ) BRIGHAM & WOMENS HOSPITAL (NPSP-) NPS PHARM INC
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                           ctggtgcatattagctatgcggccagcagcgagacgctcagcgtgaagcggcagtatccc
                                                                                                                                                    gggcaacaccacatagagctccaaggagaccttctccactattcccctacggtgctggca
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 ATTCCCCAGGTCAGTTATGCCTCCTCCAGCAGCACTCCTCAGCAACAAGAATCAATTCAAG
                                                           GTGGGAGCAACTGGCTCAGGCGTCTCCACGGCAGTGGCAAATCTGCTGGGGGCTCTTCTAC
                                                                                        gtgattgggcctgacagcaccaaccgtgctgccaccaccagccgccctgctgagccctttc
                                                                                                                         TCTTTGAACCTTGATGAGTTCTGCAACTGCTCAGAGCACATTCCCTCTACGATTGCTGTG
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                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                       50.4%;
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                                                                                                                                                                                                                                                                                                                                                                        Score 132.6;
Pred. No. 1.1e
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                        5; DB 1;
1.1e-23;
nes 389;
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27-MAR-1997; UO5031.
27-MAR-1996; US-62738.
(BGHM ) BRIGHAM & WOMENS H
Brown E, Harris HW, Hebert
WPI: 97-489640/45.
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Key
sequence; an isolated PVCR present in the plasma membranes of aquatic species, especially on the apical membrane of epithelial cells of elasmobranch fish, particularly from cells found in the collecting duct or late distal tubule in the kidney, intestine, gill, rectal gland, gonad or brain; an antibody that specifically binds to a PVCR; and a method of screening for aquatic PVCR agonists and antagonists. Modulation of the expression of the
                                                                                                                                                                                                          This cDNA clone codes for dogfish shark kidney calcium receptor related protein (SKCaR-RP, see W3205), an aquatic polyvalent cation-sensing receptor (PVCR). It was isolated from a shark kidney cDNA library using a rat kidney calcium receptor cDNA as probe. Also claimed are: a probe comprising the 4131 bp SKCaR-RP
                                                                                                                                                                                                                                                                                                                                                            New isolated Aquatic polyvalent of develop products for increasing of fish for use in aquaculture Claim 2: Fig 4A-F: 57pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dogfish shark kidney calcium receptor related protein cDNA. Calcium receptor related protein; CaR-RP; dogfish shark; SKCaR-RP; polycation-sensing receptor; aquaculture; fish farming;
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Sequence 4131 BP; 1028 A; 1161 C; 1019 G; 923 T;
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                                                                                                             Matches
                                                                                                                         Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                   07-JUN-1995; 485588.
07-JUN-1995; US-485588.
23-AUG-1991; US-834044.
11-FEB-1992; US-934161.
12-FEB-1993; US-017127.
23-FEB-1993; US-017127.
23-FEB-1993; US-141248.
19-AUG-1994; US-292827.
21-OCT-1994; WG-U12117.
21-OCT-1994; US-357844.
                                                                                                                                                                              The specification includes details of molecules that can modulate one or more inorganic ion receptor activities, and antibodies and antibody fragments targetted to inorganic ion receptor proteins. In proteins and antibodies may be used to treat disorders by modulating one or more inorganic ion receptor activities, preferably disorders of calcium homeostasis, e.g. hyperparathyroidism and osteoporosis.

Sequence 4131 BP; 987 A; 1170 C; 1053 G; 921 T;
                                                                                                                                                                                                                                                                                            DNA encoding calcium receptor polypeptide(s) - useful therapeutic purposes, e.g. hyperparathyroidism and ost Claim 15; Columns 133-142; 174pp; English.
The present sequence encodes rat kidney cell calcium receptor 3A (RakCaR 3A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus
Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rat kidney cell calcium receptor 3A; RakCaR Rat kidney cell calcium receptor 3A; RakCaR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2894
                                                                                                                                                                                                                                                                                                                                                                                                           (BGHM )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    T95860;
08-MAY-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                              Brown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              calcium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   T95860
                                                                      ctaaacataaatgagaccaaaatccagtggcacggaaagaaccaccaggtgcctaagtct 1292
                                                                                                                                                                                                                                                                                                                                                                                 98-008040/01.
AATTGCAGCCGGGACTGTCAGGCAGGGACCCAGGAAAGGGGATCATCGAGGGAGAGCCCCACC
                       gtgtgttccagcgactgtcttgaagggcac---cagcgagtggttacgggtttccatcac 1349
                                                      CTCTTCATCAATGAGGAGAAGATCTTGTGGAGTGGGTTCTCCAGAGAGGTGCCTTTCTCC
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                                                                                                             492;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   standard; cDNA
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NPS PHARM INC.
M, Fuller FH, Garrett
                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            homeostasis; hyperparathyroidism; osteoporosis;
                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers 574. .3813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product= kidney_cell_calcium_receptor_3A
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                                                                                                                        5.3%;
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                                                                                                            Score 123.4; I
Pred. No. 2.1e
0; Mismatches
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    01-SEP-1998 (first entry)
Rat kidney calcium receptor 3A
ss; calcium ion concentration;
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                                                   V26965 standard;
V26965;
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 gene 4Kb fra
parathyroid
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fragment.
oid hormone;
   homeostasis;
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PT Gaicium receptor:

PT antibody production

PS Example 30; Fig 50; 174pp; English.

CC The rat kidney calcium receptor gene encodes a 1079 amino acid protein.

CC The tissue from which this receptor and receptors from bovine parathyroid

CC and rat kidney are derived, respond to changes, and control changes, in

CC calcium ion concentration, e.g. parathyroid hormone regulates Ca2+

CC homeostasis in blood and extracellular fluid, and kidney function alters

CC through changes in Ca2+ levels in juxtaglomerular and proximal tubule

CC cells in the kidney. The purified receptors (produced

CC recombinantly) can be used to screen for compounds that modulate calcium

CC receptor activity, especially those that can be used to treat diseases

CC associated with the receptors in these tissues. They can also be used

CC to raise antibodies for use in detection assays.

CC cannence 4131 BP; 988 A; 1170 C; 1052 G; 921 T;
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Best Local :
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09-JUN-1998.
07-JUN-1995.
07-JUN-1995.
US-484565.
07-JUN-1995.
US-484565.
07-JUN-1995.
US-84044.
11-FEB-1992.
US-934161.
12-FEB-1993.
US-003389.
12-FCB-1993.
US-003389.
22-OCT-1994.
US-22827.
21-OCT-1994.
US-22827.
21-OCT-1994.
US-22827.
21-OCT-1994.
US-22827.
21-OCT-1994.
US-353784.
ORDEC-1994.
US-353784.
ORDEC-1994.
US-353784.
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US-BEC-1994.
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US-SEC-1
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Rattus sp.
Key
CDS
2494
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Calcium receptor poly:peptide(s) -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AATTGCAGCCGGGACTGTCAGGCAGGGACCAGGAAGSSGATCATCGAGSGAGAGCCCACC
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                                         cetgtggtgaggteageagggggeegeetgtgetttettatgetgggeteeetggeagea
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                                                                                                                                                               acqctqctqctqctqctqctqcttggqactqctqgcctqtttgcctgqcacctagacacc
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Pred. No. 2.1e-21;
0; Mismatches 571;
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